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tion; therapy; antibacterial; antiinflammatory; vaccine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New BASB081 polypeptides from Moraxella catarrhalis and polynucleotides encoding the polypeptides used for treating infections, or as a vaccine for preventing infections, especially those caused by M. catarrhalis
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N-PSDB; AAA50536.
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         FDEVVFFTIDPKTNOLTTDPDKLPVKRELLEQLLTVNMGEAYNLQAVRALSNDLIATRYF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALLAGVAVHKTVADNLVNPMRGYRQRYSLEVGSSGLVSDANMAIARAGISGVYSFGDNAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GFDLSTRTLEHEISRSIIQNGGWNRTYSLRYRLDKLKTQAPPETWQDLPVDFVNGKPSQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                         2000WO-EP01468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ction; otitis media; pneumonia; sinusitis;
therapy; antibacterial; antiinflammatory; vaccine;
                                                                                                                                                                                                              99GB-0004559
                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers 335
                                                                                                                                                                                                                                                                                                                                                                                             /note= "Val in sequence
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from
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  Moraxella
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  catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                               of AAY95987"
  and
polynucleotides
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encoding the polypeptides used for treating infections, or as a vaccine for preventing infections, especially those caused by \mathtt{M}. catarrhalis -
                                                                                                                                   Claim
                                                                                                                                   1; Page 61;
                                                                                                                                  97pp; English.
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BASB081 gene translation product (see AAY95987). The invention provides BASB081 polypeptides, polynucleotides, expression vectors, host cells, and a process for producting a BASB081 polypeptide. Also provided are vaccine compositions comprising a BASB081 polypeptide or polynucleotide, and optionally at least 1 other M. catarrhalis antigen. A method for diagnosing a M. catarrhalis infection and the process identifying a BASB081 polypeptide, or an antibody that is immunospecific for it, in a sample. A therapeutic composition useful in treating M. catarrhalis diseases in humans comprises an cantibody directed against a BASB081 polypeptide. The disease can be a bacterial infection, e.g. otitis media in infants and children, pneumonia in elderlies, sinusitis, nosocomial infections and accumulation in the middle ear, auditive nerve damage, delayed speech learning, upper respiratory tract infection, and inflammation speech learning, upper
of the middle ear The present sequence is that of the Moraxella catarrhalis strain Mc2391 (ATCC 43617) BASB081 mature protein. BASB081 is related the amino acid sequence homology to Neisseria meningitidis omp85 outstance protein. The sequence was deduced from PCR-amplified DR (see AAA50537), and shows 99.9% homology to the mature region of Sequence 889 AA; sequence is that of the Moraxella catarrhalis

Ş DЪ Qy Ъ δÃ Вb 20 В δÃ Qy δÃ Qy Qy рЬ 망 Ъ В В Qy Matches Query Match 481 511 421 301 451 361 391 331 241 271 181 211 121 151 61 91 31 QQNNPANIINHVPAHDTAINQAKAGNPPVLLTPEQIQARLNAAGLNAKPQSQALDVVNFD Local LAINHDDGVNRSILGRISDAVSAVARAILPDESENEVIDLPERTALANRKTPADVYQSKK DQSPISRIGEQSPPLGLDMSVIEETTPLSLEELFAQESTEMGINPNDYIPEYQGEQPNSE 150 EQLLTVNMGEAYNLQAVRALSNDLIATRY FNMVNTEIVF PEREQIQNDQVSFEQSSSSRT GRWLDRSVDVILPDNTADVSLIYDTGTQYRFDEVIFFTIDPKTNQLTTDPDKLPVKRELL GRWLDRSVDVILPDNTADVSLIYDTGTQYRFDEVVFFTIDPKTNQLTTDPDKLPVKRELL NIKAALEDITQESAMDLNGSIPRLRQTALVAARAVGYYDIDLSIIRNSIGEVDVIIHDLG VVVPPTLEPEKPGLIKRLYARLFNDGVNKVPRLKAKFYQSSQSGETSAIGSSHQKTEPYA QQNNPANTINHVPAHDTAINQAKAGNPPVLLTPEQIQARLNAAGLNAKPQSQALDVVNFD LAINHDDGVNRSILGRISDAVSAVARAILPDESENEVIDLPERTALANRKTPADVYQSKK EPAQVDESTLEPVIETVELTDGILMDISPIEFSASNLIQDKLNLVAAKARHLYDMPDDRV EPAQVDESTLEPVIETVELTDGILMDISPIEFSASNLIQDKLNLVAAKARHLYDMPDDRV EQLLTVNMGEAYNLQAVRALSNDLIATRYFNMVNTEIVFPEREQIQNDQVSFEQSSSSRT 888; Similarity Conservative 85.7%; Score 788; DB Pred. No. 0; 0; Mismatches DΒ 21; 1. Length Indels 0 Gaps 480 420 450 360 300 330 240 270 180 60 90 390 0

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541

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RESULT 3
AAY95821
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       The present sequence is that of outer membrane protein BASB067 of Haemophilus influenzae non-typeable (NtHi) strain 289. BASB067 is a Surface expressed protein that is recognised by the immune system. It shows homology to the protective surface antiqen D15 of H. influenzae and has a similar secondary structure. Its not beta-strands, and could be used as a vaccine antiqen. The anti-parallel, amphipathic beta-strands. The external loops of the beta-barrels of integral outer membrane proteins frequently
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                                                                                                                                      Claim 1; Page 81-82; 87pp; English.
                                                                                                                                                             BASB067 polypeptide and used for diagnosing and
                                                                                                                                                                                                                                               (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                                                            04-FEB-2000; 2000WO-EP00887
                                                                                                                                                                                                                                                                             09-FEB-1999;
                                                                                                                                                                                                                                                                                                                                             W0200047737-A1
                                                                                                                                                                                                                                                                                                                                                                               Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibacterial; screening;
                                                                                                                                                                                                                                                                                                                                                                                                                 Key
                                                                                                                                                                                                                                                                                                                                                                                                                               Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haemophilus influenza ntHi strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY95821 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          751
                                                                                                                                                                                                           2000-515059/46
   immunodominant B-cell epitopes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KGFTNDTKIGAGVGVRWASPVGQVRVDVATGVKEEGNPIKLHFFIGTPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KGFTNDTKIGAGVGVRWASPVGQVRVDVATGVKBEGNPIKLHFFIGTPF 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FFAGGDOSIRGYAHDSLSPISDKGYLTGGQVLAVGTAEYNYEFNKDLRLAVFGDIGNAYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FFAGGDQSIRGYAHDSLSPISDKGYLTGGQVLAVGTAEYNYEFMKDLRLAVFGDIGNAYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YRLDKLKTOAPPETWODLPVDFVNGKPSQEALLAGVAVHKTVADNLVNPMRGYRQRYSLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VGSSGLVSDANMAIARAGISGVYSFGDNAYGSNRAHQMTGGIQAGYIWSDNENHVPYRLR
                                                                                                                                                                                                   AAA50270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VGSSGLVSDANMAIARAGISGVYSFGDNAYGSNRAHOMTGGIQAGYIWSDNENHVPYRLR 810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YATKPLSHPLNDQLRATLGYQQEVFGHSTNGFDLSTRTLEHEISRSIIQNGGWNRTYSLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YATKPLSHPLNDQLRATLGYQQEVFGHSTNGFDLSTRTLEHEISRSIIQNGGWNRTYSLR
                                                                                                                                                                                                                                                                                                                                                                                                                                          outer membrane protein; antigen; vaccine; antiteral; screening; infection; diagnosis; therapy.
                                                                                                                                                                                                                                Thonnard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                        99GB-0002880
                                                                                                                                                                                                                                                                                                                                                                             /label= Signal_peptide
21..576
                                                                                                                                                                                                                                                                                                                                                                /label-
                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                  Polynucleotide from Haemophilus influenzae are treating H. influenzae infections .
                                                                                                                                                                                                                                                                                                                                                          Mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           289 BASB067 protein
   making
the C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibiotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    780
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RESULT 4
AAY95820
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is that of outer membrane protein BASB067 Haemophilus influenzae strain Rd KW20. BASB067 is a surface expressed protein that is recognised by the immune system. It shows 23% identity to the protective surface antigen D15 of H. influenzae and has a similar secondary structure. Its
                                                                          Claim 1; Page 78-80; 87pp; English.
                                                                                                   BASB067 polypeptide used for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                          Ruelle J,
                                                                                                                                                                                       (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                    09-FEB-1999;
                                                                                                                                                                                                                                    04-FEB-2000; 2000WO-EP00887.
                                                                                                                                                                                                                                                                                     WO200047737-A1.
                                                                                                                                                                                                                                                                                                                                               Domain
                                                                                                                                                                                                                                                                                                                                                                   Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                    antibacterial; screening; infection;
                                                                                                                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                      Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASB067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haemophilus influenza strain Rd KW20 BASB067 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY95820 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 domain of BASB067 a strong candidate vaccine antigen. The invention relates to recombinant materials and methods for the production of BASB067 polypeptides and polynucleotides, for use relates to methods for using such polypeptides and polynucleotides in the prevention and treatment of microbial diseases. It also in the prevention and treatment of microbial diseases, in diagostic assays for detecting diseases associated with microbial infections, and assays for detecting expression or activity of BASB067 polypeptides or polynucleotides. Antibodies raised against humans with H. influenzae disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                        AAA50269
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                                                                                                                                                                                                                                                                                                                                                                                                                                          outer membrane protein; antigen; vaccine; antibiotic;
                                                                                                                                                                      Thonnard
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237..5
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23..236
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                                                                                                    and
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                                                                                           Polynucleotide from Haemophilus influenzae treating H. influenzae infections -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.2%;
                                                                                                                                                                                                                                                                                                    "C-terminal domain"
                                                                                                                                                                                                                                                                                                                       "N-terminal domain"
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%; Pred. No. 0.0
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnosis;
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0.071;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 576;
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RESULT 5
AAY70579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C N-terminal domain is predicted to contain a mixture of alpha-helix c and beta-strands, and could be used as a vaccine antigen. The C C-terminal domain is predicted to form a beta-barrel composed of anti-parallel, amphipathic beta-strands. The external loops of the beta-barrels of integral outer membrane proteins frequently C contain immunodominant B-cell epitopes, making the C-terminal C domain of BASB067 a strong candidate vaccine antigen. The invention relates to recombinant materials and methods for the production of BASB067 polypeptides and polynucleotides, for use c specially in therapeutic and prophylactic vaccines. It also crelates to methods for using such polypeptides and polynucleotides in the prevention and treatment of microbial diseases, in diagostic assays for detecting diseases associated with microbial infections, and assays for detecting expression or activity of BASB067 c nolynearides are nolynucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 attenuation; gram-negative cell; vaccine; cytostatic; virucide; tumour; anti-arteriosclerotic; anti-Alzhelmer's; bactericide; hepatotropic; anti-Inflammatory; microbial infection; therapeutic; Salmonella infection Helicobacter pylori; stomach cancer; Herpes virus; Chlamydia pneumoniae; Alzhelmer's disease; arteriosclerosis; viral pathogen; Hepatitis virus; cervical cancer; ssef; effector; type III secretion system.
        Salmonella,
Island 2 (S
                                          The
                                                                            Claim 18;
                                                                                                           cervical cancers
                                                                                                                      Attenuated gram-negative Salmonella cells, comprising inactivated genes in the SPI2 locus and useful for vaccinating against a range of disorders associated with microbial infections such as stomach and
                                                                                                                                                                                                                                                                                                                       04-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                       03-SEP-1999;
                                                                                                                                                                                                                                                                                 (CREA-) CREATOGEN BIOSCIENCES GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                         WO200014240-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Salmonella typhimurium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Salmonella Pathogenicity Island
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Salmonella Pathogenicity Island 2 locus; SPI2 locus; antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY70579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY70579 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptides or polynucleotides. Antibodies raised against BASB067 can be used to treat human .....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       882 GVGVRWASPVG 892
||||||||||
539 GVGVRWASPVG 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
patent discloses attenuated gram-negative cells, especially monella, in which at least 1 gene in the Salmonella Pathogenicity and 2 (SPI2) locus has been inactivated resulting in attenuation/
                                                                                                                                                                                               2000-256988/22.
DB; AAZ51991.
                                                                                                                                                                                                                                                   Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                     Fig 23F; 180pp; English.
                                                                                                                                                                                                                                                 Guzman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  578 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                     98EP-0116827
                                                                                                                                                                                                                                                                                                                                                    99WO-EP06514.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein; 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to treat humans with H. influenzae disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                               Medina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 11;
Pred. No.
                                                                                                                                                                                                                                               Ę
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (SPI2) SseF protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                              Apfel H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 21;
0.071;
                                                                                                                                                                                                                                              Hueck C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            carrier;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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CCCCXXXXX DDRXRR PRXX PXX DXXXXX XXXX AXCCCCCXXXX XXXX AXCCCCXXXX XXXX AXCCCCXXXX XXXX AXCCCXXX XXXX AXCCCXXX XXXX AXCCXXX AXCXX AXCCXX AXCXX AXXX AX
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AAR41333
ID AAR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC reduction of virulence compared to the wild type cell. The attenuated CC cells are used as carriers for presenting bacterial, viral or tumour CC antigens to a host and are capable of expressing the antigen in a target CC cell, especially a macrophage. The cells may therefore be used for the CC preparation of a prophylactic or therapeutic composition for the CC treatment of a chronic disease caused by a bacterium or virus, e.g. CC Salmonella infection or a tumour The cells may also be used to vaccinate CC against a range of bacterial and viral pathogens e.g. Helicobacter pyloric CC associated with stomach cancer), Chlamydia pneumoniae (associated with CC arteriosclerosis and Alzheimer's disease), Borrella burgdorferi, CC Nanobacteria (found in the chronically diseased kidneys of patients CC with crystalline deposits), Hepatitis virus (causative agent of CC Hepatitis B and C and associated with liver cancer), Human papilloma CC virus (HPV) (associated with cervical cancer) or Herpes virus.

CC The present sequence is the SseF protein, an effector of type III cous of salmonella. Inactivation of the cancer of the section system, from the SPIZ locus of Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
  The sequences given in AAR41333-35 represent the 11 ISGF-3alpha proteins respectively. ISGF-3alpha is related receptor recognition factor which comprises substituents. The 113 kD, and the 91 and 84 kD pro
                                                                                                                                                                                                                           viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113 kD; 91 kD; 84 kD; ISGF-3alpha; interferor recognition factor; gene family; translation DNA binding protein; interferon-gamma; hairy interferon therapy; chronic viral hepatitis;
                                                                                                                                                                                                                                                                                                                                                                                       Darnell JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-MAR-1992;
23-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYRQ ) UNIV ROCKEFELLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W09319179-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         adjuvant therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113 kD ISGF-3alpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR41333 standard; Protein; 851 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sse gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43 PVLLTPEQI 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58 PVLLTPEQI 66
                                                                                                                                                                                                                                                                                                                                  1993-320745/40
                                                                                                                                             17;
                                                                                                                                                                                                                        eron receptor recognition factors - hepatitis, hairy cell leukaemia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             is
                                                                                                                                             Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       useful for producing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                       Fuχ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                          1; 131pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 kD; ISGF-3alpha; interferon-related;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92US-0854296
92US-0980498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93WO-US02569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tyrosine kinase.
                                                                                                                                                                                                                                                                                                                                                                                       Schindler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.0%;
                                                                                                                                        English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 9; [
; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                    CW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          attenuated cells.
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                                                                                                                                                                                                                - useful e.g.
     comprises several
84 kD proteins a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21;
.7;
kD proteins are
                                                                                                                                                                                                                     potentiate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein; tyrosine;
cell leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                          an interferon-
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                                                                                                                                                                                                                                              ç
                                                                                                                                                                                                                   interferon
                                                                                   16
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     derived
                                                                                   and 84
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RESULT 7
AAR72077
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Best Local s
Matches 9
                            The sequences of cDNA encoding receptor regonition factors having mol.wt. of 113 kDa (Stat113), 91 kDa (Stat92) and 84 kDa (Stat84) are given in AAQ89335-37 and the deduced amino acid sequences of the STAT proteins in AAR72077-79. These ISGF-3-derived proteins are activated by binding of interferon-alpha (all 3 Stat proteins) or
                                                                                                                                                                                                                                                                                                              24-SEP-1993;
24-SEP-1993;
11-MAR-1994;
11-MAR-1994;
                                                                                                                                                     Receptor recognition factor implicated in transcriptional stimulation of genes - useful in drug screening assays and/or treating cellular debilitations, derangements and/or
Sequence
                         interferon-gamma (Stat91)
                                                                                                                      Disclosure;
                                                                                                                                                 dysfunctions, etc.
                                                                                                                                                                                                                                                          Darnell JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal transducer and activator of transcription; ISGF-3; STAT; Statil3; receptor recognition factor; transcription factor; cellular debilitation; derangement; dysfunction; interferon-alpha;
                                                                                                                                                                                                                                                                                   (UYRQ ) UNIV ROCKEFELLER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from two different but related genes. It is clear that a gene family exists and further members are likely to be found. The 91 kD protein has the capability of acting as a translation protein and as a DNA binding protein in response to interferon-gamma stimulation. These proteins participate in rapid phosphorylation and dephosphory-lation during the course of, and as part of their activity. This phosphorylation takes place in an interferon-dependant manner on specified tyrosine residues. These proteins may be used in conjunction with interferon therapy eg. to treat chronic viral hepatitis, hairy cell leukaemia and for use with interferon in
                                                                                                                                                                                                                                                                                                                                                                                   26-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                               30-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                         W09508629-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          interferon-gamma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recognition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR72077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    adjuvant therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   756
                                                                                                                                                                                                                                1995-139598/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESTLEPVIE 764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ESTLEPVIE 465
                                                                                                                                                                                                                   AAQ89335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard; Protein;
851
                                                                                                                Page 78-81; 160pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          851 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             factor Stat113
                                                                                                                                                                                                                                                          Schindler CW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                             93US-0126598.
93US-0126595.
94US-0212184.
94US-0212185.
                                                                                                                                                                                                                                                                                                                                                                                 94WO-US10849
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100.0%; Pred. No.
                        ť
                                                                                                                                                                                                                                                        Shuai K,
                        cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             851
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                                                                                                                                                                                                                                                       Wen
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5. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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QΥ

457 ESTLEPVIE 465

Ouery Match Best Local S Matches

Similarity 9; Conser

Conservative

0;

100.0%;

Score 9; DB 1 Pred. No. 11; 0; Mismatches

DB 17;

Length 851;

0;

Indels

0

Gaps

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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 9
              kinase complexes followed by nuclear translocation and DNA binding to activate transcription. The amino acid sequence of STAT2 was deduced from a cDNA clone (AART31275) derived from HeLa cells. STAT includes a DNA-binding domain (see also AAW03175) capable of both receptor recognition and message delivery via DNA binding in a receptor-ligand specific manner. STAT procleins and their DNA binding domains (see also AAW03167-76) are useful for screening antagonists used to inhibit STAT-mediated signal transduction and activation of transcription.
Sequence
                                                                                                                                 Signal transducer and activator of transcription (STAT) protein STAT2 (AAW03166), also known as STAT113, is a 113 kDa protein having a dual purpose, i.e. signal transduction from ligand activated receptor
                                                                                                                                                                                                               New STAT protein DNA-binding domain peptide(s) - useful diagnosing, preventing or treating cellular dysfunction, oncogenesis, inflammation, parasitic disease or autoimmun
                                                                                                                                                                                        Disclosure; Page 63-66; 138pp; English.
                                                                                                                                                                                                                                                                          N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                 06-JAN-1995;
                                                                                                                                                                                                                                                                                                                                     (UYRQ ) UNIV ROCKEFELLER
                                                                                                                                                                                                                                                                                                                                                                                        28-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                          W09620954-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Кеу
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STAT; STAT2; signal transducer and activator of transcription; DNA binding protein; ligand; receptor; oncogenesis; inflammati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human STAT2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW03166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW03166
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||||||||
756 ESTLEPVIE 764
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                                                                                                                                                                                                                                                                                     1996-333941/33
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9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
851 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                             Horvath
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                        95WO-US17025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= DNA_binding_domain
/note= "Claim 3, page 111"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers 396..506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antagonist;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor; oncogenesis; inflammation;
st; therapy; STAT113.
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Pred. No.
                                                                                                                                                                                                                                                                                                           Z,
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                                                                                                                                                                                                                                                                                                           Zhong
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D. 11;
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                                                                                                                                                                                                              - useful for
sfunction, e.g.
c autoimmunity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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               The present invention relates to a crystal of an N-terminal fragment of a signal transducer and activator of transcription (STAT) protein. The crystal effectively diffracts X-rays, allowing the determination of the atomic coordinates of the N-terminal domain to a resolution of greater than 5.0 Angstroms. The present sequence is the N-terminal domain of the human STAT 2 protein. The N-terminal domain enables STAT dimers to interact and bind DNA cooperatively, a mechanism important for gene activation. The crystals are useful in drug screening and development by selecting a potential drug by performing rational drug design with the 3-dimensional structure determined for the crystal.
                                                                                                                                                                    New crystals of an N-terminal fragment of a activator of transcription that effectively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-NOV-2000
Sequence
                                                                                                                                       Disclosure;
                                                                                                                                                                                                                         Vinkemeier U,
                                                                                                                                                                                                                                               (UYRQ ) UNIV
                                                                                                                                                                                                                                                                     23-JAN-1998;
                                                                                                                                                                                                                                                                                          23-JAN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STAT: signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-terminal domain of human STAT-2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB12374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB12374 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            design;
                                                                                                                                                                                                     2000-505108/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ESTLEPVIE
                                                                                                                                                         screening
851 AA;
                                                                                                                                    Fig 1; 42pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transducer and activator of transcription; crystal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                               ROCKEFELLER
                                                                                                                                                                                                                          Moarefi I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               764
                                                                                                                                                                                                                                                                   98US-0012710
                                                                                                                                                                                                                                                                                         98US-0012710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= "Alpha helix
19..21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= "Alpha helix
12..21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label
                                                                                                                                                                                                                                                                                                                                                     /label= "Alpha helix 8"
                                                                                                                                                                                                                                                                                                                                                                  /label- "Alpha helix
102..122
                                                                                                                                                                                                                                                                                                                                                                                               /labe.
                                                                                                                                                                                                                                                                                                                                                                                                                      /labe
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                                                                                                                                                                                                                                                                                                                                                                                                                                         'label= "Alpha
                                                                                                                                                           and development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptide;
                                                                                                                                                                                                                                                                                                                                                                                              l= "Alpha
                                                                                                                                                                                                                                                                                                                                                                                                                   ∟= "Alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l= "3(10) helix of alpha helix 2"
                                                                                                                                                                                                                          Darnell
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                                                                                                                                                                                                                                                                                                                                                                                               helix
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                                                                                                                                                                                                                        Kuriyan
                                                                                                                                                                     signal transducer and diffracts x-rays, use
                                                                                                                                                                                                                         J,
                                                                                                                                                                     x-rays, useful
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Query Match Best Local Similarity

1.0%;

Score 9; Pred. No.

DB 21; . 11;

Length 851;

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RESULT 10
AAB19963
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                                                   STAT dimer. The core portion comprises a coiled-coil domain comprising 4 long helices, a DNA binding domain which contains an immunoglobulin-like fold, a C-terminal SH2 domain and a domain that links the DNA binding and SH2 domains. The crystal is of sufficient quality to perform x-ray crystallography studies. Methods of preparing the crystals are included in the invention. Knowledge of the STAT protein's 3-dimensional structure will aid in structure-based drug design. The crystal can be used in drug screening assays to
                    identify agonist and antagonist compounds. Antagonists can be use to treat inflammation, allergy, asthma and leukaemia, and agonists to treat anaemia, neutropenia, thrombocytopenia, cancer, obesity,
                                                                                                                                                 The present sequence is that of human signal transducer and activator of transcription 2 (STAT-2). The invention provides crystal of a core portion of a STAT protein in dimer form with 18 mer duplex DNA (see AAA89233) that contains a binding site f
                                                                                                                                                                                                                                    Novel crystal useful in drug screening assays, con signal transducer, activator of transcription and
                                                                                                                                                                                                                                                                        N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human signal
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            viral diseases,
                                                                                                                                                                                                               Disclosure;
                                                                                                                                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                                                                                                  (UYRQ )
                                                                                                                                                                                                                                                                                                                                                          29-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STAT-2; signal transducer and activator of transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               crystal;
                                                                                                                                                                                                                                                                         AAA89228
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                                                                                                                                                                                                                                                                                                          Darnell JE,
                                                                                                                                                                                                            Column 59-64; 206pp; English.
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                                                                                                                                                                                                                                                                                                                                   ROCKEFELLER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transducer and
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bу
                                                                                                                                                                                                                                                                                                                                                         98US-0087465
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         growth retardation, and other conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note=
486..5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "0-phosphorylated"
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"SH2 c
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                                                                                                                                                                                                                                                                                                          Kuriyan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "DNA-binding domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "C-terminal tail segment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "coiled-coil domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   activator of transcription
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                                                                                                                                                                                                                                                                                                          Vinkemeier
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                                                                                                                                                                                                                                     comprises
and duplex
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                                                                                                                                                                                                                                     portion
DNA -
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RESULT 11
AAE14649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
         treatment of diseases e.g. anaemia, neutropaenia, thron cancer, obesity, viral diseases and growth retardation
                           dimeric interactions between STAT dimers, can
                                                                                                                                                                  The invention relates to methods for detecting
                                                                                                                                                                                                Identifying compounds that bind to signal transducer and activator of transcription proteins, useful for the production of new drugs \dot{\phantom{a}}
                                                                                                                                                                                                                               WPI; 2002-033337/04.
                                                                                                                                                                                                                                                                                                                                                                                                Signal transducer and activator of transcription; STATZ; drug development; drug discovery; crystal; inflammation; allergy; asthma; leukaemia; anaemia; neutropaenia; thrombocytopaenia; cancer; obesity; viral disease; growth retardation; human.
                                                                                                                                                                                                                                                                (UYRQ ) UNIV
                                                                                                                                                                                                                                                                                 23-JAN-1998;
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                                                                                                                                                                                                                                                                                                                                   US6312887-BJ
                                                                                                                                                                                                                                                                                                                                                                      Key
                                                                                                                                                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                             Human STAT2 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE14649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE14649 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           457
     present sequence is human STAT2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             158
                                                                                                                                                                                                                                                                ROCKEFELLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                              Moarefi I,
                                                                                                                                                                                                                                                                                98US-0012710
                                                                                                                                                                                   35-40; 44pp; English
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                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1..130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein; 851 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.0%; 500
100.0%; Pro
                                                                                                                                                                                                                                                                                                                                              "Conserved N-terminal domain of the STAT family"
                                                                                                                                                                                                                                              Darnell JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 9;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                       or detecting compounds that bind transcription (STAT) proteins for
    protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB
11;
                                                                                                                                                                                                                                             Kuriyan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22;
                          be used as drugs in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                             ۲,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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The present invention relates to a method for monitoring acceptance of a C transplant or an autoimmune disease in a mammal. The method comprising content of the amount of at least one of Stat4 (signal transducer and content of transcription), Stat6, SOCS1 (suppressor of cytokine content of transplant of transplant of the host or an affected tissue sample of the transplant, taken content of transplant of the method is used to determine whether acceptance of a transplant content of the method is used to determine whether acceptance of a transplant content of the method is used to determine whether acceptance of a transplant content of the method is used to determine if autoimmune disorders (systemic content of the method is used to determine if autoimmune disorders (systemic content of the method is used to determine if autoimmune disorders (systemic content of the method is used to determine if autoimmune disorders (systemic content of the method is used to determine if autoimmune disorders (systemic content of the method is used to determine if autoimmune disorders (systemic content of the method content of transplant of the method content of transplant of transplant of transplant of the method content of the method content of the method content of the method is used to determine if autoimmune disorders (systemic content of the method is used to determine if autoimmune disorders (systemic content of the method co
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AAE15173
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    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                             Example; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Monitoring transplant acceptance or autoimmune disease, useful e.g. assessing therapy, comprises measuring levels of Stat or their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            inhibitors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hancock WW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MILL-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Crohn's disease; haemolytic anaemia; nephrotic syndrome; dermatological; diabetes mellitus; thyroiditis; inflammatory bowel disease; nephrotropic; immunosuppressive; antiinflammatory; antirheumatic; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   atopic dermatitis; multiple sclerosis; myasthenia gravis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-APR-2001; 2001WO-US12131.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200179555-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nepatotropic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; SOCS; suppressor of cytokine signalling; autoimmune disorder; Jak; Janus kinase; signal transducer and activator of transcription; Stat; transplant acceptance; systemic lupus erythematosus; glomerulonephritis; rheumatoid arthritis; Wegener's granulomatosis; chronic active hepatitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human Stat2 (signal transducer and activator of transcription) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-MAR-2002
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9; Conserv
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                                            treatment
851 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   851
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                                                                                                                                                                                                                                                                                                                                                                                                        218pp; English.
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                                          regimes.
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                              being treated successfully and may The present sequence is human Stati
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Pred. No.
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                                     Stat2
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Query Match

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Length 851;

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RESULT 13
ABG25555
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                                                                                  polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and diagnostic amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at fire, wipo.int/pub/published_pct_sequences.
Query Match
Best Local S
Matches 8
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Matches
                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                  polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The
                                                                                                                                                                                                                                                                                                                                                                                       polypeptide (II) sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ INC.
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     457
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DB; AAS89742.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chromosome mapping; gene mapping; gene therapy; forensic; upplement; medical imaging; diagnostic; genetic disorder.
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9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID No 55914; 103pp;
                                                             114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnostic protein #25546
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            0.9%;
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            Score 8;
Pred. No
                                                                                                                                                                                                                                                                                                                                                                                    (I) is useful as hybridisation probes,
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18;
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                         Length 114;
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Similarity 8; Conser

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Matches Query Match Best Local

Similarity 8; Conserv

0.9%;

Score 8; Pred. No.

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Mismatches DB 2 23;

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Length 331; Indels

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RESULT 14
ABB47876
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                                                                                                       and modulate \tilde{L}. monocytogenes-related diseases. In addition, the generations and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections \tilde{l}
                                                                                                                                                                 B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication
                                                                                                                                                                                                  encoded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific expressed from the genome sequence are useful for raising specific entibodies, identification of L. monocytogenes and related organisms, and biosynthesis and biodegradation, especially biosynthesis of Vitamin
                                                                                                                                                                                                                                                                           monocytogenes EGD-e (see ABA03041). The genome sequence and fragments it are useful for selecting probes and primers for detecting genes in monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein
                                                                          monocytogenes and related organisms. Note: The sequence data for this pat
                                                                                                                                                                                                                                                                                                                                     The present invention relates to the genome sequence of Listeria monocytogenes EGD-e (see ABA03041). The genome sequence and frag
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-010914/01.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     related polypeptides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Daniels J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dussurget O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Buchrieser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Listeria monocytogenes protein
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                                     ftp.wipo.int/pub/published_pct_sequences
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                                                  The sequence data for this patent did not form part of the printed fication, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B12;
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331
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, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P;
Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA;
lernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;
T, Domann E, Hain T, Berche P, Charbit A, Durant L;
J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
                                                                                                                                                                                                                                                                                                                                                                                            ID No 581; 192pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bacterial infection; disease
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185 LRFFAGGD 192

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CC polymertide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II) rhe conjuncted the polymerestides are also used in diagnostics as expressed sequence tags of restore normal activity of (II) or to treat disease states involving CC quantitating a polypeptide in tissue, as molecular weight markers and as conjunction of supplement. (II) and its binding partners are useful in medical CC imaging of sites expressing (II). (I) and (II) are useful for treating cC disorders involving aberrant protein expression or biological activity. CC dispnostics, forensics, gene mapping, identification of mutations in CC and to produce other types of data and products dependent on DNA and CC amino acid sequences. ABG00010-ABG30377 represent movel human cCC specification, but was obtained in electronic format directly from WIPO car af ftp wipo, intromb/oublished nor sequences.
809 LRFFAGGD 816
                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes,
                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 20; SEQ ID No 55917; 103pp; English.
                               Local Similarity
les 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ INC
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23-AUG-2000; 2000US-0649167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; chromosome mapping; gene mapping; gene therapy; forensic
food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human diagnostic protein #25549.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-FEB-2002
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)B; AAS89745
                                                                                       371 AA;
                   0.9%; Score 8; DB 2
llarity 100.0%; Pred. No. 54;
Conservative 0; Mismatches
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                               DB 22;
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                                              Length 371;
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              0;
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QУ
                                                                                                        CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC continued expressed genes. (I) is useful in gene therapy techniques (II). (II) is useful in diagnostics as expressed sequence tags (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as continued for sites expressing (II). (II) and its binding partners are useful in medical coinciders involving aberrant protein expression or biological activity. (C diagnostics, forensics, gene mapping, identification of medical cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and consolid sequences. ABG00010-ABG30377 represent novel human consolid sequence data for this patent did not appear in the printed cat first. but was obtained in electronic format directly from WIPO cat of the twist of the sequence of the invention.
                                      Matches
                                                                                          Sequence
809 LRFFAGGD 816
                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes,
                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 20; SEQ ID No 48069; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity
                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; chromosome mapping; food supplement; medical in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human diagnostic protein #17701.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG17710 standard; Protein; 474
                                            Similarity
                                                                                        474 AA;
                            Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a mapping; gene mapping; gene therapy; forensic;
medical imaging; diagnostic; genetic disorder.
                    0.9%; Score 8; DB;
100.0%; Pred. No. 67
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A
                                    DB 22;
                                               Length 474;
                   Indels
               0,
            Gaps
            0;
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RESULT 18
ABB62368
ID ABB62
XX ABB62
XX ABB62
XX DF0S0
XX DF0S0
XX Droso
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                                                                                                                                                                                                                                                                                                                               RESULT 17
                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                  The present sequence represents an antigenic protein originating infectious laryngotracheitis virus (ILTV). The DNA sequence can be incorporated into recombinant viruses (such as fowlpox, avipox or chickenpox virus) and used to produce vaccines. The vaccines are a effective means of protecting birds such as chickens, pheasants or turkeys against infectious laryngotracheitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              for
             WO200171042-A2
                                  Drosophila melanogaster
                                                                       Drosophila;
                                                                                            Drosophila melanogaster polypeptide SEQ ID NO 13896
                                                                                                                      26-MAR-2002
                                                                                                                                              ABB62368;
                                                                                                                                                                  ABB62368 standard; Protein; 1373 AA
                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Pages 38-41; 69pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antigenic protein from infectious laryngotracheitis virus and DNA coding for it - which is incorporated into recombinant avian virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Okuda T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (JAPG ) NIPPON ZEON KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W09807866-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pheasant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antigenic protein; recombinant virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW56318 standard; Protein; 582 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Infectious laryngotracheitis virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-JUL-1998
                                                                                                                                                                                                                                 277
                                                                                                                                                                                                                                                        213 KAALEDIT 220
                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                vaccine production
                                                                                                                                                                                                                                 KAALEDIT 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1998-169170/15.
                                                                                                                                                                                                                                                                               Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tsuzaki Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       turkey.
                                                                                                                                                                                                                                                                                                                               582 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    laryngotracheitis virus antigenic protein
                                                                     developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                               Conservative
                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96JP-0238580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97WO-JP02912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                infectious laryngotracheitis virus; ILTV;
fowlpox; avipox; chickenpox; vaccine; chicken;
                                                                                                                                                                                                                                                                                          0.9%;
                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                            Score 8; DB 19;
Pred. No. 81;
0; Mismatches
                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                    Length 582;
                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                              0;
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RESULT 19
AAR44425
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Best Local :
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                                                                                                                     01-DEC-1993.
                                                                                                                                                                                            Bacillus licheniformis; alpha-amylase; peptidase; mature protein; recognition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from prosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of
                              Bonekamp AJ,
                                                                                                                                                               Bacillus licheniformis
                                                                                                                                                                                     cleavage site;
                                                                                                                                                                                                                             Mutant alpha-amylase signal peptide
                                                                                                                                                                                                                                                                          AAR44425;
                                                                                                                                                                                                                                                                                              AAR44425 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence data for this patent did not form specification, but was obtained in electronic i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-MAR-2000;
11-JUL-2000;
                                                                         25-MAY-1992;
                                                                                              25-MAY-1993;
                                                                                                                                                                                                                                                    26-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                              at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 13896; 21pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genes from Drosophila and interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PEKE ) PE
                                                    KONN ) GIST-BROCADES
                                                                                                                                                                                                                                                                                                                                                    913 LTPEQIQA 920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB57737-ABB72072)
                                                                                                                                                                                                                                                                                                                                                                        61 LTPEQIQA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001-656860/75.
DB; ABL06471.
                                                                                                                                                                                                                                                                                                                                                                                             l Similarity
8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                         1373 AA;
                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adams M,
                                                                                                                                                                                                                                                   (first entry)
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2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001WO-US09231
                              Van Tilborg MWEM;
                                                                                                                                                                                     interleukin; IL-3.
                                                                         92EP-0201492
                                                                                              93EP-0201500
                                                                                                                                                                                                                                                                                              Protein;
                                                                                                                                                                                                                                                                                                                                                                                                        0.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                              29 AA
                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                              Score 8; DB 2; Pred. No. 1.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                           signal
site; n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        n part of the printed
format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1373;
                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention
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WPI; 1993-379003/48

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RESULT 20
AAR44426
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
         The two cleavage sites of B. licheniformis alpha-amylase signal peptide may give rise to two different mature proteins (AAR44429). To obtain a proper mature prod., the second recognition site has to be destroyed without interfering with the first recognition site. The combination of the B. licheniformis alpha-amylase
   signal sequence
                                                                                             Claim
                                                                                                                                                          WPI; 1993-379003/48.
                                                                                                                                                                                                           (KONN ) GIST-BROCADES NV
                                                                                                                                                                                                                                    25-MAY-1992;
                                                                                                                                                                                                                                                                                        01-DEC-1993
                                                                                                                                                                                                                                                                                                                                                              peptidase; mature protein; i
cleavage site; interleukin;
                                                                                                                                                                                                                                                                                                                                                                                    Bacillus licheniformis; alpha-amylase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         site. The combination of the B. licheniformis alpha-amylase signal sequence with human II-3 shows a third possible cleavage site since mature II-3 starts with Ala (AAR51699). In practice the third site is not used, as the signal peptidase is not active when the Ala-X-Ala is upstream of a Pro.

Mutant signal sequences with fewer potential cleavage sites reduce the processing ambiguity of signal peptidases. Mutated Bacillus alpha-amylase sequences in combination with II-3 are illustrated in AAR44425-28
                                                                                                                                                                                                                                                            25-маү-1993;
                                                                                                                                                                                                                                                                                                                                        Bacillus licheniformis
                                                                                                                                                                                                                                                                                                                                                                                                               Mutant alpha-amylase signal peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                        26-MAY-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR44426 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The two cleavage sites of B. licheniformis alpha-amylase signal peptide may give rise to two different mature proteins (AAR44429). To obtain a proper mature prod., the second recognition site has to be destroyed without interfering with the first recognition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        166 KRLYARL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      reduce processing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 KRLYARL 11
                                                                                                                               mutant signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oligonucleotide probes used to obtain the desired given in AAQ52516-25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mutant
                                                                                           7;
                                                                                                                   processing
                                                                                          Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
7; Conser
                                                                                                                                                                                  Ą
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                          15;
                                                                                                                                                                              Van Tilborg MWEM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15,
                                                                                                                                                                                                                                   92EP-0201492
                                                                                                                                                                                                                                                           93EP-0201500
                                                                                                              sequences with fewer potential cleavage
ambiguity of signal peptidase(s)
                                                                                      23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequences with fewer potential cleavage sites ambiguity of signal peptidase(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein;
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  IL-3 shows
                                                                                                                                                                                                                                                                                                                                                                           recognition
                                                                                                                                                                                                                                                                                                                                                               IL-3
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
a third possible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
53;
                                                                                                                                                                                                                                                                                                                                                                        signal peptide;
site; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                             sites
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RESULT 21
AAR44427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                            signal sequence with human IL-3 shows a third possible clear site since mature IL-3 starts with Ala (AAR51699). In pract the third site is not used, as the signal peptidase is not active when the Ala-X-Ala is upstream of a Pro.

Mutant signal sequences with fewer potential cleavage sites reduce the processing ambiguity of signal peptidases.

Mutated Bacillus alpha-amylase sequences in combination with
                                                                                                                                                       The two cleavage sites of B. licheniformis alpha-amylase signal peptide may give rise to two different mature proteins (AAR4429). To obtain a proper mature prod, the second recognition site has to be destroyed without interfering with the first recognition site. The combination of the B. licheniformis alpha-amylase
Sequence
                                                   IL-3 are illustrated in AAR44425-28
                                                                                                                                                                                                                                                 Claim 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus licheniformis; alpha-amylase; signal peptidase; mature protein; recognition site; m cleavage site; interleukin; IL-3.
                                                                                                                                                                                                                                                                     New mutant signal sequences with fewer potential cleavage sites reduce processing ambiguity of signal peptidase(s)
                                                                                                                                                                                                                                                                                                                     WPI; 1993-379003/48
                                                                                                                                                                                                                                                                                                                                              Bonekamp AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-1993.
                                                                                                                                                                                                                                                                                                                                                                          (KONN ) GIST-BROCADES NV
                                                                                                                                                                                                                                                                                                                                                                                                   25-маү-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EP572088-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus licheniformis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mutant alpha-amylase signal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              site since mature II-3 starts with Ala (AAR51699). In practithe third site is not used, as the signal peptidase is not active when the Ala-x-Ala is upstream of a Pro. Mutant signal sequences with fewer potential cleavage sites reduce the processing ambiguity of signal peptidases. Mutanted Bacillus alpha-amylase sequences in combination with II-3 are illustrated in AAR44425-28.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR44427 standard; Protein; 29 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The oligonucleotide probes used to are given in AAQ52516-25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   166 KRLYARL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                         oligonucleotide probes used to given in AAQ52516-25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 KRLYARL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Conserv
                                                                                                                                                                                                                                             Page 15; 23pp; English.
29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             172
                                                                                                                                                                                                                                                                                                                                           Van Tilborg MWEM;
                                                                                                                                                                                                                                                                                                                                                                                                   92EP-0201492
                                                                                                                                                                                                                                                                                                                                                                                                                             93EP-0201500
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100.0%; Pr
0;
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                   obtain the desired mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   obtain the desired mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14;
                                                                combination with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                   In practice is not
                                                                                                                                               cleavage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 practice
not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>,,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                               RESULT 22
AAR44428
 В
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Best Local Similarity
~*~hes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy
                                                                     Query Match
                                                                                                                                         peptide may give rise to two different mature proteins (AAR44729). To obtain a proper mature prod., the second recognition site has to be destroyed without interfering with the first recognition site. The combination of the B. licheniformis alpha-amylase signal sequence with human IL-3 shows a third possible cleavage site since mature IL-3 starts with Ala (AAR31699). In practice the third site is not used, as the signal peptidase is not active when the Ala-X-Ala is upstream of a Pro. Mutant signal sequences with fewer potential cleavage sites reduce the processing ambiguity of signal peptidases. Mutated Bacillus alpha-amylase sequences in combination with TL-3 are illustrated in AAR4445-28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptidase; mature protein; recognition site; mutant; cleavage site; interleukin; IL-3.
                                                                                              Sequence
                                                                                                                                                                                                                                                                                           The two cleavage sites of B.
                                                                                                                                                                                                                                                                                                                   Claim 7; Page 15; 23pp; English.
                                                                                                                                                                                                                                                                                                                                         New mutant signal sequences with fewer potential cleavage sites reduce processing ambiguity of signal peptidase(s)
                                                                                                                                                                                                                                                                                                                                                                               WPI; 1993-379003/48.
                                                                                                                                                                                                                                                                                                                                                                                                       Bonekamp AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                               (KONN ) GIST-BROCADES NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-MAY-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus licheniformis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mutant alpha-amylase signal peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR44428 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-MAY-1994
                        166 KRLYARL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             166 KRLYARL 172
                                             Local Similarity
nes 7; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ç
                                                                                                                      given
KRLYARL 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KRLYARL 11
                                                                                                                   nucleotide probes used to obtain the desired mutations in AAQ52516\hbox{--}25
                                                                                              29
                                            0.8%;
(larity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                              Ą,
                                                                                                                                                                                                                                                                                                                                                                                                      Van Tilborg MWEM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      92EP-0201492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93EP-0201500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein; 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.8%;
                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 7; DB 1; Pred. No. 53; 0; Mismatches
                                                                                                                                                                                                                                                                                        licheniformis alpha-amylase signal
                                                          Score 7;
Pred. No.
                                           Mismatches
                                                          DB 14;
D. 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 14;
5. 53;
                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                   Length 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                            0;
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RESULT

23

Homo sapiens

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AAW51936
ID AAW5
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                                                                                                                                                                                                                                                                                                                                AAR74559
                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                 different protease specificities and/or increased rate association constants compared to the native PN-1. The variants can be used as urokinase inhibitors (to treat inflammation and tumour cell invasion), as elastase inhibitors (to treat emphysema and septic shock) and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New protease nexin-1 variant with altered active site - for inflammation etc., also proteins modified by polyethylene glattached to Cys thiol residues, related DNA and nexin fusion
                                            Nexin I type alpha; PN-1; serine protease inhibitor; serpin; antlinflammatory; cysteine-PEGylated protein; polyethylene gl
                                                                                    Human
                                                                                                                                                            AAW51936 standard;
                                                                                                                                                                                                                                                                                                                                                                                                      AAR74559 is the protease Nexin-1 (PN-1) N-terminal peptide, it was used to isolate the complete PN-1 sequence, from which the active site variants described in AAR74533-R74546 were derived. These variants have different protease specificities and/or increased rate association
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protease Nexin-1 N-terminal peptide; PN-1; variants; protease inhibitors; urokinase inhibitor; inflammati tumour cell invasion; elastase inhibitor; emphysema;
                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-MAY-1995.
                                                                                                             26-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Braxton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09511987-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   septic shock; wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protease Nexin-1 N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR74559 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                       wound healing stimulators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (INCY-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-OCT-1994;
                                                                                                                                                                                                                                                     117 PLSLEEL 123
                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                            5 PLSLEEL 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1995-178879/23
                                                                                    protease nexin I N-terminal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SM,
                                                                                                                                                                                                                                                                            Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INCYTE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 73; 122pp; English.
                                                                                                                                                                                                                                                                                                                                34 AA;
                                                                                                                                                                                                                                                                              Conservative
                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scott RW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93US-0144758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94WO-US11624
                                            cysteine-PEGylated protein; polyethylene glycol;
                                                                                                                                                              Peptide;
                                                                                                                                                                                                                                                                          100.08;
                                                                                                                                                               34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide
                                                                                                                                                                                                                                                                                       Score 7; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34
                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                        DB 16;
o. 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inflammation;
                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                    Length 34;
                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       glycol
                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                           Gaps
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RESULT 25
AAU88768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This amino acid sequence comprises an N-terminal peptide of human C protease nexin I (PN-1, see also AAW51933-34) isolated from human C foreskin fibroblasts. Claimed chemically modified PN-1 variants C (see AAW30592-56) comprise PN-1 polypeptides in which the amino acid cresidues at positions adjacent to the reactive site centre are which at least cysteine residue of the polypeptide is coupled to CC which at least cysteine residue of the polypeptide is coupled to CC polyethylene 91ycol (PEG). Other claimed PEGylated PN-1 variants CC proteins have a prolonged half-life in vivo. They cause decreased CC immunogenicity and antigenicity while retaining the same level of CC polyethylene 1 capable of inhibiting elastase in the presence of CC proteins have a prolonged half-life in vivo. They cause decreased CC biological activity as the naturally occurring protein. Specific CC PN-1 variants are capable of inhibiting elastase in the presence of
                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                            Cytostatic; antidiabetic; neuroprotective; cerebroprotective; ophthalmological; insulin; receptor; gene therapy; diabetes; insulin-like growth factor-1; IGF-1; tumour; prostate; breast; diabetic retinopathy; neurological diseases; stroke; diabetic neuropathy.
    29-MAR-2000;
                                                        WO200172771-A2
                                                                                    Synthetic
                                                                                                                                                                          Insulin/insulin-like growth factor receptor-binding peptide #724
                                                                                                                                                                                                                  18-JUN-2002
                                                                                                                                                                                                                                                               AAU88768 standard; Peptide; 39
                                                                                                                                                                                                                                                                                                                                                   117 PLSLEEL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chemically modified protease nexin-1 variants - comprise the amino acid sequence of protease nexin-1 with certain residues replaced with cysteine residues modified with polyethylene glycol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-APR-1995;
21-JUN-1990;
03-AUG-1992;
29-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example A; Column 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-361691/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Braxton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (INCY-) INCYTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US5766897-A
                                                                                                                                                                                                                                                                                                                                         5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-JUN-1998
                                                                                                                                                                                                                                                                                                                                       PLSLEEL 11
                                                                                                                                                                                                                                                                                                                                                                                       Similarity 100
7; Conservative
2000WO-US08528.
                                                                                                                                                                                                                                                                                                                                                                                                                                              34
                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                            ξ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95US-0427100.
90US-0542484.
92US-0924294.
93US-0144758.
94WO-US11624.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90US-0542484
                                                                                                                                                                                                                                                                                                                                                                                                  0.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                               Score 7; [
                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                 DB 19;
5. 61;
                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                        Length 34;
                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                            0,
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RESULT 26
AAP60714
AAP60714
AXX AAP60
XX AAP60
AXC AAP60
DT 23-JU
XX Vectr
CX Vectr
XX Bac11
XX Bac11
XX Hegio
FT Regio
FT Prote
FT Prote
XX W0860
AX W0860
AX W9-OC
XX PF M9-OC
XX PF M9-OC
XX PF M9-OC
XX PF M9-OC
XX PAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
           28-MAR-1986;
                                    09-OCT-1986
                                                         W08605812-A
                                                                                               Protein
                                                                                                                     Region
                                                                                                                                                                                                                 Sequence of the fusion of the alpha-amylase signal sequence alkaline phosphatase in the vector pNH218.
                                                                                                                                            Peptide
                                                                                                                                                                               Bacillus
                                                                                                                                                                                                    Vectro; Gram
                                                                                                                                                                                                                                                               23-JUL-1991
                                                                                                                                                                                                                                                                                     AAP60714;
                                                                                                                                                                                                                                                                                                       AAP60714 standard; Protein; 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a method of modulating insulin activity in mammalian cells by administering a peptide that binds the insulin receptor (IR). A composition containing a peptide, optionally expressed agonist are useful for treating diabetes. Also, peptides that are useful for treating diabetes. Also, peptides that are useful for treating insulin-like growth factor (IGF-1) receptor are (e.g. of prostate and breast) and diabetic retinopathy, while IGF-1 including stroke and diabetic neuropathy. The peptides are also useful including stroke and diabetic neuropathy. The peptides are also useful interapeutics and research reagents. AAU88034-AAU90957 represent IR and/or IGF-1 receptor-binding peptides and related amino acid sequences of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                 523 ILGRISD 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Beasley J, B
Brissette R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Figure 1H; 390pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modulating insulin activity in mammalian cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           insulin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-025774/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NOVO ) NOVO NORDISK AS.
                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-MAR-2000; 2000WO-US08528
                                                                                                                                                                                                                                                                                                                                                                        6
                                                                                                                                                                                                                                                                                                                                                                     ILGRISD 12
                                                                                                                                                                           licheniformis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DGI BIOTECHNOLOGIES LLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and tumours,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39
                                                                                                                                                                                                  positive
                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ravera
          86WO-US00636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Blume AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ΑĄ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      growth factor receptors
                                                                                             /label= linker
37..41
                                                                                                                     30.
                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Spetzler
                                                                                                                           /label= signal
                                                                                                                                                                                                bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                        0.8%; Score 7; 1
100.0%; Pred. No.
                                                                         "starts at AA residue 5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              comprises using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schaeffer L,
r J, Cheng W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hsiao
                                                                                                                                                                                                                                                                                                                                                                                                                0;
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                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pillutla R,
Ostergaard :
                                                                                                                                                                                                                                                                                                                                                                                                                         DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ran cells, for treating e.g. peptides that bind to insulin
                                                                                                                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ß
                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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, Mandecki WS;
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                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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RESULT 27
AAB65038
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
  The present invention relates to 26 secreted human proteins. The proteins may be used in the prevention, diagnosis and treatment diseases associated with inappropriate polypeptide expression.
                                                                 preventing,
healing -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vectors useful for transforming Gram positive bacteria - contg. secretory signal encoding sequence of Bacillus licheniformis alpha-amylase gene
                                          Disclosure;
                                                                                                                                        Ruben SM,
                                                                                                                                                                                07-JUN-1999;
                                                                                                                                                                                                                        14-DEC-2000
                                                                                                                                                                                                                                                                                    Secreted protein; gene therapy; vaccine; cancer; autoimmune disease; allergy; inflammation; graft hyperproliferation; cardiovascular; infection.
                                                                                                                                                                                                                                                                                                                              Gene #5 associated peptide #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB;
                                                                                   Nucleic
                                                                                                       WPI; 2001-061741/07.
                                                                                                                             Lafleur
                                                                                                                                                                                                    02-JUN-2000; 2000WO-US15187.
                                                                                                                                                                                                                                                                                                                                                    23-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                           AAB65038 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The vectors of the invention may be used to transform Gram positive bacteria for prodn. of polypeptides e.g. growth hormone. Using the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1986-278825/42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stephens MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-MAR-1986;
29-MAR-1985;
                                                                                                                                                                                                                                             WO200075375-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bacteria for prodn. of polypeptides e.g. growth hormovectors contg. a gene for alkaline phosphatase fused encoding growth hormone, expression can be monitored
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example;
                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BIOT-) BIOTECHNICA INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   166 KRLYARL 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                               KRLYARL
                                                                                                                                                                                                                                                                  sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 7; Conserv
                                                                       acids encoding ing, diagnosing
                                                                                                                             DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAN60673.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fig 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activity.
                                                                                                                           Birse CE,
1, Olsen HS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41
                                         Page 23; 530pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                11
                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>Α</u>,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rudolph
                                                                                                                                                                                99US-0137725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86US-0845864.
85US-0717321.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60pp;
                                                                                                                            Duan RD,
5, Ebner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.8%;
                                                                      26 human secreted polypeptides, and/or treating cancers and for
the prevention, h inappropriate p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hannett NM,
                                                                                                                                                                                                                                                                                                                                                                                             41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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                                                                                                                                                                                                                                                                                                                                                                                             ₽
                                                                                                                            Soppet DR, Florence
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 polypeptide expression
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                                                                                                                           KA,
                                                                                                                           Rosen CA,
KA, Ni J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                                                                                              leukemia;
rejection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to a gene
by observing
                                                                      useful e.g. for promoting wound
                                                                                                                          Shi Y;
Young
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JG;
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           of
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RESULT 28
AAP60715
ID AAP60
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                 Vectors useful for transforming Gram positive bacteria - consecretory signal encoding sequence of Bacillus licheniformis alpha-amylase gene
                                                                                                                                          WPI; 19
N-PSDB;
                   enzymatic
                            The vectors of the invention may be used to transform Gram positive bacteria for prodn. of polypeptides e.g. growth hormone. Using the vectors conty. a gene for alkaline phosphatase fused to a gene encoding growth hormone, expression can be monitored by observing
                                                                                                                                                                                                                                                                                                                                                                     Key
                                                                                                                                                                                                                                                                                                                                                                                                                               alkaline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAP60715;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  graft rejection, hyperproliferation, cardiovascular diseases (particularly critical limb ischemia and coronary disease) and involving abnormal angiogenesis, neurodegeneration and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                For example, they may be used in gene therapy or in vaccines Typical of diseases which are potentially treatable are canc (including leukemia), autoimmune diseases, allergies, inflam
Sequence
                                                                              Example; Fig 10; 60pp;
                                                                                                                                                                       Stephens
                                                                                                                                                                                                               28-MAR-1986;
29-MAR-1985;
                                                                                                                                                                                                                                                                  09-OCT-1986
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                                                                                                                                                                                                                                                                                                                    Protein
                                                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                                                                        Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                            Vectro;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                           (BIOT-)
                                                                                                                                                                                                                                              28-MAR-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          infectious diseases.
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4 DRVLAIN 10
                                                                                                                                          1986-278825/42.
DB; AAN60674.
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7; Conserv
                                                                                                                                                                                           BIOTECHNICA INT INC
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                                                                                                                                                                       MA,
                                                                                                                                                                                                                                                                                                                                                                                        licheniformis
                                                                                                                                                                                                                                                                                                                                                                                                                              phosphatase in
                                                                                                                                                                                                                                                                                                                                                                                                                                         of the fusion of the alpha-amylase
                    activity.
 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.8%;
ilarity 100.0%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                           positive
 AA;
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                                                                                                                                                                                                               86US-0845864
85US-0717321
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                                                                                                                                                                                                                                                                                                                    40.
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                                                                                                                                                                                                                                                                                                                             /label= linker
                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                               /label= signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein;
                                                                                                                                                                       CF,
                                                                                                                                                                                                                                                                                                                                                                                                           bacteria
                                                                              English
                                                                                                                                                                                                                                                                                                         "starts
                                                                                                                                                                                                                                                                                                                                                                                                                                the vector
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42
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Pred. No. 73;
0; Mismatches
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                                                                                                                                                                                                                                                                                                          residue
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                                                                                                                                                                       Stassi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22;
                                                                                                                                                                                                                                                                                                                                                                                                                                         signal sequence
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                                                                                                                     contg.
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Query Match

0.8%;

Score

7;

DB

7;

Length

42;

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CC AAX43052. The 5' ESTs can be used for proteins. AAX64651 to AAX6343052. The 5' ESTs can be used for producing secreted human gene CC Products. They can be used for producing secreted human gene CC Products. They can be used to identify and isolate 5' untranslated CC Iocation, development stage, rate, and quantity of protein synthesis, as CC chromosome mapping, and to obtain full length cDNA clones. The ESTs can CC diagnostic procedures to identify individuals, or in CC diagnostic procedures to identify individuals, or in CC diagnostic procedures to identify individuals, or in CC constituting from abnormal gene expression. The products may also be used in core as the expression. The products may also be used in core as the core of the case of constituting from abnormal gene expression. The products may also be used in core of a polypeptide or the core of the 
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AAY64841
                                                       Best Local
                                     Matches
                                                                            Query Match
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                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Page 657-658; 837pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ42265 to AAZ43075 represent novel 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel secreted protein 5' expressed sequence tag sequences used in diagnostic, forensic, gene therapy, and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-038446/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; 5' EST; expressed sequence tag; secreted protein; diagnosis; gene therapy; chromosome mapping; upstream regulatory sequence; forensic; location; development; protein synthesis; stability;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-OCT-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY64841 standard; Protein; 51 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              166 KRLYARL 172
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                                     Similarity
7; Conserv
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                                                                                                                 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             location; development;
                                   Conservative
                                                                                                                 AA;
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98US-0069047
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                                                                                                                                                  the exemplification
                          0.8%; Score 7; I
100.0%; Pred. No.
tive 0; Mismatc
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                              Mismatches
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                                                                                                                                                of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ID
                                                                  DB 21; Length 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expressed sequence tag (EST)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NO:1002
                                                                                                                                              present invention
                          0;
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                      Gaps
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RESULT 30
AAU22430
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                                                                        14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
18-AUG-2000;
22-AUG-2000;
22-AUG-2000;
22-AUG-2000;
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26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
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30-JUN-2000;
07-JUL-2000;
07-JUL-2000;
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14-AUG-2000;
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19-MAY-2000;
07-JUN-2000;
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11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antirheumatic; antiproliferative; cytostatic; cardiant; neuroprotective; cerebroprotective; nootropic; antibacterial; virucide; fungicide; cancer; ophthalmological; vulnerary; gene therapy; autoimmune disease; neoplasm; hyperproliferative disorder; breast; liver; cardiovascular disorder; cerebrovascular disorder; nervous system disorder; bacterial infection; fungal infection; viral infection; coular disorder; endocrine disorder; gastrointestinal disorder; renal disorder; respiratory disorder; wound healing; skin aging; organ transplantation; tissue regeneration; anti-infer-til;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-MAR-2000;
17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    anti-infertility.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cardiovascular system antigen; human; mouse; rabbit; goat; horse; chicken; sheep; immunosuppressive; antiarthritic; vasotropic; dog;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human cardiovascular system antigen polypeptide SEQ ID No 1204.
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2 LTDGILM 8
        2000US-0225268
2000US-0225470
2000US-0225477
2000US-0225759
2000US-0225759
2000US-0226279
2000US-022681
2000US-0226868
2000US-0226868
2000US-0226868
2000US-02268924
2000US-0227182
2000US-0227182
2000US-022709287
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2000US-0217487
2000US-0217496
2000US-0218290
2000US-0220963
2000US-0220964
2000US-0224518
2000US-0224519
2000US-0225213
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2000US-0215135.
2000US-0216647.
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2000US-0209467
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2000US-0198123
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2000US-0189874
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01-SEP-2000 01-SEP-2000 05-SEP-2000 05-SEP-2000 06-SEP-2000 06-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000

2000US-0229344. 2000US-0229345. 2000US-0229509. 2000US-0229513. 2000US-0239513. 2000US-0230438. 2000US-0231242.

2000US-0232401. 2000US-0233063. 2000US-0233064.

2000US-0234274 2000US-0234997

2000US-0233065 2000US-0234223 2000US-0232397. 2000US-0232398. 2000US-0232399.

2000US-0232400

2000US-0231414. 2000US-0231414. 2000US-0232080. 2000US-0232081. 2000US-0231968.

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RESULT 31
AAM87002
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Best Local
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01-DEC-2000
01-DEC-2000
01-DEC-2000
05-DEC-2000
06-DEC-2000
08-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequences AAU21852-AAU22466 represent the cardiovascular system antigen polypeptides of the invention. Cardiovascular system antigens and their associated polynucleotides are useful in the diagnosis, treatment and prevention of various types of disorders in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A pathological condition can be determined by detecting the presence or absence of a mutation in cardiovascular system antigen polynucleotide. The treatable disorders include autoimmune diseases such as reumatoid arthritis, hyperproliferative disorders such as repulsams of the breast or liver, cardiovascular disorders such as cardiac arrest, cerebrovascular disorders such as cardiac arrest.
                                                                                                                                                                                                                          Note: The sequence data for this patent did not specification, but was obtained in electronic for at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                            Alzheimer's disease, infections caused by bacteria, viruses and fungi, ocular disorders such as corneal infection, endocrine disorders such as premature labour and infertility, gastrointestinal disorders such as Crohn's disease, renal disorders such as glomerulonephritis and respiratory disorders such as asthma and pleurisy. The polypeptides can also be used to aid wound healing, to prevent skin aging due to sunburn, to maintain organs before transplantation, to regenerate tissues and in
                                                                                                                                                                                                                                                                                  chemotaxis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cardiovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New cardiovascular system related polynucleotides and polypeptides, useful for diagnosing, treating and/or preventing disorders of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-451930/48.
N-PSDB; AAS35704.
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                                                                                                             234 LRQTALV 240
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                                                                                                                                                                                                                        ecification, but was obtained in electron:
ftp.wipo.int/pub/published_pct_sequences
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2000US-0249297.
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2000US-0240960. 2000US-0241221. 2000US-0241785. 2000US-0241786. 2000US-0241787.

2000US-0239935 2000US-0239937

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2000US-0241808 2000US-0241809 2000US-0244617 2000US-0246474 2000US-0246474 2000US-0246475 2000US-0246476 2000US-0246477 2000US-0246477 2000US-0246477 2000US-0246477 2000US-0246473 2000US-0246523 2000US-0246524

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WO200157182-A2. 17-JAN-2001; 2001WO-US01354. 31-JAN-2000; 2000US-0186350. 16-MAR-2000; 2000US-0186350. 16-MAR-2000; 2000US-0189874. 11-JUN-2000; 2000US-0199123. 19-MAY-2000; 2000US-0299467. 28-JUN-2000; 2000US-02168350. 07-JUL-2000; 2000US-02168350. 07-JUL-2000; 2000US-02168350. 07-JUL-2000; 2000US-0216836. 07-JUL-2000; 2000US-0216836. 07-JUL-2000; 2000US-0216847. 07-JUL-2000; 2000US-0216847. 11-JUL-2000; 2000US-0216847. 11-JUL-2000; 2000US-0216847. 11-JUL-2000; 2000US-0216847. 11-JUL-2000; 2000US-0216847. 11-JUL-2000; 2000US-0216849. 11-JUL-2000; 2000US-0224518. 14-AUG-2000; 2000US-0224518. 14-AUG-2000; 2000US-0225266. 14-AUG-2000; 2000US-0252566. 14-AUG-2000; 2000US-0252566. 14-AUG-2000; 2000US-0252568. 14-AUG-2000; 2000US-0225447. 14-AUG-2000; 2000US-0252568. 14-AUG-2000; 200US-02568. 14-AUG-2000; 200US-02568. 1	Hum Gyt	AAM87002 standard; Pi AAM87002; 07-NOV-2001 (first
PR 25-SEP-2000, 2000US-0234997 PR 25-SEP-2000, 2000US-0234997 PR 29-SEP-2000, 2000US-0235834 PR 29-SEP-2000, 2000US-0235834 PR 29-SEP-2000, 2000US-0235834 PR 29-SEP-2000, 2000US-0235837 PR 29-SEP-2000, 2000US-0235935 PR 20-CCT-2000, 2000US-0237039 PR 13-CCT-2000, 2000US-0237039 PR 13-CCT-2000, 2000US-0241785 PR 20-CCT-2000, 2000US-0241785 PR 20-CCT-2000, 2000US-0241786 PR 20-CCT-2000, 2000US-0241886 PR 20-CCT-2000, 2000US-0241886 PR 20-CCT-2000, 2000US-0241886 PR 20-CCT-2000, 2000US-0246477 PR 08-NOV-2000, 2000US-0246614 PR 08-NOV-2000, 2000US-0246624 PR 08-NOV-2000, 2000US-0246624 PR 08-NOV-2000, 2000US-0246613 PR 08-NOV-2000, 2000US-0246613 PR 11-NOV-2000, 2000US-0246611 PR 11-NOV-2000, 2000US-0249211	14-SEP-2000; 2000U 14-SEP-2000; 2000U 14-SEP-2000; 2000U 14-SEP-2000; 2000U 21-SEP-2000; 2000U 21-SEP-2000; 2000U 21-SEP-2000; 2000U	14-SEP-2000; 2000U 14-SEP-2000; 2000U 14-SEP-2000; 2000U

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) cc proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For cexample, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome ct that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) collective proteides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, and diagnose and treat immune/haematopoietic related diseases, especially cancers and cancer metastases of haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 cancers the present invention.
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06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
                                                                                           Homo sapiens
                                                                                                                                                                             forensic; gene therapy; chromosome mapping; signal peptide; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopoiesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
                                                                                                                                                                                                                                                                                                  Human; secreted protein; EST; expressed sequence tag; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                        Human 5′
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DB; AAK59783.
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                                                                                                                                                       anti-inflammatory; tumour
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1.1e+02;
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human secreted proteins, and encode the proteins given in AxY11374 to CAXY11531, respectively. The proteins given represent the signal peptide cand an N-terminal fragment of a secreted protein. The nucleic acid cand an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for products for diagnosis and therapy. The CC can also be used to develop products for diagnosis and therapy. The proteins obtained may have cytokine activity, cell crotiferation/differentiation activity, haematopoiesis regulating cc regulating activity, tissue growth regulating activity, reproductive hormone regulating activity, chemotactic/ chemokinetic activity, haematory crotiferation activity, receptor/ ligand activity, anti-inflammatory activity, tumour inhibition activity or other activities. The products can be used in forensic, gene therapy and chromosome mapping promoter The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptide can be used for oliventide into a cell of a colventide into a cell of a
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Best Local :
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                                             29-SEP-1999;
03-NOV-1999;
                                                                                                                                                                                                                                                                                                  colorectal carcinoma
                                                                                                                                                                                                                                                                                                                       Human; colon cancer;
                                                                                                                                                                                                                                                                                                                                                                   Human colon cancer antigen protein SEQ ID NO:7835
                                                                                                                                                                                                                                                                                                                                                                                                                     03-SEP-2001
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(HUMA-) HUMAN GENOME SCI INC
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                                           99US-0157137
99US-0163280
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                                                                                                                                                                                                                                                                                                                       colon cancer antigen; diagnosis; detection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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RESULT 34
AAW75000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                02-OCT-1997;
07-MAR-1997;
07-MAR-1997;
07-MAR-1997;
07-MAR-1997;
07-MAR-1997;
07-MAR-1997;
07-MAR-1997;
07-MAR-1997;
                                                                                                                                                       06-MAR-1998;
                                                                                                                                                                                 11-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene diagnosis and vaccine production. N and P may be used in the prevention, expression. For example, N and P may be used to treat disorders in a patient's genome that affect the activity of P by expressing in a patient's genome that affect the activity of P by expressing in a patient's or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 necessity expresent sequences used in the exemplification of the
                                                                                                                                                                                                                                                            diagnosis; neurodegenerative disease.
                                                                                                                                                                                                                                                                                                            Human secreted protein encoded by gene 146 clone HSNAK17.
                                                                                                                                                                                                                                                                             fusion
                                                                                                                                                                                                                                                                                           Human;
                                                                                                                                                                                                                                                                                                                                          19-JAN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                    AAW75000 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present invention.

N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding useful for preventing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                768 GISGVYS 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-235357/24
N-PSDB; AAH36476.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                      sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GISGVYS
                                                                                                                                                                                                                                                                            secreted protein;
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7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 AA;
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               97US-0061060
97US-0038621
97US-0040161
97US-0040163
97US-0040163
97US-0040333
97US-0040334
97US-0040336
                                                                                                                                                    98WO-US04493
                                                                                                                                                                                                                                                                      protein; testis; tumour;
cancer; central nervous;
                                                                                                                                                                                                                                                                                                                                                                                                 Protein; 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.8%;
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Pred. No. 1.1e+02;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                colon cancer-associated polypeptides,
and/or treating colorectal cancers -
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                                                                                                                                                                                                                                                                        system; seizure;
                                                                                                                                                                                                                                                                                 foetal brain tissue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and proteins (P), where cancer antigens. The colon
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     11 - APR-1997
23 - MAY - 1997
24 - AUG - 1997
25 - AUG - 1997
26 - AUG - 1997
27 - AUG - 1997
28 - AUG - 1997
29 - AUG - 1997
22 - AUG - 1997
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11-APR-1997;
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11-APR-1997;
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97US-0056874.
97US-0056875.
97US-0056876.
97US-0056877.
97US-0056878.
97US-0056879.
97US-0056880.
97US-0056881.
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970S-0043569

970S-0043569

970S-0043670

970S-0043671

970S-0043672

970S-0047500

970S-0047500

970S-0047500

970S-0047501

970S-0047502

970S-0047583

970S-0047583

970S-0047588

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970S-0047593

970S-0047613

970S-0047632

970S-0047633

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970S-0047633

970S-0046631

970S-0056630

970S-0056631

970S-0056632

970S-0056633
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97US-0056864
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97US-0043312.
97US-0043313.
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AAG01031
ID AAGC
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AC AAGC
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AC AAGC
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DT 06-C
DT 06-C
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KW Huma
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Best Local S
Matches 7
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                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents a secreted human protein encoded by the nucleic acid molecule designated Gene 146 from the human cDNA clone HSNAKI7 (deposited as clone ATCC 97903 and ATCC 209049).

The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin FC portion (e.g. AAV59502) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 186 novel genes and their fragments (nucleic acid sequences: AAV59511-V59812; amino acid sequences AAW74731-W75026) which are useful for preventing, treating or ameliorating medical conditions can be diagnosed by determining the amount of the new polynucleotides. Specific uses are described for each of the 186 notward the new polynucleotides. Specific uses are described for each of the 186 notward the new polynucleotides.
Human; 5' EST;
gene therapy;
                                          Human secreted protein, SEQ ID NO: 5112.
                                                                           06-OCT-2000
                                                                                                                                     AAG01031 standard; Protein; 69 AA.
                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 694; 721pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated human genes and the secreted polypeptide(s) they encode - useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, I
Feng P, Ferrie AM, Fischer CL, Florence KA, Greene JM
Kyaw H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS,
Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-506364/43.
N-PSDB; AAV59785.
                                                                                                                                                                                                                                                                                                                                                                              polynucleotides, based on which tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                          388 ELLEQLL 394
                                                                                                                                                                                                                51
                                                                                                                                                                                                                                                                        Local Similarity 100 les 7; Conservative
                                                                                                                                                                                                             ELLEQLL 57
                                                                                                                                                                                                                                                                                                                                    69
                                                                         (first entry)
 chromosome
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                                                                                                                                                                                                                                                                                                                                                              for described uses).
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97US-0056903.
97US-0056908.
97US-0056909.
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97US-0056911.
97US-0057650.
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                                                                                                                                                                                                                                                                                     0.8%;
              sequence tag; secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                     Score 7; |
Pred. No.
                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                     DB 19; Loo. 1.2e+02;
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                                                                                                                                                                                                                                                                                                   Length 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Greene JM, hu Greene CA;
                                                                                                                                                                                                                                                                       Indels
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Query Match
Best Local Similarity
Tatches 7; Conserva
Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 were prepared from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream
                                                                                                                                                                                                                                                                                                                                                                         482 FSASNLI 488
|||||||
59 FSASNLI 65
                                                                                                                                                                Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                            26-FEB-1999;
                                                                                                                                                                                                                Human secreted protein, SEQ ID NO: 5113.
                                                                                                                                                                                                                                                                                                      AAG01032 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 13;
                                                       21-FEB-2000; 2000EP-0200610
                                                                                                                EP1033401-A2
                                                                                                                                                                                                                                             06-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        regulatory sequences and to design expression and secretion vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present sequence is a polypeptide encoded by one of a large number 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAC01037
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                               100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 7;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                              DB 21; LC.
NO. 1.2e+02;
0;
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(GEST) GENSET

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RESULT 37
AAW74874
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                   02-OCT-1997
07-MAR-1997
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07-MAR-1997
07-MAR-1997
11-APR-1997
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Best Local :
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                                                                                                                                                 06-MAR-1998;
                                                                                                                                                                                                                                                                          Human; secreted protein; testis; tumour; foetal brain tissue; fusion protein; cancer; central nervous system; seizure; diagnosis; neurodegenerative disease.
                                                                                                                                                                                            W09839448-A2
                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                 Human secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs different tissues. EST sequences usually correspond mainly to the 3' from oligo-dT primed cDNA libraries. Such ESTs are not well suited for those cases where longer cDNA sequences have been obtained, the full 5' ends and can therefore be used to obtain full length cDNAs and genomic chromosome mapping procedures. They are used to obtain upstream converges and to design and to design serior and secretion vactors.
                                                                                                                                                                                                                                                                                                                                                        25-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                AAW74874 standard; Protein; 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       482 FSASNLI 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              regulatory sequences and to design expression and secretion vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 13; SEQ ID 5113; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dumas Milne Edwards
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7; Conserv
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               97US-0061060
97US-0038621
97US-0040161
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97US-0040163
97US-0040333
97US-0040334
97US-0040336
97US-0040336
97US-00403311
                                                                                                                                                                                                                                                                                                                                                       (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                            98WO-US04493
                                                                                                                                                                                                                                                                                                                     Protein encoded by gene 146 clone HSNAK17.
                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                              /label= unknown
                                                                                                                                                                                                                                                                                                                                                     entry)
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%; Pred. No. 1.2
0; Mismatches
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No. 1.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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    23-MAY-1997
22-AUG-1997
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11-APR-1997;
23-MAY-1997;
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11-APR-1997;
11-APR-1997;
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        97US-0056874.
97US-0056875.
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ABP05664
ID ABP
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AC ABP
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DE Hum
KW Hum
KW Hyp
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22-AUG-1997
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Kyaw H,
Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                        conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 186 polynucleotides, based on which tissues they are most highly expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                         The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. AAV59502) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 186 novel genes and their fragments (nucleic acid sequences: AAV59511-V59812; amino acid sequences AAW74731-W75026) which are useful for preventing, treating or ameliorating medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated human genes and the secreted polypeptide(s) they encode - useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
                                                          Human ORFX protein sequence SEQ ID NO:11310.
                                                                                                                    ABP05664;
                                                                                                                                              ABP05664 standard;
                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 628; 721pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents a secreted human protein encoded by the nucleic acid molecule designated Gene 146 from the human cDNA clone HSNAK17 (deposited as clone ATCC 97903 and ATCC 209049).
                                                                                                                                                                                                                                               388 ELLEQLL 394
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                                                                                      (first entry)
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ie AM, Fischer CL,
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97US-0056909.
97US-0056910.
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97US-0057650
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                                                                                                                                                                                                                                                                                                      0.8%;
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                                                                                                                                                                                                                                                                            0;
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Pred. No.
                                                                                                                                              79
                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                    DB 19; LC.
No. 1.2e+02;
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Greene JM,
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                                                                         ABB16701
                                                                                           RESULT 39
                                                                                                                                                                                                                                                                                                                                                                                                                                               treating or preventing a pathology associated with an ORFX-associated collision or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a cyndrome associated with ORFX-associated disorder. ORFX polynucleotide sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders related to organ transplantation, cardiovascular diseases, diabetes mellitus, systemic transplantation, cardiovascular diseases, diabetes mellitus, systemic transplantation, cardiovascular diseases, diabetes mellitus, systemic trupus erythematosus, hypertension, hypothyroidism, cholesterol ester storage disease, various immune deficiencies and disorders, infectious diseases, autoimmune disorders such as multiple sclerosis, rheumatoid arthritis, autoimmune inflammatory eye disease. ORFX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut
                                                                                                                                                                                                                       Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes substantially purified human prote (referred to as open reading frame, ORFX, where X is 1-11491 (see in the specification). ABN15762 to ABN27252 encode the human ORFX proteins given in ABP00010 to ABP11500. ORFX proteins are useful if
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cardiovascular disease; diabetes mellitus; systemic lupus erythema hypertension; hypothyroidism; cholesterol ester storage disease; lumune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                                                                                                                                                                                                                                                                                                                                          N.B. The sequence data for this patent did not specification, but was obtained in electronic for
                                                                                                                                                                                                                                                                                                                                                                                                reperfusion injury in various tissues and conditions resulting systemic cytokine damage.
                                                                                                                                                                                                                                                                                                                                                                                                                                      bone degenerative disorders, or periodontal disease, and f protection or regeneration and treatment of lung or liver
                                                     ABB16701 standard; Protein;
                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID 11310; 1037pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-2000; 2000US-206132P.
29-AUG-2000; 2000US-228716P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-MAY-2001; 2001WO-US10836
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                                                                                                                                                  56
                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2002-106308/14.
                                                                                                                                                                                                                           Similarity 7; Conser
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                                                                                                                                                                                                                           Conservative
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100.0%; Pr
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NO. 1.3e+02;
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ABB16701

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	2000US-0231968. 2000US-0231968. 2000US-0232397	2000US-0231414. 2000US-0232080.	2000US-0231244. 2000US-0231413.	2000US-0231242. 2000US-0231243.	20000S-0230438.	2000US-0229513.	2000US-0229345. 2000US-0229509.	2000US-0229344.	2000US-0229287.	2000US-022B924.	2000US-0227182. 2000US-0227009.	2000US-0226868.	2000US-0226279. 2000US-0226681	2000US-0225759.	2000US-0225758	2000US-0225447.	2000US-0225270.	200008-0225267.	2000US-0225266.	2000US-0225213.	2000US-0224519.	2000US-0224518.	200005-0220963.	; 2000US-021/496.	2000US-0217487.	; 2000US-0216647. ; 2000US-0216880.	; 2000US-0215135.	; 2000US-0209467.	2000US -0205515.	; 2000US-0198123.	2000US-0189874.	; 2000US-0186350.	2000US-0180628.	; 2000US-0179065	; 2001WO-US01334.		- AZ:			nephrotr	disorder: cardioussant; antif	erebroprotective; antiarthritic; cancer;	i-HIV; antibacterial;	ive; cytostatic: dermatological:	ous system related polypeptide SEQ ID NO 5358.	2 (first entry)	
PR	PR PR	PR PR	קק	אק אק	PR	PR	PR	PR	PR	PR	קי אים	אַק	יק קי	PR	PR	PR	קים קים	אַם אַם	PR	יים דים		PF	PH	PI	PI	ld.	P	ים פי	9	יי סי	טי ס	י סי	טי נ		- G	 G' G	יי טי										
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05-DEC-2000;
06-DEC-2000;
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08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
11-DEC-2000;
              17-MAY-2001
                                           WO200134810-A2
                                                                       Escherichia coli.
                                                                                                    Escherichia coli; grobacterial infection;
                                                                                                                                              E. coli growth and proliferation related protein sequence SEQ ID NO:370
                                                                                                                                                                                                                 AAG98900;
                                                                                                                                                                                                                                            AAG98900 standard; Protein; 82 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoitis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
                                                                                                                                                                               26-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format direfrom WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and parasitic infections
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2000US-0251869.
2000US-0251989.
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2000US-0254097.
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                                                                                                                  growth; proliferation; microbial; antimicrobial;
                                                                                                                                                                                                                                                                                                                                                                                               0.8%;
                                                                                                      microorganism
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D. 1.4e+02;
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Matches Query Match Best Local

Similarity 7; Conserv

Conservative

0.8%; Score 7; 100.0%; Pred. No. live 0; Mismatc

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Search completed: April 28, 2003, 16:33:09 Job time: 97 secs

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cc new antimicrobial agents, and for identification of compounds which conteract with the gene products of (I). In addition the expression of (I) and the purification of the proteins, the purified proteins can be cused to generate reagents and screen small molecule libraries or other candidate compound libraries for compounds that can be further developed to yield novel antimicrobial compounds. In addition, nucleic acid probes complementary to (I) that are specific for particular species of complementary to (I) that are specific for particular microorganism species in clinical specimens, therefore, providing a rapid and dependable comethod by which to identify the causative agents of a bacterial infection. Also, antibodies generated against proteins translated from mRNA transcribed from proliferation-required sequences can also be used to screen for specific microorganisms that produce such proteins in a species-specific manner. AAH84371 and AAH8470 represent sequencing primers used in the isolation of E. coll growth and proliferation related sequence, which are used in an example from the present
                                                                                                                                                                                                                                                                                                                                                                                                   AAH84373 to AAH84499 represent Escherichia coli growth and proliferation related DNA sequences (I). AAH84500 to AAH84670 encode the E. coli growth and proliferation related proteins given in AAG99078 and AAG98830 to AAG98999. (I) can be used as potential targets for the generation of new antimicrobial agents, and for identification of compounds which
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel nucleic acids that inhibit Escherichia coli proliferation, useful for screening for homologous genes and for designing expression vectors
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                                          invention
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DB; AAH84571.
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Α,
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APPLICANT: James E. Darnell, Jr.
APPLICANT: 21long Wen
APPLICANT: Cutr M. Horvath
APPLICANT: Chong Zhong
TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
                                                                          Gaps
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CURRENT APPLICATION DATA:
PPLICATION NUMBER: US/08/852,091
FILING DATE: 06-MAY-1997
CLASSIFICATION: 424
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-08-820-754-2
Sequence 2, Application US/08820754 '
Fatent No. 5976835
GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christlan W.
APPLICANT: Fu, Xian-Yuan
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Schindler, Christian W.
Fu, Xian-Yuan
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APPLICATION NUMBER: 08/369,796
FILING DATE: 06-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 600-1 TELECHNUNE: 201 487-5800 TELEFRX: 201 343-1684
                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08852091
Patent No. 5883228
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 2:
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Best Local Similarity 100.
Matches 9; Conservative
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MOLECULE TYPE: protein
US-08-852-091-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity
The 9; Conserva
                                                                                                                      457 ESTLEPVIE 465
                                                                                                                                                                    756 ESTLEPVIE 764
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756 ESTLEPVIE 764
                                                                                                                                                                                                                                                                          US-08-852-091-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: James E. Darnell, Jr.
APPLICANT: Lilong Wen
APPLICANT: Lilong Wen
APPLICANT: Curt M. Horvath
APPLICANT: Long Zhong
TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                         sequence 6, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 3, Appli
Sequence 462, Appli
Sequence 462, Appli
Sequence 462, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 2, Appli
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MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: TBM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
GURBERT APPLICATION DATA:
APPLICATION NUMBER: US/08/369,796
FILING DATE: 06-JAN-1995
CLASSIFICATION NUMBER: 05/742
ATORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 26,742
REGISTRATION SEQ. ID NO: 2:
RELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 851 amino acids
TYPE: amino acids
TYPE: Amino acids
TYPE: MILIORATICIDES
MATERIAL STATEMENT
MATERIAL S
US-09-194-612A-1

US-08-9139-572-13

US-08-884-985-2

US-08-91-988-2

US-08-619-554-4

US-08-619-554-4

US-08-619-554-4

US-08-804-227C-9

US-08-804-198-3

US-09-071-035-465

US-09-071-035-465

US-09-071-035-465

US-09-071-035-465

US-09-045-201A-2

US-09-045-201A-2

US-09-045-201A-2

US-08-905-817-7

US-08-905-853-2

US-08-569-853-1

US-08-569-853-1

US-08-569-853-1

US-08-569-853-1

US-08-455-543A-4

US-08-455-543A-4
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STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-369-796-2
Sequence 2, Application US/08369796
Patent No. 5716622
GENERAL INFORMATION:
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1865
1865
1865
1986
2032
2032
2052
2052
2233
2233
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                                                                                                                                                          Sequence 2, Application US/08956652 Patent No. 6013475
                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201487-5800
                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/
FILING DATE: 23-NOV-1992
PRIOR APPLICATION DATA:
                                                   APPLICANT:
APPLICANT:
APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECI
TITLE OF INVENTION: SEQU
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 851 amino acids
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FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US
FILING DATE: 19-MAR-1993
                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEITITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                   756 ESTLEPVIE 764
                                                                                                                                                                                                                                                                                                  457 ESTLEPVIE 465
                                                                                                                                                                                                                                                                                                                                       Local Similarity hes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 851 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/820,754 FILING DATE: 19-MAR-1997 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Hackensack
STATE: New Jerse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Klauber & Jackson
411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    201 343-1684
                                                                                                      Darnell Jr., James E. Schindler, Christian W.
                                                                                      Fu, Xian-Yuan
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                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                     Wen, Zilong
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER: US 07/854,296
19-MAR-1992
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                                                                                                                                                                                                                                                                                                                                                     1.0%; Score 9;
100.0%; Pred. No
 SEQUENCES AND METHODS OF USE THEREOF 25
                                  RECEPTOR RECOGNITION FACTORS, PROTEIN
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                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                         NO.
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                                                                                                                                                                                                                                                                                                                                                                      Length 851;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Jackson Esq., David A.
RECISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEPHOX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                              Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                            APPLICANT: Darnell Jr., J
APPLICANT: Schindler, Chr
APPLICANT: Fu, Xian-Yuan
APPLICANT: Wen, Zilong
APPLICANT: Zhong, Zhong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 851 amino acids
TYPE: amino acid
                               ADDRESSEE: Klauber & Jackson
                                                                     TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US OF FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                               756 ESTLEPVIE 764
                                                                                                                                                                                                                                                                                                                                                                                                  457 ESTLEPVIE 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
               ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 1.0%; Score 9; DB; Local Similarity 100.0%; Pred. No. 3; ess 9; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/854,296 FILING DATE: 19-MAR-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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No. 6030808
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Hackensack
                                                                                                                                                                                                                                                                  Application US/08956869
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                                                                                                                                                                   Fu, Xian-Yuan
                                                                                                                                                                                     Darnell Jr., James E. Schindler, Christian W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 us/08/956,652
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 3;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

COUNTRY:

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RESULT 6
US-09-012-710-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09012710 Patent No. 6087478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local :
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ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201.487.5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 851 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Vinkemeler, Uwe
APPLICANT: Woarefi, Ismail
APPLICANT: Moarefi, Jr., James E.
APPLICANT: Darnell, Jr., James E.
APPLICANT: Kuriyan, John
TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A
TITLE OF INVENTION: STAT PROTEIN AND METHODS OF USE THEREOF
                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IHM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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FILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                             COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 756 ESTLEPVIE 764
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          457 ESTLEPVIE 465
                                                                                                                                                                                                                                                                                                             STREET: 411 Hack
CITY: Hackensack
STATE: New Jerse
                                        SOFTWARE:
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nes 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
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APPLICATION DATA:
                                                                                                                                                                                                                                                                                                         New Jersey
                                                                                                                                                                                                                                                                                                                                                                          411 Hackensack Avenue, 4th Floor
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                                Patentin Release #1.0,
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100.0%; Pred. No.
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                                Version #1.30
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RESULT 7
US-08-948-547-2
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Best Local Similarity
Watches 9; Conserv
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TELEEX: 133521
TINFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
FENGTH: 851 amino acids
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                                                                                               CLASSIFICATION:
PRIOR APPLICATION NUMBER: US/08/212,185
APPLICATION NUMBER: US/08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                   COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/948,547
                                 PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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                                                                                    PRIOR APPLICATION DATA:
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ADDRESSEE: Klauber &
STREET: 411 Hackensa
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TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
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ZIP: 076
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                                                   APPLICATION NUMBER: WO US93/02569 FILING DATE: 19-MAR-1993
                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Hackensack
STATE: New Jersey
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Ternaler, Christian W.
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JMBER: US 08/126,588
24-SEP-1993
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Pred. No.
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US-09-364-970-2
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GENERAL INFORMATION:
APPLICANT: Bromberg, Jacqueline
APPLICANT: Bromberg, Jacqueline
TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR
TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING
TITLE OF INVENTION: DYSPROLIFERATIVE CELLULAR CHANGES
FILE REFERENCE: 600-1-252
CURRENT APPLICATION NUMBER: US/09/364,970
CURRENT FILING DATE: 1999-07-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 2
LENGTH: 851
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APPLICANT: Vinkemeler, Uwe
APPLICANT: Chen, Xiaomin
APPLICANT: Chen, Xiaomin
APPLICANT: Darnell Jr., James E
APPLICANT: Kuriyan, John
TITLE OF INVENTION: A CRYSTAL OF THE CORE PORTION OF A STAT AND METHODS
TITLE OF INVENTION: USE
                                                                                                                                                                                                                 Sequence 2, Application US/09364970 Patent No. 6235873
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LENGTH: 851
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CURRENT APPLICATION NUMBER: US/09/087,465A
CURRENT FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin Ver. 2.0
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TELEX: 133521
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 851 amino acids
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100.0%; Pred. No.
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TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
APPLICANT:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Kuriyan, John
TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A
TITLE OF INVENTION: STAT PROTEIN AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 201-487-5800 TELEFAX: 201-343-1684
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                           457 ESTLEPVIE 465
756
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REFERENCE/DOCKET NUMBER: 600-1-194
                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
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les 9; Conservative
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ESTLEPVIE 764
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                                                         Conservative
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/ 100.0%; Pre
                                                       1.0%; Score 9; DB
100.0%; Pred. No. 3;
tive 0; Mismatches
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b; Pred. No. 3;
0; Mismatches
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                                                                       DB 4;
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RESULT 11 US-08-956-653A-2

Sequence 2, Application US/08956653A

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RESULT 12
PCT-US95-17025-2
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                                      Sequence 2, Application PC/TUS9517025
GENERAL INFORMATION:
APPLICANT: James E. Darnell, Jr.
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                                                                                                                                                                                                                     Matches
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                   NFORMATION FOR SEQ ID NO:
   APPLICANT:
                   APPLICANT:
                                 APPLICANT:
                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 0 FILING DATE: 24-SEP-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:
                                                                                                                                                     756 ESTLEPVIE 764
                                                                                                                                                                                  457 ESTLEPVIE 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 201
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                                                                                                                                                                                                           y Match
1.0%; Score 9; DB
Local Similarity 100.0%; Pred. No. 3;
nes 9; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN SEQUENCES AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07
FILING DATE: 23-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: WO US FILING DATE: 19-MAR-1993
                                                                                                                                                                                                                                                                                                                                     ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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              Zilong Wen
Curt M. Horvath
Zhong Zhong
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Zhong, Zhon
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Schindler, Christian W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                343-1684
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RESULT 13
US-08-276-099A-13
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Best Local Similarity
"-+ has 9; Conserv
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GENERAL INFORMATION:
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TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                      APPLICANT: Hou, Jinzhao TITLE OF INVENTION: INTETITLE OF INVENTION: BINI NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DDS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                         COUNTRY:
ZIP: 94:
                                                                                                                                                                                                                                                                                                                                                                                                                                 457 ESTLEPVIE 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                    756 ESTLEPVIE 764
APPLICATION NUMBER: US/O
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TYPE: amino acid
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ADDRESSEE: Klauber & Jackson
                                                                                                                                                      STATE:
                                                                                                                                                                 STREET: 4 Embarcadero Center, Suite 3400 CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 201 ... 1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 06-JAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 2
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                      94111-4187
                                                                                                                                                   California
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                                                                                                                                       USA
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                                                                                                                                                                                                                                                                                McKnight,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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100.08; Pr
                                                                                                                                                                                                                                    BINDING ASSAYS
                                                                                                                                                                                                                                               INTERLEUKIN-4 SIGNAL TRANSDUCERS AND
                                                                                                                                                                                                                                                                                Steven L
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                US/08/276,099A
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                                            Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5;
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RESULT 14
US-08-781-890-13
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                                                                                                                                                                                                            APPLICATION NUMBER: US/08/781,890
FILING DATE: 05-JAN-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,099
FILING DATE: 15-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: OSMBAI, Richard Aron
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-59451-1/RAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 1.0%; Score 9; Best Local Similarity 100.0%; Pred. No. Matches 9; Conservative 0; Mismatc
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REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-59451-1/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 13:
                                                                                              TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                            TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: INTERLEUKIN-4 SIGNAL TRANSDUCERS TITLE OF INVENTION: BINDING ASSAYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 852 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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                                                                                LENGTH:
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                                                          amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94111-4187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  California
                                                                            852 amino acids
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Hou, Jinzhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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lo. 3;
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FILING DATE:
FILING DATE:
FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
MAME: MURASHIGE, KATE H.
RAGISTRATION UNMBER: 29,959
REFERENCE/DOCKET NUMBER: 24615
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
(202) 887-0763
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US-09-242-632A-2
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LENGTH: 582
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 0.9%; Score 8; Best Local Similarity 100.0%; Pred. No. Matches 8; Conservative 0; Mismatc
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/242,632A
CURRENT FILING DATE: 1999-02-19
PRIOR APPLICATION NUMBER: JP 8-238580
PRIOR FILING DATE: 1996-08-21
NUMBER OF SEQ ID NOS: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Nippon Zeon
TITLE OF INVENTION: Antigen protein derived
TITLE OF INVENTION: laryngotracheitis virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Amino acid sequence of L32h polypeptide of OTHER INFORMATION: infectious laryngotracheitis virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Infectious laryngotracheitis virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: BONEKAMP, ALFONSUSJOHANNES
APPLICANT: VAN TILBORG E., MARCELLIS W.
TITLE OF INVENTION: MODIFIED SIGNAL SEQUENCES
NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    277 KAALEDIT 284
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                                                                                                                                                                                 APPLICATION NUMBER: US/07/960,510 FILING DATE: 19921013
                                                                                                                                                                                                                                                                                                                                                                                 STREET: 2000 Pen
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                            ZIP: 20006-1888
                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                     2000 Pennsylvania Ave., Suite 5500
                                                                                                                                                                                                                                                                                                                                                                  USA
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100.0%; Pred. No.
                                                                                   24615-20034.00
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o. 21;
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Query Match
Best Local Similarity
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SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
US-07-960-510-4
                                           RESULT 18
US-07-960-510-6
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Best Local Similarity
Thickes 7; Conserv.
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US-07-960-510-5
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              Sequence 6, Application US/07960510 Patent No. 5705362
                                                                                                                                                                                                                                                                                               NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2461:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFA: (202) 887-0763
TELEFA: 90-4030
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/960,510
FILING DATE: 19921013
                                                                                                                      166 KRLYARL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: BONEKAMP, ALFONSUSJOHANNES
APPLICANT: VAN TILBORG E., MARCELLIS W.
TITLE OF INVENTION: MODIFIED SIGNAL SEQUENCES
TUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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TOPOLOGY: Lin
                                                                                                                                                                                                                                                                   LENGTH: 29 amino acids
TYPE: AMINO ACID
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CITY: Washington
STATE: D.C.
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2000 Pennsylvania Ave., Suite 5500
                                                                                                                                                               Conservative
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Pred. No
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RESULT 19
US-07-960-510-7
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                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:

APPLICANT: BONEKAMP, ALFONSUSJOHANNES

APPLICANT: VAN TILBORG E., MARCELLIS W.

TITLE OF INVENTION: MODIFIED SIGNAL SEQUENCES

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON 6 FOERSTER
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ZIP: 20006-1850
COMPUTER READABLE FORM:
COMPUTER EIDAPY disk
MEDIUM TYPE: IBM PC compatible
TYPEM: PC-DOS/MS-DOS
TYPEM: PC-DOS/MS-DOS
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TELEX: 90-4030
INFORMATION FOR SEQ ID NO:
                                                                     ZIP: 20006-1888

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/960,510
FILING DATE: 19921013
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
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TELEPHONE: (202) 887-0763
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     166 KRLYARL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: BONEKAMP, ALFONSUSJOHANNES
APPLICANT: VAN TILBORG E., MARCELLIS W.
TITLE OF INVENTION: MODIFIED SIGNAL SEQUENCES
NUMBER OF SEQUENCES: 18
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APPLICANT:
                                                                                                                                                                                                                                                          STREET: 2000 Pen
CITY: Washington
STATE: D.C.
                                                          CLASSIFICATION:
                                                                                                                                                                                                                                     COUNTRY:
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FILING DATE: 199210
CLASSIFICATION: 435
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CITY: Washington
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)N: 435
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                                                                                                                                                                                                                                                                                          Suite 5500
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RESULT 21
5457090-5
;Patent No.
RESULT 22
5495001-16
;Patent No.
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5457090-5
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                                                                                                                                                                                                                                FILING DATE: 21-JUN-1990; SEQ ID NO:5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 2461
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEPAX: (202) 887-0763
TELEYAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO:8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELASTASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.8%;
Best Local Similarity 100.0%;
Matches 7; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                       Query Match
Best Local S
                                                                                                                                        Matches
                                                                                                                                                                                                                                                         ent No. 5457090
ent No. 5457090
applicawn: SCOTT, RANDY W.; GOLINI, FRED; MCGROGAN, MICHAEL TITLE OF INVENTION: PROTEASE NEXIN-I VARIANTS NUMBER OF SEQUENCES: 7
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/924,294
FILING DATE: 03-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 542,484
APPLICATION NUMBER: 542,484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 11
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 21-JUN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ent No. 5187089

APPLICANT: SCOTT, RANDY W.; GOLINI, FRED; MCGROGAN, MICHAEL TITLE OF INVENTION: PROTEASE NEXIN-I VARIANTS WHICH INHIBIT
                                                                                                          117 PLSLEEL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            166 KRLYARL 172
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                                                                                                                                       Local Similarity nes 7; Conserv
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                                                                           <sub>5</sub>
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                                                                           PLSLEEL 11
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llarity 100.0%; Pred. No. 13
Conservative 0; Mismatches
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                                                                                                                                     0.8%; Score 7; DB 6;
100.0%; Pred. No. 15;
ive 0; Mismatches
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Pred. No.
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o. 13;
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GENERAL INFORMATION:

APPLICANT: ROSEN et al.

TITLE OF INVENTION: 186 Human Secreted proteins

FILE REFERRICE: p2002p1

CURRENT APPLICATION NUMBER: US/09/149,476

CURRENT FILING DATE: 1998-09-08

EARLIER APPLICATION NUMBER: PCT/US98/04493

EARLIER FILING DATE: 1998-03-06

EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/040,162

EARLIER APPLICATION NUMBER: 60/040,333

EARLIER APPLICATION NUMBER: 60/040,333

EARLIER FILING DATE: 1997-03-07

EARLIER FILING DATE: 1997-03-07
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5171673-7
;Patent No.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: SLOMA, ALAN; HANNETT, NANCY M.; STEPHENS, M.A.; RUDOLPH, CATHY F.; RUFO JR., GERALD A.; PERO, JANICE TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS DNA USING THE BACILLUS COAGULANS AMYLASE GENE NUMBER OF SEQUENCES: 10

CURRENT APPLICATION DATA:

COURSENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/
FILING DATE: 18-JUL-1988
SEQ ID NO:7:
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Best Local Similarity
Matches 7; Conserv
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FILING DATE: 10-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 111,111
FILING DATE: 24-AUG-1993
APPLICATION UMBER: 25,450
APPLICATION UMBER: 25,450
FILING DATE: 13-MAR-1987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         166 KRLYARL 172
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FILING DATE: 06-JUN-1986
APPLICATION NUMBER: 870,232
FILING DATE: 03-JUN-1986
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100.0%; Pred. No. 15;
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APPLICATION NUMBER: 60/040,334
FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,336
FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,163

1997-03-07

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R APPLICATION NUMBER: 60/04
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/04 ER ETLING DATE: 1997-08-22

ER APPLICATION NUMBER: 60/056,911

ER FILING DATE: 1997-08-22

ER APPLICATION NUMBER: 60/056,636

ER FILING DATE: 1997-08-22

ER APPLICATION NUMBER: 60/056,874

ER FILING DATE: 1997-08-22

ER APPLICATION NUMBER: 60/056,910

ER FILING DATE: 1997-08-22

ER APPLICATION NUMBER: 60/056,864

ER APPLICATION NUMBER: 60/056,864

ER FILING DATE: 1997-08-22

ER APPLICATION NUMBER: 60/056,864

ER FILING DATE: 1997-08-2

ER APPLICATION NUMBER: 60/056,631

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ER APPLICATION NUMBER: 60/056,631 ER FILING DATE: 1997-08-22

ER APPLICATION NUMBER: 60/056,882

ER FILING DATE: 1997-08-22

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ER APPLICATION NUMBER: 60/056,637

ER FILING DATE: 1997-08-22

ER APPLICATION NUMBER: 60/056,903

ER FILING DATE: 1997-08-22

ER APPLICATION NUMBER: 60/056,888

ER FILING DATE: 1997-08-22

ER APPLICATION NUMBER: 60/056,879

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ER APPLICATION NUMBER: 60/056,879 FILING DATE: 1997-05-23 A APPLICATE: 1997-06
BR FILING DATE: 1997-08-22
BR APPLICATION NUMBER: 60/06
BR APPLICATION NUMBER: 60/06 FILING DATE: 1997-05-20
APPLICATION NUMBER: 60/C
APPLICATION 1997-05-20/C FILING DATE: APPLICATION APPLICATION NUMBER: FILING DATE: 1997-08 APPLICATION NUMBER: R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/0
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/08
R FILING DATE: 1997-08-22 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/0 FILING DATE: 1997-08-22 FILING DATE: APPLICATION NUMBER: 60/056,880 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,894 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/ FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,872 APPLICATION NUMBER: 60/1 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/ FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,889 FILING DATE: 1997-08-22 APPLICATION NUMBER: 6
FILING DATE: 1997-08-NUMBER: 60/043,578: 1997-04-11 NUMBER: 60/047,614: 1997-05-23 1997-08-22 1997-08-22 60/047,593 60/047,589 60/047,594 60/047,590 60/047,586 60/047,585 60/047,588 60/047,599 60/047,595 60/057,761 60/056,892 60/056,662 60/056,878 60/056,630 60/056,877 60/056,893 60/056,886 60/048,974

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ER APPLICATION NUMBER: 60/043,580
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,568
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,314
ER TILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,569
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,671
ER APPLICATION NUMBER: 60/043,671
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,674
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,312
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ER FILING DATE: 1997-05-23
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ER FILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/047,612
ER FILING DATE: 1997-05-23
ER FILING DATE: 1997-05-23
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R FILING DATE: 1997-05-23
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ER APPLICATION NUMBER: 60/047,587
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ER FILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/047,492
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APPLICATION NUMBER: 60/047,584
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,500
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R APPLICATION NUMBER: 60/047,503
R FILLING DATE: 1997-05-23
RA APPLICATION NUMBER: 60/047,592
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RA APPLICATION NUMBER: 60/047,581
REFILLING DATE: 1997-05-23

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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,618
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60/047,617 60/047,583 60/047,633

FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/1 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/1

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RESULT 25
US-09-149-476-465
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COURTENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER APPLICATION NUMBER: 60/040,333
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EARLIER FILING DATE: 1997-03-07
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EARLIER APPLICATION NUMBER: 60/040,626
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,334
EARLIER APPLICATION NUMBER: 60/040,336
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,163
EARLIER FILING DATE: 1997-03-07
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CURRENT APPLICATION NUMBER: US/09/149,476
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TITLE OF INVENTION: 186 Human Secreted proteins
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51 ELLEQLL 57
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ER APPLICATION NUMBER: 60/057,650
ER FILING DATE: 1997-09-05
ER APPLICATION NUMBER: 60/056,884
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ER APPLICATION NUMBER: 60/056,862
ER FILING DATE: 1997-08-22
IER APPLICATION NUMBER: 60/056,887
IER APPLICATION NUMBER: 60/056,908
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2R FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,908
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/048,964
ER APPLICATION NUMBER: 60/067,650
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ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,909
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,875
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FER FILING DATE: 1997-08-22
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FILING DATE: 1997-06-13
APPLICATION NUMBER: 60/061,060
FILING DATE: 1997-10-02
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ER APPLICATION NUMBER: 60/043,315
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/048,974
ER FILING DATE: 1997-06-06
ER APPLICATION NUMBER: 60/056,886
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,877
ER FILING DATE: 1997-08-22
                                                                                                                                                 ER APPLICATION NUMBER: 60/043,671
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,674
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,669
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,312
ER FILING DATE: 1997-04-11
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ER FILING DATE: 1997-04-11
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FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,311
FILING DATE: 1997-04-11
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APPLICATION NUMBER: 60/043,580
FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,568
FILING DATE: 1997-04-11
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APPLICATION NUMBER: 60/047,632
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FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,492
FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,587
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FILING DATE: 1997-05-23
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ER FILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/047,586
ER FILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/047,590
ER FILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/047,594
ER FILING DATE: 1997-05-23
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                          FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/047,501
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/043,670
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FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,879
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,903
FILING DATE: 1997-08-22
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FILING DATE: 1997-08-3
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FILING DATE: 1997-08-22
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STATE: CA
STATE: CA
COUNTRY: USA
LIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/438,753B
FILING DATE: 10-MAY-1995
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US-08-438-753B-24
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FILING DATE: 19-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/847,741
FILING DATE: 09-MAR-1992
PRIOR APPLICATION UNMBER: US 07/318,050
FILING DATE: 02-MAR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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PRIOR APPLICATION NUMBER: US 08/139,891
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         388 ELLEQLL 394
|||||||
51 ELLEQLL 57
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CITY: F
                                                                                             APPLICATION NUMBER: US 0 FILING DATE: 19-OCT-1993
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2R APPLICATION NUMBER: 60/056,908

2R FILING DATE: 1997-08-22

2R APPLICATION NUMBER: 60/048,964

2R FILING DATE: 1997-05-06

2R APPLICATION NUMBER: 60/057,650

2R REPLICATION NUMBER: 60/057,650
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2R FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,862
ER FILING DATE: 1997-08-22
2R APPLICATION NUMBER: 60/056,887
ER FILING DATE: 1997-08-22
ER FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/
FILING DATE: 1997-10-02
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APPLICATION NUMBER: 60/049,610
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/057,669
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FILING DATE: 1997-08-22
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NUMBER: 60/056,664
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                    EMBL; U32752;
TIGR; HI0698;
                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                    Langen H., Takacs B., Evers S., Berndt P., Lahm H.W., Wipf B., Gray C., Fountculakis M.;
"Two-dimensional map of the proteome of Haemophilus influenzae Electrophoresis 21:411-429(2000).

1. SIMILARITY: STRONG, TO E.COLI YTFM.
                                                                                                                                                                                                                                  Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F. Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M. McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Ulterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fitchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
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01-NOV-1995
15-JUN-2002
                                                                                                                                                                        IDENTIFICATION BY MASS SPECTROMETRY. MEDLINE=20137488; PubMed=10675023;
                                                                                                                                                                                                              Rd
                                                                                                                                                                                                      Science
                                                                                                                                                                                                                    "Whole-genome random sequencing
                                                                                                                                                                                                                                                                                                                 STRAIN=Rd / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
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l103; Bac_surface_Ag; 1.
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CPF3_HUMAN
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TSTATE IS A LIANSCIPATIONAL ACTIVATOR THAT REQUIRES SEQUENCE-Specific Contacts provided by statl and p48 for stable interaction with DNA.";

LJ. Biol. Chem. 272:4600-4605(1997).

C. I. FUNCTION: TRANSCRIPTION FACTOR THAT BINDS TO THE IFN-STIMULATED CONTRANSCRIPTION FACTOR THAT BINDS TO THE MULTIPROTEIN CONTRANSCRIPTION FACTOR IS TERMED ISSTS.

C. I. SUBUNIT: IN RESPONSE TO IFN ALEHA/BETA.

C. C. SUBUNIT: IN RESPONSE TO IFN ALEHA/BETA.

C. ALEHA, STATI-BETA, STAT2) OF ISSES, BECOME PHOSPHORYLATED ON TYROSINE, MIGRATE INTO THE NUCLEUS, AND ASSEMBLE INTO A COMPLEX CONTRESINE, MIGRATE INTO THE NUCLEUS, AND ASSEMBLE INTO A COMPLEX TOGETHER WITH ISSES GAMMA (P48), A DNA-BINDING PROTEIN THAT SPECIFICALLY BINDS TO THE IFN-STIMULATED RESPONSE ELEMENT.

C. I. SUBCELLULAR LOCATION: Nuclear; translocated into the nucleus in response to phosphorylation.

C. I. ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A CHAPTEN AND ALTERNATIVE COLUMN.
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Best Local Similarity
Matches 11; Conser
                                                           SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING-!- PTM: TYROSINE PHOSPHORYLATED IN RESPONSE TO IFN-!- SIMILARITY: BELONGS TO THE STAT FAMILY OF TRANSCI-!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
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MEDLINE=97172544; Pubmed=9020188;
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P52630; Q16430; Q16431;
Q1-OCT-1996 (Rel. 34, Created)
O1-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Signal transducer and activator of transcription 2 (p113).
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FEBS Lett. 381:191-194(1996).
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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           SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
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MP63_MYCTU
GRA1_TOXGO
RS7_AVIMR
INO1_BOVIN
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STA2_HUMAN
NAPC_ECOLI
KAG2_CAEEL
YTFM_ECOLI
MCCA_ARATH
CARB_THEAC
SALM_DROME
SALM_DROVI
CLDI_MOUSE
PURR_LACLA
LIGE_PSEPA
YITT_BACSU
THTR_HUMAN
THTR_MOUSE
34KD_MUSA
0YEE_HUMAN
MRAW_FUSNN
MOCA_RHIME
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VATD_THETH
GPH_VIBCH
COX2_ASCSU
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CLDI_HUMAN
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       ISPB_ECOLI
E13K_TOBAC
HITA_HAEIN
YPFG_ECOLI
GP21_HUMAN
HRCA_CAUCR
PCE_TACTR
Y62B_MYCTU
ALR_ANASP
WH4 2_STRCO
GDN_ECOLI
FRHA_METTH
DGT1_AGRT5
TIG_BACSU
C124_MYCTU
YB48_MYCTU
YJ45_MYCTU
     GPC2 RAT
DSD2-PSEAE
REB1_KLULA
ILVD_VIBCH
AMYG_AEEL
AMYG_AEEL
MCM3_KULA
MCM3_HUMAN
P11A_HUMAN
P11A_HUMAN
P11A_BACST
NRCA_CHICK
FRPA_NEIMB
XDH_DROSU
CA1E_HUMAN
CA1E_HUMAN
CHD2_HUMAN
CHD2_HUMAN
CHD2_HUMAN
FRPC_NEIMG
RGSC_HUMAN
FRCAGAC
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TPSI_KIUIA
DLJ3_YEAST
SRM_MOUSE
FSC3_HIUMAN
MOSB_RHIME
AMY_BACLI
YMY3_YEAST
AMYG_SACFI
AMYH_SACFI
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Q02294
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Q04539
P81079
P21536
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Q03735
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P91711
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2 drosophila
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Result

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A48075
60K Stress-related protein - chicken (fragments)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 16-Feb-1994 #sequence_revision 07-Feb-1997 #text_change 11-Jan-2000
C;Accession: A48075; B48075; C48075; D48075; E48075; F48075; G48075
R;Smith, D.F.; Sullivan, W.P.; Marion, T.N.; Zaitsu, K.; Madden, B.; McCormick, D.J.; Td.
Mol. Cell. Biol. 13, 869-876, 1993
A;Title: Identification of a 60-kilodalton stress-related protein, p60, which interacts
A:Reference number: A48075; MUID:93140785; PMID:8423808
                                                                                                       A;Gene: AGR_C_3548
A;Map position: cir
C;Superfamily: Esci
                                                                                                                                                                A;Cross-references:
C;Genetics:
                                                                                                                                                                                                                                                                      R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldn A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, Science 294, 2323-2328, 2001

A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium A;Reference number: A97359; PMID:11743194
                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-129 <KUR>
                                                                                                                                                                                                                                                                                                                                                                     50s ribosomal protein L22 [imported] - Agrobacterium tumefaciens (strain C58, C;Species: Agrobacterium tumefaciens C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002 C;Accession: F97593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Note: sequence extracted A; Accession: D48075
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A; Note: Particular SM3>
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Escherichia coli rib
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Science 294, 849-852, 2001
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J. A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AC1545
                                                                                                                                                                         A;Cross-references: GB:AL592022; pIDN:CAC96131.1; A;Experimental source: strain Clip11262
                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-130 <GLA>
                                                                                                                                                                                                                                                                                                                                                                                                  R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi,
                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein lin0899 [imported] - Listeria innocua (strain Clip11262) C;Species: Listeria innocua (c;Species: Listeria innocua (c;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001 C;Accession: AC1545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Felly, P., Outster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens
A;Reference number: AB2577; PMID:11743193
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A;Molecule type: DNA
A;Residues: 1-129 <KUR>
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A;Experimental source: strain C58 (Dupont)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50s ribosomal protein L22 [imported] - C; Species: Agrobacterium tumefaciens
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D.; Kutyavin,
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                                                                                                                                                                                              PID:g16413349; GSPDB:GN00178
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T.; Levy, R.; Li, N
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Voss, H.; Wehla
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A;Cross-references: EMBL:U42580; NID:g4028896; PIDN:AAC96869.1
A;Experimental source: specific host Chlorella strain NC64A
C;Genetics:
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N;Alternate names: hypothetical protein G1607

C;Species: Saccharomyces cerevisiae

C;Date: 23-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 19-Apr-2002

C;Accession: S61135; S64199

R;Bertani, I.; Coglievina, M.; Zaccaria, P.; Klima, R.; Bruschi, C.V.

submitted to the EMBL Data Library, September 1995

A;Description: The sequence analysis of a 7.9 kb DNA fragment from the left arm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-95 <GRA>
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w353 homolog G12_orf109 - Mycoplasma pneumoniae (strain ATCC 29342)
C; Species: Mycoplasma pneumoniae
A; Variety; ATCC 29342
C; Date: 27-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 07-Dec-1999
C; Accession: $73639
R; Himmelreich, R.; Hibert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R. Nucleic Acids Res. 24, 4420-4449, 1996
A; Title: Complete sequence analysis of the genome of the bacterium Mycoplasma A; Reference number: $73327; MUID:97105885; PMID:8948633
A; Accession: $73639
A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA
A; Residues: 1-109 <HIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-107 - GBRU>
A; Residues: 1-107 - GBRU>
A; Cross-references: EMBL: Z72704; NID: g1322794; PIDN: CAA96894.1; PID: g1322795; MIPS: YGL18
A; Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-107 <BER>
A; Cross-references: EMBL: X91489;
R; Bruschi, C.V.; Coglievina, M.;
submitted to the Protein Sequence
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A; Accession: S64199
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A; Accession: S61135
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ina, M.; Bertani, I.; Klima, R.; Zaccaria, P.; Delneri,
Sequence Database, May 1996
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RESULT

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R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997

A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch A;Reference number: A69250; MUID:98049343; PMID:9389475

A;Accession: A69441
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        conserved hypothetical protein AF1530 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
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C:Superfamily: conserved hypothetical protein mJ0039
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A;Molecule type: DNA
A;Residues: 1-119 <KUR>
                                                                                                                                                    C; Superfamily: Escherichia coli ribosomal protein
                                                                                                                                                                        A; Gene:
Db
                                    QY
                                                                                                                                                                                            C; Genetics:
                                                                                                                                                                                                           A; Cross-references: GB: AE006914;
                                                                                                                                                                                                                                                                                          A; Accession: A97825
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                                      491 KLNLVAA 497
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  KLNLVAA
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                                                                           Similarity 7; Conserv
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Pred. No. 74;
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                                                                                 red. No. 74
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A;Gene: ECs387
C;Superfamily:
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Qasawara, N.; Yasunaga, T.; Kullara, C., 2004
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia
                                                                                                                                                                                                                                                hydrogenase-2 operon protein HybG [imported] - Escherichia coli (strain 0157:H7, C;Species: Escherichia coli (c;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 17-May-2002 C;Accession: C91113
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C91113
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C;Superfamily:
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A; Residues: 1-82 <STO>
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A;Reference number: A85480; MUID:21074935; PMID:11206551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein hybG [imported] - Escherichia C;Specles: Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001
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C;Superfamily: hydrogenase expression/formation protein hypc
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Kasunaga, T.; Kuhara, S.;
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Pred. No
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Shinagawa, H.
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              C; Accession: T18004
R; Graves, M.V.;
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hypothetical protein A502L - Chlorella C:Species: Chlorella virus PBCV-1 C:Date: 15-Oct-1999 #sequence_revision
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R;Parkhill, J.; Achtman, M.; James,
R;Parkhill, J.; Achtman, M.; James,
R;Parkhill, J.; Achtman, M.; James,
                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-91 < PAR>
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Nature 404, 502-506, 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein NMA2123 [imported] - Neisseria meningitidis (strain z2491 serogr
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A; Residues: 1-88 < KUR>
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C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
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Pred. No. 58;
0; Mismatches
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S.; Moule, S.;
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ismatches
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red. No. 57;
Mismatches
                               virus PBCV-1
    15-Oct-1999
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#text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                 S.D.; Chu
Mungall,
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                                                                                                                                                                                                 Length 91;
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                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                 Neisseria menigitidis
                                                                                                                                                                                                                                                                     PIDN:CAB85336.1; PID:g738
                                                                                                                                                                                                                                                                                                                                                                                                 K.; Quail, M.A.;
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Van Etten,

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A;Experimental source: strain 9a5c

R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H Briones, L. Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigu, Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A. F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Silva, R.G.; Santellij, R.V.; Sawasak A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; M.S.; Santellij, R.V.; Sawasak A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; M.S.; Santellij, R.V.; Sawasak A;Authors: da Silva, M.H.; Vanlada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; M.S.; Santellij, R.V.; Sawasak A;Authors: da Silva, M.H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; M.S.; Santellij, R.V.; Sawasak A;Authors: da Silva, M.H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; M.S.; Santellij, R.V.; Sawasak A;Authors: da Silva, M.H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; M.S.; Santellij, R.V.; Sawasak A;Authors: da Silva, M.H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; M.S.; Santellija, R.V.; Sawasak A;Authors: da Silva, M.S.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; M.S.; Santellija
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R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Nature 406, 151-157, 2000
Nature 406, 151-157,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: T00661
R;Federspiel, N.A.; Palm, C.J.; Conway, A.B.; Kurtz, D.B.; Conway, Yysotskaia, V.S.; Yu, G.; Ecker, J.; Theologis, A.; Davis, R.W. submitted to the EMBL Data Library, February 1998
hypothetical protein ssr2201 - C;Species: Synechocystis sp. A;Variety: PCC 6803 C;Date: 25-Apr-1997 #sequence_r
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C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: G82667
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A;Residues: 1-66 <STM>
A;Cross-references: GB:AE003984; GB:AE003849; NID:g9106581; PIDN:AAF84352.1; GSPDB:GN00:
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A;Residues: 1-1417 <FED>
A;Cross-references: EMBL:ACC002396; NID:g2749918; PID:g2829883; GSPDB:GN00059; ATSP:F316
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A; Accession: T00661
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Best Local :
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     25-Apr-1997 #text_change 08-Oct-1999
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     hydrogenase-2 component protein [imported] - Salmonella enter c; Species: Salmonella enterica subsp. enterica serovar Typhi A; Note: this species has also been called Salmonella typhi C; Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_char C; Accession: AG0884 R; Parkhill, J; Dougan, G.; James, K.D.; Thomson, N.R.; Picka th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; I, S.; Moule, S.; O'Gaora, P.
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R;Menon, N.K.; Chatelus, C.Y.; Dervartanian, M.; Wendt, J.C.; Shanmugam, K.T.; Peck J. Bacteriol. 176, 4416-4423, 1994
A;Title: Cloning, sequencing, and mutational analysis of the hyb operon encoding Esch A;Reference number: A55516; MUID:94292472; PMID:8021226
A;Accession: G55516
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A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocy
                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross references: GB:U09177; NID:g501051; PIDN:AAA21595.1; PID:g544489 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-72 <KAN>
A;Cross references: EMBL:D90911;
A;Note: the nucleotide sequence v
                                                                                                                                                                             A; Gene: hybG
C; Superfamily:
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                                                                                                                                                                                                                                                                                          A;Status: preliminary; nucleic acid
A:Molecule type: DNA
A;Residues: 1-82 <BLAT>
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A; Residues: 1-82 <MEN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Species: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: S74322; MUID:97061201; PMID:8905231 A; Accession: S75519
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7 GQVLAVG 13
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was submitted
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to the EMBL Data Library, June 1996
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Salmonella enterica

subsp. enterica

#text_change 17-May-2002

R.M.; Dowd, L.;

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White,

Wain,

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hypothetical protein all7659 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120be C:Species: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 C:Accession: AH2546 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, Shar Res. 8, 205-213, 2001 Right Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Analized Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Analized Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Analized Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Analized Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Analized Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Analized Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Analized Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Analized Cyanobacterium Anal
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A; Residues: 1-731 <KUR>
A; Cross references: GB: AP003602; PIDN: BAB77302.1;
A; Cross references: Strain PCC 7120
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A;Molecule type: DNA
A;Residues: 1-582 <HEI>
A;Cross-references: GB:AE004323;
A;Experimental source: serogroup
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Nature 406, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A;Reference number: A82035; MUID:20406833; PMID:10952301

A;Accession: F82064
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A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: F86119
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-577 <5TO>
A;Cross-references: GB:AE005174; NID:g12519219; PIDN:AAG59418.1;
A;Experimental source: strain O157:H7, substrain EDL933
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C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: F82064
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C; Species: Vibrio cholerae
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MUID:21074935; PMID:11206551
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H.; Dragoi, I.; Sellers,
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hypothetical protein F316.24 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999
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A;Gene: FlyBase:Dvir/salm
A;Cross-references: FlyBas
C;Keywords: DNA binding; t
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                                                                                                                                                                                                                                                                                                     finger protein - fruit fly (Drosophila virilis) (fragment) C:Species: Drosophila virilis C:Date: 20-Oct-1994 #sequence_revision 26-May-1995 #text_c
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A; Residues: 1-1402 <SCH>
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S42748
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A;Introns: 51/1; 1329/3 1355/2
C;Keywords: zinc finger
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A; Residues: 1-1355 < KVUE>
A; Cross references: EMBL: X75541; NID: 9414106;
A; Note: the authors translated the codon GAC A; Note: mRNA sequencing has also been done
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Genetics:
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C;Species: Drosophila melanogaster
C;Date: 19-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jul-2000
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S40022
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EMBO J. 13, 168-179, 1994
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Best Local (
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934 LTPEQIQA 941
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                             61 LTPEQIQA 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              212 IKAALEDI 219
                                                                                                                  DNA binding;
                                                       Similarity 100 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
8; Conserv
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                                                                                                                              FlyBase:FBgn0013137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Frommer, G.;
                                                                                                                                                                      EMBL: 227444; NID: g426461; PID: g426462
                                                                                                               transcription regulation
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                                                                                   Score 8;
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                                                      Mismatches
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                                                                     NO.
                                                                   DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gonzalez-Gaitan, M.; Weber, A.; Wagner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N
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                                                                                 Length 1402;
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#text_change

22-Oct-1999

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hypothetical protein SC10H5.07 SC10H5.07 - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999 C;Accession: T34645
R;Ollver, K.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, August 1998
A;Reference number: 221550
A;Accession: T34645
A;Accession: T34645
A;Status: prelininary; translated from GB/EMBL/DDBJ
A;Residues: 1-469 <OLI>A;Residues: 1-469 <OLI>A;Cross-references: EMBL:AL031232; PIDN:CAA20279.1; GSPDB:GN00070; SCOEDB:SCABCCOST-TESTATION:CAA20279.1; GSPDB:GN00070; SCOEDB:GN00070; SCOED
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R:Penfold, C.N.; Bender, C.L.; Turner, J.G.
Gene 183, 167-173, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     coronafacic acid synthetase component cfa3 [imported] - Pseudomonas syringa N;Contains: 3-oxoacyl-[acyl-carrier-protein] synthase (EC 3.2.1.-) C;Species: Pseudomonas syringae C;Date: 24-Jan-1998 #sequence_revision 13-Mar-1998 #text_change 20-Jun-2000 C;Accession: JC5747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Start codon: GTG
C;Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I; 3-oxoacyl-[acyl-carrier-prot
C;Keywords: glycosidase; hydrolase; transferase
C;Keywords: glycosidase; hydrolase; transferase
F;26-372/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene 183, 167-173, 1996
A;Title: Characterisation of genes involved in biosynthesis A:Reference number: JC5745; MUID:97149295; PMID:8996103
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A; Residues: 1-380 < PEN>
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C; Species: Escherror
C; Date: 28-Oct-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: strain A3(2)
C; Genetics:
A; Gene: SCOEDB:SC10H5.07
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                                               hypothetical 64.8K protein (msra-chpbi intergenic N;Alternate names: hypothetical protein o577 C;Species: Escherichia coli
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nes 8; Conser
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8; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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Pred. No
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Pred. No.
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Mismatches
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                             03-Nov-1995 #text_change 01-Mar-2002
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24;
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A; Start codon:
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                                                                                    hypothetical protein ytfM [imported] - Escherichia coli (strain O157:H7, substrain C;Species: Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C;Accession: F86119
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; IR;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; linc, A.; Dimalanta, E.; Potamousis, K.; App; iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; App; iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; App; iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; App; iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; App; iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; App; iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; App; iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; App; iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; App; iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; App; iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; App; iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; App; iller, L.; Davis, R.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, R.; Davis, R.; Dav
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                                        iller, L.; Grotbeck, E.J.; Davis, N.W.; Nature 409, 529-533, 2001
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A; Residues: 1-577 <HAY>
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                                 Nature 409,
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8; Conserv
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1433-1462, 1997 A;Tille: The committee.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Burland, V.; Plunkett III, G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R. Nucleic Acids Res. 23, 2105-2119, 1995
A;Title: Analysis of the Escherichia coli genome VI: DNA sequence of the region A;Reference number: S56314; MUID:95334362; PMID:7610040
A;Accession: S56445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; nucleic acid sequence not shown; to A;Molecule type: DNA
A;Rosleus: 1-577 <BLAT>
A;Cross-references: GB.AE000493; GB:U00096; NID:g2367360; A;Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: The complete genome sequence of Escherichia coli K-12. A;Reference number: A64720; MUID:97426617; PMID:9278503 A;Accession: G65233
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                                                                                                                                                                                                                                                                                                                                                         hypothetical protein ECs5198 [imported] - Escherichia coli (strain O157:H7, C;Species: Escherichia coli C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001 C;Accession: F91278
                                                                                                                                                                                                                          A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 A; Reference number: A99629; MUID:21156231; PMID:11258796 A; Accession: F91278
                                                                                                                   A;Cross-references: GB:BA000007; PIDN:BAB38621.1; PID:g13364675;
A;Experimental source: strain O157:H7, substrain RIMD 0509952
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Pred. No. 28
0; Mismatches
                    Score
Pred.
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Mismatches
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Shiba, T.;
                      No.
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28;
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Indels
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Shinagawa,
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A.; Dimalanta,

.; May Apoda

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MreB-like protein homolog mb1 [imported] - Listeria innocua (strain Clip11262) C;Species: Listeria innocua (Cip11262) C;Species: Listeria innocua (Cip11262) C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001 C;Accession: AG1765 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; F.; Jones, L.M.; Karst, U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MreB-like protein homolog mbl [imported] - Listeria monocytogenes (strain EGD-e)
C:Species: Listeria monocytogenes
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C:Accession: AE1390
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
D: Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
C:Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mack, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AE1390
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C; Genetics:
A; Gene: mbl
C; Superfamily: rod shape-determining protein envB
                                                                                                                                                                  AG1765
                                                                                                                                                                                    RESULT 11
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A; Residues: 1-331 <GLA>
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C;Superfamily: denitrification system component nirT; nirT homology
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R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Filler, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamou Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: E85859
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nes 8; Conserv
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8; Conser
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100.0%; Pred. No
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o. 17;
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Potamousis,
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K.; Apodaca
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Fsihi, H.
                       Fsihi,
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                                                                                                     A; Gene: CESP: ZC434.8
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C; Superfamily:
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Query Match
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A; Map position: 1
A; Introns: 13/3; 109/3;
C; Superfamily: creatine
                                                                                                                          A; Experimental source: clone ZC434 C; Genetics:
                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-360 <WIL>
A;Cross-references: EMBL:Z75714; PIDN:CAB00062.1; GSPDB:GN00019; CESP:ZC434.8
                                                                                                                                                                                                                                                                                                                     hypothetical protein ZC434.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
C;Accession: T27569
                                                                                                                                                                                                                                                               submitted to the EMBL Data A; Reference number: Z20388
                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein MLCB1450.24 [imported] - Mycobacterium leprae C;Species: Mycobacterium leprae C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
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A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; A; Title: Comparative genomics of Listeria species.
A; Reference number: AB1077; MUID:21537279; PMID:11679669
A; Accession: AG1765
A; Status: preliminary
A; Molecula turn.
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A;Experimental source: strain Clip11262
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A; Residues: 1-331 <GLA>
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Best Local Similarity
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January 1998
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Voss, H.; Wehla
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C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 18-Aug-2000
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 18-Aug-2000
C;Accession: A46160; S71908; S53873
R;Fu, X:Y; Schindler, C; Improta, T; Aebersold, R; Darnell Jr., J.E.
Proc. Natl. Acad. Sci. U.S.A. 89, 7840-7843, 1992
A;Title: The proteins of ISGF-3, the interferon alpha-induced transcriptional A;Reference number: A46160; MUID:92366558; PMID:1502204
A;Accession: A46160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:U18671; NID:g1293919; PIDN:AAA98760.1; PID:g1293920 R;Yan, R.; Qureshi, S.; Zhong, Z.; Wen, Z.; Darnell Jr., J.E. Nucleic Acids Res. 23, 459-463, 1955 A;Title: The genomic structure of the STAT genes: multiple exons in coincider A;Reference number: S53873; MUID:95192056; PMID:7885841 A;Accession: S53873
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                                                                                                                                                                                                                                                                                                                                 Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the blology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: A70551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein Rv3072c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
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C; Superfamily: human signal trans
C; Keywords: signal transduction;
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A; Accession: S71908
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Note: sequence extracted from NCBI backbone (NCBIP:110820) R; Yan, R; Qureshi, S; Zhong, Z; Wen, Z; Darnell, J.E.
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R; Cole, S.T.; Brosc
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A; Residues: 1-196; 392-591; 684-730 < YAW>
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A;Residues: 1-851 <YAN>
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A; Residues: 1-174 <COL>
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                                                                                                                                                                                                                                     A;Cross-references: GB:Z83866; GB:AL123456; NID:g3261691;
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Best Local
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9; Conser
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8; Conserv
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llarity 100.0%; Pred. No.
Conservative 0; Mismatch
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Pred. No.
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A;Gene: napc
C;Superfamily: denitrification system component nirT; nirT homology
C;Superfamily: denitrification system component nirT; nirT homology
C;Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein
F;18-192/Domain: nirT homology <NIRT>
F;18-192/Domain: nirT homology
Ccvalent) #status predicted
F;192/Domain: nirT homology
C;NIRT>
F;183/Domain: nirT homology
C;NIRT>
F;184/Domain: nirT homology
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F;184/Domain: nirT homology
C;NIRT-
F;184/Domain: nirT homology
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F;184/Domain: nir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cytochrome c-type protein [imported] - Escherichia coli (strain C;Species: Escherichia coli C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change C;Accession: C91015
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A;Molecule type: DNA
A;Residues: 1-200 <HAY>
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A; Reference number: A99629;
A; Accession: C91015
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A; Residues: 1-200 <BLAT>
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C; Superfamily:
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                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:BA000007; PIDN:BAB36514.1; PID:g13362560; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
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8, 11-22, 2001
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; Makino, K.; Oh
"""""""" T.; K
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; Kuhara, S.; Shiba, T.; Hat
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Shinagawa, H.
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R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; Whit S; Moule, S; O'Gaora, P.

Nature 413, 848-852, 2001
A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.
A; Title: Complete genome sequence of a multiple drug resistant Salmonella A; Reference number: AB0502; PMID:11677608
A; Accession: AD1055
                                                                                                                                                                   probable exported protein ytfM [imported] - Salmonella enterica subsp. enterica C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001 C;Accession: ADI055
A; Molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: AE0428
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Iil, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Snature 413, 523-527, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable exported protein YPO3524 [imported] - Yersinia pestis (strain CO92) C.Species: Yersinia pestis (c.Species: Yersinia pestis (pate: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text change on no not consider the constant of the cons
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A; Residues: 1-578 < KUR>
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A; Status Process DNA A; Status (Process CB: AE004682; GB: AE004091; NID: g9948598; PIDN: AAG05931.1; A; Cross-references: GB: AE004682; GB: AE004091; NID: g9948598; PIDN: AAG05931.1;
Q
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R;Stover, C.K.; Pham, X.Q.;
adman, S.; Yuan, Y.; Brody,
                                                                                                                                                                                                                    Nature 406, 959-964, 2000
A; Title: Complete genome :
                                                                                                                                                                                                                                                                                                    conserved hypothetical protein PA2543 [imported] - Pseudomonas aeruginosa (strain C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; Fleischmann, R.D.; Adams, M.D.; White, Gocayne, J.D.; Scott, J.; Shirley, R.; D.M.; Brandon, R.C.; Fine, L.D.; Fritc Science 269, 496-512, 1995
A; Authors: Gnehm, C.L.; McDonald, L.A.; Authors: Gnehm, C.L.; McDonald, L.A.;
                                                                                                                                                                          A; Status: preliminary
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C:Species: Haemophilus influenzae
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999
C:Accession: B64012
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A; Residues: 1-578 <TIGR>
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A; Cross-references: GB: C; Genetics: A; Gene: ytfM
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L.L.; (
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MUID:20437337; PMID:10984043
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Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman
, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
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C83015
S26023
H82010
B64917
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F70595
C86907
F69398
A49921
A43749
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S51572
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Chen, Jian

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APPLICANT: Wood William I.

APPLICANT: Zhang,Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P3430R1C36

CURRENT FILING NUMBER: US/10/174,582

CURRENT FILING DATE: 2002-06-18

PRIOR APPLICATION NUMBER: US/10/174,582

CURRENT FILING DATE: 2002-06-18

NUMBER OF SEQ ID NO 35E

SEQ ID NO 35E

LENGTH: 261

TYPE: PRT

ORGANISM: Homo Sapien

US-10-174-582-356
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US-10-174-582-356

Sequence 356, Application US/10174582

Publication No. US20030027265A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Desnoyers, Luc

APPLICANT: Goddard, Audrey

APPLICANT: Goddwski, Paul J.

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Smith, Victoria

APPLICANT: Smith, Victoria

APPLICANT: Smith, Victoria

APPLICANT: Smith, Victoria
Search completed: April 28, 2003, 16:41:50 Job time: 88 secs
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C31
CURRENT APPLICATION NUMBER: US/10/174,579
CURRENT FILING DATE: 2002-06-18
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 356
LENGTH: 261
TYPE: PRT
ORGANISM: Homo Sapien
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Watanabe, Colin K.
Wood, William I.
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Godowski, Paul J.
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RESULT 37
US-10-173-700-356
US-10-173-700-356; Sequence 356, Application US/10173700; Sequence 356, Application US/20030027262a1; Publication No. US20030027262a1; GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
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US-10-180-557-356
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 356
LENGTH: 261
TYPE: PRT
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Best Local Similarity
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 356
LENGTH: 261
TYPE: PRT
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CURRENT FILING DATE: 2002-06-25
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Watanabe, Colin K.
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APPLICANT: Smith, VICULIAN APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Whood, William I.
APPLICANT: Zhang, Zemin
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION NUMBER: US/10/174,572
CURRENT APPLICATION NUMBER: US/10/174,572
CURRENT APPLICATION NUMBER: US/10/174,572
CURRENT APPLICATION NUMBER: US/10/174,572
CURRENT FILING DATE: 2002-06-18
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 356
LENGTH: 261
TYPE: PRT
ORGANISM: Homo Sapien
US-10-174-572-356

0.8%; Score 7; DB 9; Length 261;
O: Gaps
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US-10-174-572-356
; Sequence 356, Applica
; Publication No. US200
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; GENERAL INFORMATION:
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LENGTH: 261
TYPE: PRT
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RESULT 39
US-10-174-579-356
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Goddard, Audrey
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o. US20030027263A1
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                                                                                                                                                 0.8%; Score 7; lilarity 100.0%; Pred. No. Conservative 0; Mismatcl
                                                                            82
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Pred. No.
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5. 2e+02;
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; Sequence 356, Application US/10174579 ; Publication No. US20030027264A1 ; GENERAL INFORMATION: ; APPLICANT: Baker, Kevin P.

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Sequence 356, Application US/10176757
PUDIICATION NO. US20030022297A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Baker, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
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                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo Sapien US-10-176-482-356
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US-10-176-482-356
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; ORGANISM: Homo Sapien
US-10-175-752-356
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 356
LENGTH: 261
TYPE: PRT
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APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Gurney, Austin I
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      APPLICANT:
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 356
LENGTH: 261
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Best Local
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CURRENT FILING DATE: 2002-06-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Zhang,Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C70
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CURRENT APPLICATION NUMBER: US/10/175,752
CURRENT FILING DATE: 2002-06-19
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nes 7; Conserv
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Watanabe, Colin K.
Wood, William I.
Watanabe, Colin K. Wood, William I.
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1 100.0%; Pr
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100.0%; Pr
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RESULT 35
US-10-180-552-356
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                   Sequence 356, Application US/10180552
Publication No. US20030022300A1
GEMERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
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Best Local :
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SEQ ID NO 356
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APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J
APPLICANT: Godowski, Paul J
APPLICANT: Gurney, Austin L
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
         APPLICANT:
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CURRENT FILING DATE: 2002-06-20
Prior Application removed - See File Wrap:
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 356
LENGTH: 261
TYPE: PRT
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Publication No. US20030022298A1
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 261
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo Sapien
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C86
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Goddard, Audrey
Godowski, Paul
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Goddard, Audrey
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100.0%; Pr
0;
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100.0%; Pred. No.
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0. 2e+02;
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c. 2e+02;
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APPLICANT:

Gurney, Austin L. Pan, James

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: NUMBER OF SEQ ID NOS: 6:
: SEQ ID NO 356
: LENGTH: 261
: TYPE: PRT
: ORGANISM: Homo Sapien
US-10-175-737-356
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Best Local Similarity
7; Conserve
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; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-502-118
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US-10-173-706-356
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Best Local Similarity
'Atches 7; Conser'
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NUMBER OF SEQ ID NOS: 170
SEQ ID NO 118
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APPLICANT:
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APPLICANT:
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APPLICANT:
APPLICANT:
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CURRENT FILING DATE: 2002-05-01
                                                                                                                                                                                                     APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian APPLICANT: Desnoyers, Luc
                               APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C7
CURRENT APPLICATION NUMBER: US/10/173,706 CURRENT FILING DATE: 2002-06-17
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Gurney, Austin L.
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                                                                                                                          Smith, Victoria
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                                                                                            Wood, William I.
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100.0%; Pred. No. 2e
tive 0; Mismatches
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o. 2e+02;
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lo. 2e+02;
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; Prior Application removed - St; NUMBER OF SEQ ID NOS: 612; SEQ ID NO 356; LENGTH: 261; TYPE: PRT; ORGANISM: Homo Sapien US-10-173-706-356
                                                                                                                                                                                                                                                                                                                                                                                                                   Prior application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
SEQ ID NO 356
LENGTH: 261
TYPE: PRT
ORGANISM: Homo Sapien
US-10-175-738-356
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Best Local Similarity
Thes 7; Conserve
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US-10-175-752-356
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                              Publication No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                            Sequence 356,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: 93430R1C45 CURRENT APPLICATION NUMBER: US/10/175,738 CURRENT FILING DATE: 2002-06-19
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APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audre
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APPLICANT:
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APPLICANT: Zhang, Zemin TITLE OF INVENTION: SECTITITLE OF INVENTION: ACI
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Godowski, Paul
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                                                             Smith, Victoria Watanabe, Colin K.
                                                Wood, William I.
                                                                                           Pan, James
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o. US20030022295A1
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   SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME
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b. 2e+02;
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RESULT 24
US-10-174-590-356
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US-10-176-758-356
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Best Local Similarity
7; Conserve
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; ORGANISM: Homo Sapien
US-10-174-590-356
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APPLICANT:
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SEQ ID NO 356
LENGTH: 261
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APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Cosnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Goddowski, Paul J
APPLICANT: Gurney, Austin I
                  APPLICANT: Zhang, Zemin TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C104 CURRENT APPLICATION NUMBER: US/10/176,758 CURRENT FILING DATE: 2002-06-21
Prior Application removed NUMBER OF SEQ ID NOS: 612
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TITLE OF INVENTION: SCRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C42
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                                                                                                                 Watanabe, Colin K. Wood, William I.
                                                                                                                                                                             Godowski, Paul J.
Gurney, Austin L.
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                                                                                                                                                Smith, Victoria
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Godowski, Paul J.
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Watanabe, Colin K.
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2002-06-21
oved - See File Wrapper or Palm
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100.0%; Pred. No.
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RESULT 27
US-10-175-737-356
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Best Local Similarity
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; ORGANISM: Homo Sapien
US-10-063-616-118
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Best Local Similarity
Thes 7; Conserve
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APPLICANT: Chen, Jian
APPLICANT: Desmoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J
APPLICANT: Gurney, Austin I
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NUMBER OF SEQ ID NOS: 170
SEQ ID NO 118
LENGTH: 261
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LENGTH:
                  CURRENT APPLICATION NUMBER: US/10/175,737 CURRENT FILING DATE: 2002-06-19
                                                TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C50
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261
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Godowski, Paul J.
                                                                                                   Zhang, Zemin
                                                                                                               Watanabe, Colin | Wood, William I.
                                                                                                                                                  Smith, Victoria
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100.0%; Pred. No.
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100.0%; Pred. No. 2e+02;
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; TYPE: PRT
; ORGANISM: Glycine
US-10-062-254-162
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US-09-764-868-956
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US-09-825-414
Sequence 60, Application US/09825414
Patent No. US20020083489A1
GENERAL INFORMATION:
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US-09-764-868-956
CURRENT APPLICATION NUMBER: US/09/825,414
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/194,160
PRIOR FILING DATE: 2000-04-03
PRIOR APPLICATION NUMBER: 60/224,604
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/249,548
PRIOR APPLICATION NUMBER: 60/249,548
PRIOR FILING DATE: 2000-11-17
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Best Local S
Matches 7
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ32
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LENGTH: 188
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Best Local Similarity 100.0%;
Matches 7; Conservative (
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LENGTH: 214
TYPE: PRT
ORGANISM: Homo saplens
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                                                                                                                                                APPLICANT: COllmer, Alan
APPLICANT: Alfano, James R.
APPLICANT: Charkowski, Amy O.
APPLICANT: Charkowski, Amy O.
TITLE OF INVENTION: DNA MOLECULES AND POLYPEPTIDES OF PSEUDOMONAS SYRINGAE
TITLE OF INVENTION: HRP PATHOGENICITY ISLAND AND THEIR USES
FILE REFERENCE: 19603/3243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prior application data removed - refer to
NUMBER OF SEQ ID NOS: 1510
SOFTWARE: Patentin Ver. 2.0
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OTHER INFORMATION: Xaa
NAME/KEY: SITE
LOCATION: (209)
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46 LLTVNMG 52
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nes 7; Conservative
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Pred. No.
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APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Sleeman, Matthew
APPLICANT: Murison, James G.
APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated From Sk
TITLE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 11000.1011c4U
CURRENT APPLICATION NUMBER: US/09/866,050A
CURRENT FILING DATE: 2001-05-24
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Best Local Similarity
Thes 7; Conserv
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SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 705

LENGTH: 255

TYPE: PRT

ORGANISM: Mouse
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CURRENT APPLICATION NUMBER: US/10/063,547
CURRENT FILING DATE: 2002-05-02
Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 170
SEQ ID NO 118
LENGTH: 261
TYPE: PRT
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Best Local
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                                                                                                                       TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3230R1C1
                                                                                                                                                                                                                                                                                   APPLICANT: Eaton, Dan L.
APPLICANT: Filvaroff, E
APPLICANT: Gerritsen, M
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APPLICANT:
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                                                                                                                                                                                Wood, William I.
                                                                                                                                                                                                Watanabe, Colin K.
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100.0°; Pr
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100.0%; Pred. No.
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s; Pred. No. 1.7
0; Mismatches
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o. 1.7e+02;
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o. 2e+02;
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RESULT 18
US-09-986-480-368
; Sequence 368, Application US/09986480
; Publication No. US20030027999A1
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CURRENT FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: US 60/239,531
PRIOR FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 28
LENGTH: 173
TYPE: PRT
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Best Local Similarity
7; Conserve
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; OTHER INFORMATION: tagged IL-3 amino acid
US-09-975-132A-28
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Sequence 27, Application US/09975132A
Diblication No. US20020182672A1
GENERAL INFORMATION:
APPLICANT: Kolkman, Marc
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TITLE OF INVENTION: Enhanced Secretion of a Polypeptide by
TITLE OF INVENTION: Microorganism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: GC636-2
                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
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TYPE: PRT
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100.0%; Pred. No. 1.3e+02;
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PRIOR APPLICATION NUMBER: 60/157287
PRIOR APPLICATION NUMBER: 60/169767
PRIOR PELING DATE: 1999-10-01
PRIOR PELING DATE: 1999-12-09
PRIOR PELING DATE: 1999-12-09
PRIOR PELING DATE: 1999-12-16
PRIOR PELING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: 60/1712958
PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: 60/171515
PRIOR APPLICATION NUMBER: 60/171535
PRIOR APPLICATION NUMBER: 60/173535
PRIOR APPLICATION NUMBER: 60/173535
PRIOR FILING DATE: 1999-12-29
PRIOR FILING DATE: 1999-12-29
PRIOR FILING DATE: 1999-12-29
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SEQ ID NO 368
LENGTH: 187
TYPE: PRT
                                                                                                                                                                                                                                                                                                                      APPLICANT: Zheng, Peizhong
APPLICANT: Zhu, Qun
TITLE OF INVENTION: Polynucleotides Encoding Proteins Involved In Plant Metabolism
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/062,254
CURRENT FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 09/630,346
PRIOR APPLICATION NUMBER: 60/146511
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: 60/156006
PRIOR FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: 60/156006
PRIOR FILING DATE: 1999-09-30
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Best Local Similarity
Matches 7; Conserv
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CURRENT APPLICATION NUMBER: US/09/986,48C
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: PCT/US00/12788
PRIOR FILING DATE: 2000-05-11
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PRIOR FILING DATE: 1999-05-13
NUMBER OF SEQ ID NOS: 456
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TITLE OF INVENTION: 143 Human Secreted Proteins
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Microsoft Office 97
                        SEQ ID NOS:
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Zheng, Peizhong
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Fang, Yiwen
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100.0%; Pred. No. 1.9
tive 0; Mismatches
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NO. 1.5e+02;
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US-10-042-141-91

; Sequence 91, Application US/10042141

; Publication No. US20020183503A1
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: Sequence 91, Application US/09726643

: Patent No. US20020028449A1
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Best Local Similarity
"hehes 7; Conserve
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CURRENT APPLICATION NUMBER: US/10/042,141
CURRENT FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: 09/726,643
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: PCT/US00/15187
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: 60/137,725
PRIOR APPLICATION NUMBER: 60/137,725
PRIOR FILING DATE: 1999-06-07
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; ORGANISM: Homo sapiens
US-10-042-141-91
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Best Local Similarity
7; Conserv
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 140
LENGTH: 106
TYPE: PRT
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                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                 SOFTWARE:
SEQ ID NO 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ruben et al. TITLE OF INVENTION: 26 Human secreted proteins
                                                                                                  PRIOR APPLICATION NUMBER: PCT. PRIOR EILING DATE: 2000-06-02-07-08-108 APPLICATION NUMBER: 60/PRIOR FILING DATE: 1999-06-07
                                                                                                                                                                   FILE REFERENCE: PZ040P1
CURRENT APPLICATION NUMBER: US/09/726,643
CURRENT FILING DATE: 2000-12-01
                                                                                                                                                                                                                 APPLICANT: Ruben et al.
TITLE OF INVENTION: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 190 SOFTWARE: Patentin Ver. 2.0
                                                                                  NUMBER OF SEQ ID NOS:
                   TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
ORGANISM: Homo sapiens
                               LENGTH: 122
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o. 88;
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US-09-764-868-1129
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LOCATION: (138)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-764-868-1129
                                                                     , OTHER INFORMATION: IL-3 encoded by plasmid pLATIL-3 us-09-975-132A-26
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SEQ ID NO 1129
LENGTH: 150
TYPE: PRT
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Best Local 9
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ32
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
Query Match 0.8%; Sometive 0.00%; If Best Local Similarity 100.0%; If Matches 7; Conservative 0;
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                                                                                                                                                                                                          FILE REFERENCE: GC636-2
CURRENT APPLICATION NUMBER: US/09/975,132A
CURRENT FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: US 60/239,531
PRIOR FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 30
                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Enhanced Secretion of a Polypeptide by TITLE OF INVENTION: Microorganism
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LOCATION: (125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                              TYPE: PRT
                                                                                                         FEATURE:
                                                                                                                                                         LENGTH: 158
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45 DRVLAIN 51
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     Score 7; DB 9
s; Pred. No. 1.3
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Pred. No. 1.2e+02;
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 DB 9; L.,
NO. 1.3e+02;
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b. 1e+02;
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RESULT 9
US-09-925-297-506
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Best Local Similarity
7; Conserve
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Sequence 506, Application US/09925297 Patent No. US20020081659A1
                                                                                                                                                                                                                                                                                                                          TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 95 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 28,006
REFERENCE/DOCKET NUMBER: 560
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/969,890
FILING DATE: 30-OCT-1992
                                                                                                                               389 LLEQLLT 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 30-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Dehlinger, Peter J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: UFILING DATE: 09-MAR-1 PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/139,891
FILING DATE: 19-0CT-1993
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite
                                                                                                42 LLEQLLT 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Dehlinger, Peter J. REGISTRATION NUMBER: 28,(
                                                                                                                                                                                                                                            INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 0 FILING DATE: 02-MAR-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE:
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09-MAR-1992
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Interferon Tau Compositions and
Methods of Use
                                                                                                                                                                                              0.88;
                                                                                                                                                                                                                                     predicted amino acid coding sequence of SEQ ID NO:23 (HuIFNtau7).
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RESULT 11
US-09-764-855-140
; Sequence 140, Application US/09764855
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                                                                                                                                     Query Match
Best Local Similarity
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SEQ ID NO 140
LENGTH: 106
TYPE: PRT
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Matches
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CURRENT FILING DATE: 2002-02-11
                                                                                                                                                                                                                                                                                               Prior Application removed - NUMBER OF SEQ ID NOS: 334
                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PA110C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/925,297
CURRENT FILLING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05989
PRIOR FILING DATE: 2000-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: SITE LOCATION: (92)
OTHER INFORMATION:
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PRIOR APPLICATION NUMBER: 60/124,270
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LOCATION: (80)
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TYPE: PRT
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                                                                                                         178 NKVPRLK 184
                                                                                          69 NKVPRLK 75
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les 7; Conserv
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(45)
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100.0%; Pred. No.
Live 0; Mismatch
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5. 85;
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GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA110

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GENERAL INFORMATION:
APPLICANT: ROSEN et al.
TITLE OF INVENTION: NUCLEIC ACIDS, Proteins, an
FILE REFERENCE: PC007
CURRENT APPLICATION NUMBER: US/09/764,869
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM
NUMBER OF SEO ID NOS: 2442
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1204
LENGTH: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LENGTH: 41
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-726-643-93
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US-10-091-504-1204
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US-10-091-504-1204
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Best Local Similarity
Thehes 7; Conserve
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US-09-764-869-1204
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FILE REFERENCE: PC007C1
CURRENT APPLICATION NUMBER: US/10/091,504
CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 2442
Prior Application removed - See File Wrapper or Palm
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1204
LENGTH: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1204, Application US/10091504 Publication No. US20030059908A1 GENERAL INFORMATION:
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Best Local Similarity 100
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                   Sequence 1204, Application US/09764869 Patent No. US20020061521A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature LOCATION: (20)
OTHER INFORMATION: Xaa e NAME/KEY: misc_feature LOCATION: (40)
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               LOCATION: (20)
OTHER INFORMATION: X
NAME/KEY: SITE
LOCATION: (40)
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                                                                                                        LENGTH: 51
TYPE: PRT
ORGANISM: Homo sapiens
                                                                             FEATURE:
NAME/KEY: SITE
OTHER INFORMATION: Xaa equals any of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            508 DRVLAIN 514
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Pred. No.
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US-09-809-391-465
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Best Local Similarity
7; Conser
                                                                                                          : NAME/KEY: SITE
| LOCATION: (70)
| OTHER INFORMATION: Xaa equals stop translation
| US-09-809-391-465
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SEQ ID NO 601
LENGTH: 69
                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 465
LENGTH: 70
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                  Sequence 465, Application US/09809391 Publication No. US20030049618A1 GENERAL INFORMATION:
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ruben et al. TITLE OF INVENTION: 186 Human Secreted proteins FILE REFERENCE: PZ002P2
                                                   Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                           APPLICANT: Ruben et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P2
                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/809,391
CURRENT FILING DATE: 2001-03-16
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                                                                                                                                                                                                                                                    Prior application data removed - NUMBER OF SEQ ID NOS: 761
                                                                                                                                                                   FEATURE:
                                                                                                                                                                                ORGANISM: Homo sapiens
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                         388 ELLEQLI 394
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les 7; Conserv
51 ELLEQLL 57
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RESULT 8 US-09-746-919-24

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RESULT 1
US-10-045-792-2
Sequence 2, Application US/10045792
Publication No. US20030003563A1
GENERAL INFORMATION:
                                                                                  APPLICATION NUMBER: US/10/045,792
FILING DATE: 19-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/012,710
FILING DATE: <Unknown>
                         ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-194
                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                  TELECOMMUNICATION
                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A STAT PROTEIN AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Vinkemeier, Uwe
                                                                                                                                                                                                                                                                            CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                     STREET: 411 Hackensack Avenue,
                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Darnell, Jr., James E. Kuriyan, John
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10 US-09-815-242-13784
10 US-09-815-242-13784
10 US-09-738-625-130
10 US-09-904-615-130
10 US-09-9864-761-36218
10S-09-738-626-6762
10S-09-738-626-5014
10S-09-898-751A-6
10S-09-834-794A-1
10US-09-834-794A-1
10US-09-834-795A-1
10US-09-834-795A-1
10US-09-834-795A-1
10US-09-931-381A-2
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9 US-10-051-643-78
9 US-09-880-505-78
9 US-09-974-879-188
9 US-09-974-879-188
10 US-09-925-300-1011
1 US-09-925-300-1011
1 US-08-979-847-90
10 US-09-867-550-1670
9 US-10-101-4648-581
10 US-08-979-441
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US-09-925-299-1128
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US-10-023-896-82
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Sequence 5014, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1128, Ap
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Sequence 14, Appl
Sequence 10421, A
Sequence 13784, A
Sequence 130, App
Sequence 130, App
Sequence 130, App
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Sequence 43059, A
Sequence 43059, A
Sequence 78, Appl
Sequence 78, Appl
Sequence 188, Appl
Sequence 34124, A
Sequence 1011, Ap
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Sequence 16
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1670, Ap
Sequence 93, Application US/09726643
Patent No. US20020028449A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 26 Human secreted proteins
FILE REFERENCE: P2040P1
CURRENT APPLICATION NUMBER: US/09/726,643
CURRENT FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: PCT/US00/15187
PRIOR APPLICATION NUMBER: 60/137,725
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 190
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
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US-10-042-141-93
; Sequence 93, Application US/10042141
; Publication No. US20020183503A1
; GENERAL INFORMATION:
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US-09-726-643-93
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TITLE OF INVENTION: 26 Human secreted proteins
FILE REFERENCE: PZ040p1
CURRENT APPLICATION UNBER: US/10/042,141
CURRENT FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: 09/726,643
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: PCT/US00/15187
PRIOR APPLICATION NUMBER: PCT/US00/15187
PRIOR APPLICATION NUMBER: 60/137,725
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: 60/137,725
PRIOR FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 190
SOFTWARE: Patentin Ver. 2.0
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LENGTH: 41
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TELEX: 13521
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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nes 9; Conserv
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HYPOTHETICAL: NO
SEQUENCE DESCRIPTION: SEQ ID NO:
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TELEFAX: 201-343-1684
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sequence 219, App Sequence 219, App Sequence 219, App Sequence 40, Appl Sequence 70, Appl Sequence 70, Appl Sequence 959, App Sequence 2, Appli Sequence 4, Appli	Sequence 219, Appendix	219	999	166, 166, 166,	166, 166,	e 166,	equence 166, equence 166,	166,	166, 166,	Sequence 219, App Sequence 40, Appl Sequence 166, App	166	166	166 166	166	166	100	166	166	100	99	991 991	99	99	999
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Sequence 2, Appli
Sequence 93, Appl
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Sequence 140, Appl
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US-10-175-78-356

US-10-175-78-356

US-10-176-98-356

US-10-176-98-356

US-10-176-98-356

US-10-176-98-356

US-10-176-98-356

US-10-174-582-356

US-10-174-582-356

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Sequence 356
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Sequence 60,
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Search completed: April 28, 2003, 16:36:30 Job time: 67 secs

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US-08-465-971B-2
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SOFTWARE: FASTSEQ I
SEQ ID NO 64
LENGTH: 264
RESULT 38
US-09-134-001C-5150
Sequence 5150, Application US/09134001C
Patent NO. 6380370
Patent NO. 6380370
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
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Patent No. 5942414
GENERAL INFORMATION:
APPLICANT: Y1 L1 and Mark D. Adams
TITLE OF INVENTION: Human G-Protein Receptor HIBEF51
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Best Local Similarity
Matches 7; Conser
                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/46
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
ATTORNEY_AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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LENGTH: 349 amino acid
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nes 7; Conserv
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STATE: NJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Carella, Byrne, Bain, Gilfillan.
ADDRESSEE: Cecchi, Stewart & Olstein
STREET: 6 Becker Farm Road
                                                                                                                                             233 SSQSGET 239
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                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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                                                                                                                                                                                                                                                                                                          B: 349 amino acids
amino acid

OGY: Linear
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100.0%; Pred. No. 1.4e+02;
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o. 1e+02;
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           TO
           STAPHYLOCOCCUS
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117 PLSLEEL 123

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ORGANISM: Staphylococcus epidermidis US-09-134-001C-5150
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US-09-325-932A-191
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                                                                                                                                                                                                 RESULT 40
5187089-2
;Patent no. 5187089
; PATENT: SCOTT, RANDY W.;GOLINI, FRED;MCGROGAN, MICHAEL
TITLE OF INVENTION: PROTEASE NEXIN-I VARIANTS WHICH INHIBIT
                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
7; Conserve
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US-09-325-932A-191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Fai
SEQ ID NO 191
LENGTH: 355
TYPE: PRT
                                                                 5187089-2
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SEQ ID NO 5150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Flinn, Barry
APPLICANT: Lasham, Annette
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification of forestry plant dev
TILE REFERENCE: 1022
CURRENT APPLICATION NUMBER: US/09/325,932A
CURRENT FILING DATE: 199-06-04
NUMBER OF SEO ID NOS: 206
NUMBER OF SEO ID NOS: 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REBERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                     ELASTASE
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                                                                                                 SEQ ID NO:2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 191, Application US/09325932A Patent No. 6451604
              Query Match
Best Local
 Matches
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                                                                                                                                 NUMBER OF SEQUENCES: 11
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   546 EVIDLPE 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  321 EVIDLPE 327
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                                                                                                                 FILING DATE: 21-JUN-1990
                                                                                 LENGTH: 397
Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FastSEQ for Windows Version 3.0
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 Conservative
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100.0%; PI
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 0.8%; Score 7; DB
100.0%; Pred. No. 1.
ntive 0; Mismatches
                                                                                                                                        US/07/542,484
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                                       DB 6;
       1.5e+02;
hes 0;
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                                       Length 397;
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            Gaps
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/600,993A
FILING DATE: 1-MAR-1996
CLASSIFICATION #35
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/245,511
FILING DATE: 18-MAY-1994
CLASSIFICATION: 435
CLASSIFICATION: 435
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US-08-245-511-26
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Best Local
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/116,541
FILING DATE: 01-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: BACTERIAL EXPORTED PROTEINS AND TITLE OF INVENTION: ACELULAR VACCINES BASED THEREON NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Masure, H Robert
APPLICANT: Pearce, Barbara J
APPLICANT: Tuomanen, Elaine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-069 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
PRIOR TOATTON NUMBER: US 08/116,541
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                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                               CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 202
TELEFAX: 133521
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nes 7; Conserv
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100.0%; Pred. No. 70;
vative 0; Mismatches
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IN Release #1.0, Version #1.25
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RESULT 36
US-09-724-864-64
: Sequence 64, Application US/09724864
: Patent No. 6380362
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Best Local Similarity
7; Conserv
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GENERAL INFORMATION:
APPLICANT: Watson, James D
APPLICANT: Watson, James G.
TITLE OF INVENTION: Polynucleotides, polypeptides expressed
TITLE OF INVENTION: by the polynucleotides and methods for t
FILE REFERENCE: 11000.1050U1
CURRENT APPLICATION NUMBER: US/09/724,864
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
PRIOR FILING DATE: 1999-12-23
                                                                                                                                                                                                                                                                                                                                                                                                             US-09-323-872A-12
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US-09-323-872A-12
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US-08-600-993A-26
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Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12, Application US/09323872A Patent No. 6395539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 58
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/323,872A CURRENT FILING DATE: 2001-06-15 PRIOR APPLICATION NUMBER: 09/072,433 PRIOR FILING DATE: 1998-05-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Coschigano, Peter
TITLE OF INVENTION: Compositions and Methods for Bioremediation
FILE REFERENCE: OHU 03640
                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Azorhizobium caulinodans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 211
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HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                           197 ALLAGVA 203
                                                                                                                                                                                                                                                                                                          721 ALLAGVA 727
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            354 DTGTQYR 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: ZUI TELEPHONE: ZUI TELEPHONE: ZUI TELEPHONE: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600
                                                                                                                                                                                                                                                                                                                                        Conservative 0;
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100.0%; Pred. No. 70;
tive 0; Mismatches
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                                                                               their use.
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LLEQLLT 48

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INDIVIDUAL ISOLATE: predicted amino acid coding sequence of SEQ ID NO:23 (HuIFNtau7).

SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-045-467-24
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                                      RESULT 32
US-08-796-792-2
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                                                                                                                  В
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GENERAL INFORMATION:
APPLICANT: Johnson,
Sequence 2, Application US/08796792 Patent No. 6087163
                                                                                                                                                                                          Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                      389 LLEQLLT 395
                                                                                                                    42 LLEQLLT 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/045,467
FILING DATE: 20-Mar-1998
CLASS.FICATION: CUNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 5600-0001.36
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Dehlinger, Peter J.
REGISTRATION NUMBER: 28,006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/139,891
FILING DATE: 19-OCT-1993
APPLICATION NUMBER: US 07/847,741
FILING DATE: 09-MAR-1992
APPLICATION NUMBER: US 07/318,050
FILING DATE: 02-MAR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/455,021
FILING DATE: 31-MAY-1995
FILING DATE: 10-MAY-1995
FILING DATE: 10-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/969,890 FILING DATE: 30-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 95 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/09045467
                                                                                                                                                                                              Conservative
                                                                                                                                                                                        100.0%; F1.
                                                                                                                                                                                              0.8%; Score 7; DB
100.0%; Pred. No. 39
ive 0; Mismatches
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Methods of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Howard M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carol H.
                                                                                                                                                                                                                                      DB 4;
                                                                                                                                                                                                                                    Length 95;
                                                                                                                                                                                                0;
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                                                                                                                                                                                                Indels
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                                                                                                                                                                                                  Gaps
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Вb
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US-08-245-511-26
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                                                                                                                                                                                                                                                                                                            Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 0.8%; Score 7; DB Best Local Similarity 100.0%; Pred. No. 64 Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                           Sequence 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/796,79:
FILING DATE: 06-FEB-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/011,364
FILING DATE: 09-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hone, William J.
REGISTRATION NUMBER: 26,739
REFERENCE/DOCKET NUMBER: 07763/0
TELEPHONE: 212-765-5070
TELEPHONE: 212-765-5070
                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Masure, H Robert
APPLICANT: Pearce, Barbara J
APPLICANT: Tuomanen, Elaine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION: APPLICANT: Gennar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lyashchenko, Konstai
APPLICANT: Manca, Claudia M.A.
TITLE OF INVENTION: MYCOBACTER:
TITLE OF INVENTION: SPECIFIC PI
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS: ADDRESSE: Fish & Richardson, P.C.
ADDRESSEE: Fish & Richardson, Suite 2800
STREET: 45 Rockefeller Plaza, Suite 2800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 10111
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: FRAGMENT TYPE:
                                                                                                                                                                                                TITLE OF INVENTION: BACTERIAL EXPORTED PROTEINS AND TITLE OF INVENTION: ACELLULAR VACCINES BASED THEREON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 212-258-2291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER:
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                                                    COUNTRY: UZIP: 07601
                                                                                                                                                                                                                                                                                                                                                                                                                   25 PVALAAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                       STATE:
                                                                                                            CITY: Hackensack
                                                                                                                           STREET:
                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New York
                                                                                                                                                                                                                                                                                                           5, Application US/08245511
5928900
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                                                                                       New Jersey
                                                                                                                           411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   159 amino acids
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                                                                        USA
                                                                                                                                                                                                                                                        Masure, H Robert
Pearce, Barbara J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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                                                                                                                                               Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MYCOBACTERIUM TUBERCULOSIS
                                                                                                                                                                                     58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US/08/796,792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07763/03301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 159;
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US-08-455-524B-24
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US-08-455-524B-24
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Best Local
                                                                                                                                                                                                                                                         TELEFAX: 415-324-0960
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                             MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 56
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/438,753
FILING DATE: 10-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/847,741
FILING DATE: 09-MAR-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ott, Troy L.

APPLICANT: Van Heeke, Gino
TITLE OF INVENTION: Interferon Tau Compositions and
TITLE OF INVENTION: Methods of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Bazer, Fuller W. APPLICANT: Johnson, Howard M. APPLICANT: Pontzer, Carol H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 350 STREET
                        INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Sholtz, Charles K. REGISTRATION NUMBER: 38,
                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/139,891
FILING DATE: 19-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 31-MAY
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                                                                                                                                                                                                                             LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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nes 7; Conserv
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o. 5942223
                                                                                                                                                                                           amino acid
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                                                                                                                                                                                                                          95 amino acids
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100.0%; Pr
          predicted amino acid coding sequence
of SEQ ID NO:23 (HuIFNtau7).
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; Pred. No.
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Query Match

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Score 7;

DB 2;

Length 95;

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                          Best Local Similarity
Matches 7; Conserv
                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 24, Application US/08455021B GENERAL INFORMATION:
                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 95 amino acide
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity Matches 7; Conserv
                                                                                                                               MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07 FILING DATE: 30-OCT-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 09-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 02-MAR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/139,891
FILING DATE: 19-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
389 LLEQLLT 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Imakawa, Kazuhito
TITLE OF INVENTION: Interferon Tau Compositions and
TITLE OF INVENTION: Methods of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                   INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 38, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     389 LLEQLLT 395
                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 07/847,741 FILING DATE: 09-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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Van Heeke, Gino
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Pontzer, Carol H.
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IBM PC compatible
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                                        100.0%;
                     0.8%; Score 7; DB ;
100.0%; Pred. No. 39;
ive 0; Mismatches
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                                                                                                amino acid coding sequence NO:23 (HuIFNtau7).
                                        DB 2;
5. 39;
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Best Local Similarity
Trahes 7; Conserva
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US-08-443-883A-24
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                                                                                   APPLICATION UNMBER: US/08/443,883A
FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/139,891
APPLICATION NUMBER: US 08/139,891
FILING DATE: 19-0CT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847,741
FILING DATE: 09-MAR-1992
PRIOR APPLICATION DATA:

OPENAR-1992
PRIOR APPLICATION DATA:
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TELEFAX: 415-324-0960
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US 0
FILING DATE: 30-OCT-1992
ATTORNEY/AGENT INFORMATION:
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
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APPLICATION NUMBER: US 07/318,050
FILING DATE: 02-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/969,890
FILING DATE: 30-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Interferon Tau Compositions TITLE OF INVENTION: Methods of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Van Heeke, Gino
APPLICANT: Imakawa, Kazuhito
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                                                                                                                                                                                                                                                                                                                                                                                               ZIP:
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100.0%; Pred. No. 39;
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; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: !
; INDIVIDUAL ISOLATE: !
US-08-443-883A-24
INDIVIDUAL ISOLATE:
US-08-631-328-24
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INFORMATION FOR SEQ ID NO:
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REFERENCE/DOCKET NUMBER: 56
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-324-0880
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LENGTH: 95 amino acids
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APPLICATION NUMBER: US 08/438,753
FILING DATE: 10-MAY-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Subramaniam, Prem S. TITLE OF INVENTION: Hybrid Inte TITLE OF INVENTION: Methods of NUMBER OF SEQUENCES: 55
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                                                         ORIGINAL SOURCE:
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REFERENCE/DOCKET NUMBER: 5600-0001.34
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                                                                                                                                                                                                                                                                 NAME: Sholtz, Charles K. REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
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350 Cambridge Ave., Suite
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of SEQ ID NO:23 (HuIFNtau7).
                                         predicted amino acid coding sequence
of SEQ ID NO:23 (HulfNtau7).
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01-FEB-1994 (Rel. 28, Last
16-OCT-2001 (Rel. 40, Last
Cytochrome c-type protein n
NAPC OR B2202 OR 23459 OR E
                                                                                                           [2]
SEQUENCE FROM N.A.
SERAIN=K12 / MC1655;
MEDLINE=97426617; PubMed=9278503;
MEDLINE=97426617; PubMett G. III, Bloch C.A., Perna N.T., Burland V., Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Riley M., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                       Science
   SEQUENCE FROM (
STRAIN=0157:H7
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bichterich P., Lakey N.,
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P33932;
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SEQUENCE
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EMBL; M97934; -; NOT_ANNOTATED_CDS.
EMBL; S81491; AAB36225.1; -.
EMBL; S81491; AAB36227.1; ALT_SEQ.
HSSP; P42224; 1BF5.
TRANSFAC; T01494; -.
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PROSITE; PS0019
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EMBL; AE000309; AAC75262.1; --
EMBL; AE0005452; AAC57337.1; --
EMBL; AP002560; BAB36514.1; --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "A reassessment of K-12.";
Escherichia coli K-12.";
FEMS Microbiol. Lett. 119:89-94(1994).
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InterPro; IPR005126; Cyt_NNT.
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STRAIN=0157:H7
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MEDLINE=21156231; PubMed=11258796;
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HSSP; P51541; 1BG0.
WormPep; ZC434.8; CE06583.
InterPro; IPR000749; ATP-gua_Ptrans.
Pfam; PF00217; ATP-gua_Ptrans; 1.
Pfam; PF02807; ATP-gua_PtransN; 1.
PROSITE; PS00112; GUANIDO_KINASE; 1.
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01-FEB-1995 (Rel. 31, Created)

01-FEB-1995 (Rel. 31, Last sequence up

16-OCT-2001 (Rel. 40, Last annotation

Hypothetical protein ytfM precursor

YTFM OR B4220 OR 25831 OR ECS5198.
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                                                                                                 Escherichia coli, and Escherichia coli 0157:H7
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Rhabditidae; Peloder
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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nes 8; Conser
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CATALYTIC ACTIVITY: ATP + L-arginine = ADP + N-phospho-L-arginine.
SIMILARITY: BELONGS TO THE ATP:GUANIDO PHOSPHOTRANSFERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LNLVAAKA 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KPGLIKRL 14
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8; Conser
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(Rel. 36, Last sequence update)
(Rel. 38, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Pred. No. 6.6
0; Mismatches
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                                                             subdivision;
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9 ;
                                                             Enterobacteriaceae;
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RESULT 6
MCCA_ARATH
MCCA_ARATH
STANDARD; PRT; 734 AA.

ID MCCA_ARATH
STANDARD; PRT; 734 AA.

AC Q42523; Q9SA61;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Methylcrotonyl-CoA carboxylase alpha chain, mitochondrial precursor
DE (EC 6.4.1.4) (3-Methylcrotonyl-CoA carboxylase 1) (MCCase alpha
DE subunit) (3-methylcrotonyl-CoA:carbon dioxide ligase alpha subunit).
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                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
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SEQUENCE FROM N.A.
STRAIN=K12 / MG165
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000184; Bac_surray___.

Pfam; PF01103; Bac_surface_Ag; 1.

Hypothetical protein; Signal; Complete proteome.

SIGNAL 1 21

POTEMTIAL.

HYPOTHETICAL PROTEJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U14003; AAA97116.1; --
EMBL; AE0000493; AAC77177.1; --
EMBL; AE005554; AAC59418.1; --
EMBL; AP002568; BAB38621.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyi Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe I Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunac Kuhara S., Shiba T., Hattori M., Shinagawa H.; "Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12."; DNA Res. 8:11-22(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genome sequence of enterohaemorrhagic Escherichia Nature 409:529-533(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=0157:H7 / F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-0157:H7 / EDL933 / ATCC 700927;
MEDLINE-21074935; PubMed-11206551;
Perna N.T., Plunkett G. III, Burland V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EcoGene; EG12513; ytfM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Blattner F.R.; "Analysis of the region from 92.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-95334362; PubMed=7610040;
Burland V.D., Plunkett G. III, Sofia H.J.,
                                                                                                                                                                                                                                                               809
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[2]
                                                                                                                                                                                                                               466
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                                                                                                                                                                                                                                                                 LRFFAGGD
                                                                                                                                                                                                                             LRFFAGGD
                                                                                                                                                                                                                                                                                                  Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                      22
577 AA;
                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                    Pred.
                                                                                                                                                                                                                                                                                                  Mismatches
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Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

white O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

Buehler E., Chan A., Chao Q., Chen H., Cheu R.F., Chin C.W.,

Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

Chung M.K., Conn L., Conway A.B., Conway A.R., Fujii C.Y.,

Chan J. J., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

Kim C.J., Koo H.L., Kremenetskala I., Kuritz D.B., Kwan A., Lam B.,

Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

Chan X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Mazziali A.,

Militscher J., Miranda M., Nguyen M., Nierman M.C., Osborne B.I.,

A Militscher J., Miranda M., Nguyen M., Nierman M.C., Osborne B.I.,

A Mai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,

Sakano H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

Mu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.,

"Sequence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                           This
                                                                                                                                                                                                                                                                                                                                                                                                                                                              3-methylcrotonyl-CoA carboxylase.";
J. Biol. Chem. 275:5582-5590(2000).
-i- CATALYTIC ACTIVITY: ATP + 3-methylcrotonyl-CoA + HCO(3)(-) = ADP phosphate + 3-methylglutaconyl-CoA.
-i- COFACTOR: Biotin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Weaver L.M., Lebrun L., Franklin A., Huang L., Wurtele E.S., Nikolau B.J.;
"Molecular cloning of the biotinylated subunit coenzyme A carboxylase of Arabidopsis thaliana. Plant Physiol. 107:1013-1014(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shinozaki K., Davis R.W., Ecker J.R., Theologis A.; "RIKEN Arabidopsis full length cDNA clones (RAFLs) seque SSP consortium (Salk/Stanford/PGEC)."; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
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STRAINE-95.232183; PubMed-7716229;
MEDLINE-95232183; PubMed-7716229;
Lebrun L., Franklin A.,
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=cv. Landsberg erecta, and omedLINE=20148760; PubMed=10681539
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Theologis A., Ecker J.R., Palm C.J.,
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"Molecular characterization of the |
"Molecular characterization of the |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            McKean A.L., Ke J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-CV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-CV.
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                                                                                                                                                                                                                                                                                                                                             PATHWAY: Leucine catabolism.
SUBUNIT: Probably a heterodimer composed of biotin-containing alpha subunits and beta subunits (By similarity).
SUBCELLULAR LOCATION: Mitochondrial matrix.
   s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EM European Bioinformatics Institute. There are no restr by non-profit institutions as long as its content
                                                                                                                                                                                                                                                        ovaries, siliques and embryos MISCELLANEOUS: Temporal and sp
                                                                                                                                                    gene model
                                                                                                                                                                                   CAUTION: Ref. 2
                                                                                                                                                                                                                                         beta
                                                                                                                                                                                                                                                                                                                     TISSUE SPECIFICITY: In roots, cotyledons,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   408:816-820(2000).
                                                                                                                                                                                                                                   subunits during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Columbia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Columbia;
                                                                                                                                                 prediction.
                                                                                                                                                                            sequence
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                                                                                                                                                                                                                                   development
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                                                                                                                                                                                                                          spatial accumulation coment at approximately
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long
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Columbia;
                                                                                                                                                                            that
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                                                                                                                                                                                                                                                                                                                        leaves,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               man C.L., Brooks S.Y., F., Chin C.W., Creasy T.H., Dewar K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of 3-methylcrotonyl-
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y equal molar
                              restrictions
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                                                EMBL outstation
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                                                            a collaboration
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Best Local S
Matches
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                                                                                                                                                                                                        "The genome sequence of the acidophilum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NP_BIND
ACT_SITE
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                   Nature 407:508-513(2000).

-i- CATALYTIC ACTIVITY: 2 ATP + L-glutamiphosphate + L-glutamate + carbamoyl phosphate + carbamoyl phosphat
                                                                                                                                                                                                                                    Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C., Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.; "The genome sequence of the thermoacidophilic scavenger Thermoplasm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pfam; pF02785; Biotin_carb_C; 1.
pfam; pF00364; biotin_lipoy1; 1.
pfam; pF00289; CPSase_L_chain; 2.
pfam; PF02786; CPSase_L_D2; 2.
                                                                                                                                                                                                                                                                                                     MEDLINE=20479972;
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=DSM 1728;
                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=2303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carbamoyl-phosphate synthase large chain phosphate synthetase ammonia chain).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001882; Biotin_attach.
InterPro; IPR000089; Biotin_lipoyl.
InterPro; IPR000901; CPSase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                  Thermoplasmataceae;
                                                                                                                                                                                                                                                                                                                                                                                                                            Archaea; Euryarchaeota;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Thermoplasma acidophilum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 AARAVGYY
                                   SUBUNIT: Composed of two chains; the small promotes the hydrolysis of glutamine to am the large (or ammonia) chain to synthesize
                                                                                                 PATHWAY: Arginine biosynthesis. PATHWAY: Pyrimidine biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OR TA079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AARAVGYY 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THEAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC006550; AAD25800.1; AY070723; AAL50065.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS00188; BIOTIN; 1
PS00866; CPSASE_1;
PS00867; CPSASE_2;
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BELONGS TO
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                                                                                                                                                                                                                                                                                                     PubMed=11029001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biotin; ATP-binding; Transit peptide MITOCHONDRION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                          Thermoplasmata;
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THE CARB FAMILY
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V -> D (IN REF. 1).
A -> AK (IN REF. 1).
MISSING (IN REF. 1).
W -> L (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALT_SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATP (POTENTIAL).
                                                                                                                                                        + L-glutamine + CC carbamoyl phosphat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -> L (IN REF. 1).
251CACF6464B046B
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                                      synthesize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  update)
                                                                                               first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                          Thermoplasmatales;
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                                                                                                                                     (Ву
                                                         ammonia,
                                                                                                 step
                                                                                                                                       similarity)
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                                                                                                                                                                             CO(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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                                   carbamoyl phosphate (By
                                                                         (or glutamine)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRC64;
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                                                                                                                                                                           + H(2)0
                                                           which
                                                                                                                                                                                                                                      Thermoplasma
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Best Local
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InterPro: IPR005479; CPase_L_D2.
InterPro: IPR005481; CPase_L_D3.
InterPro: IPR005481; CPase_L_N.
InterPro: IPR005481; CPase_L_N.
InterPro: IPR004362; MGS_like.
Pfam: PF00289; CPSase_L_chain; 2.
Pfam: PF002786; CPSase_L_D2; 1.
Pfam: PF02787; CPSase_L_D3; 1.
Pfam: PF02787; CPSase_L_D3; 1.
                                MEDLINE-94139659; PubMed-7905822;
MEDLINE-94139659; PubMed-7905822;
Kuehnlein R.P., Frommer G., Friedrich M., Gonzalez-Gaitan M.,
Weber A., Wagner-Bernholz J.F., Gehring W.J., Jaeckle H., Schuh R.,
"Spalt encodes an evolutionarily conserved zinc finger protein of
"Spalt encodes an evolutionarily conserved zinc finger protein of
                                                                                                                                                                                                        SALM.
                                                                                                                                                                                                                          01-FEB-1995 (Rel. 31, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                   DROME
                                                                                                                                                                            Drosophila melanogaster (Fruit fly). Eukaryota; Metazoa; Arthropoda; Manc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NP_BIND
NP_BIND
METAL
                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                        SALM_DROME P39770;
                                                                                                                                                                                                                   Homeotic
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METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00866; CPSASE_1; FALSE_NEG.
PROSITE; PS00867; CPSASE_2; 2.
Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;
ATP-binding; Manganese; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P00968;
                                                                                                                                                                                                                                                                                                                                                                 626 KGVKLYAT 633
                                                                                                                                                                                                                                                                                                                                                      941 KGVKLYAT 948
                                                                                                                                                                                                                                                                                                                 œ
 FUNCTION: REQUIRED
               l structure which provides homeotic gene
region of the Drosophila embryo.";
J. 13:168-179(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Evenopean Bioinformatics Institute. There are no restroy by non-profit institutions as long as its content
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                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PR00098; CPSASE
                                                                                                                                                                                                                   protein
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153
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                                                                                                                                                                                                                   spalt-major.
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915
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 FOR THE ESTABLISHMENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP (POTENTIAL).

ATP (POTENTIAL).

ATP (POTENTIAL).

MANGANESE 1 (BY SIMILARITY).

MANGANESE 1 AND 2 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                Score 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OLIGOMERIZATION DOMAIN CARBAMOYL PHOSPHATE SY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALLOSTERIC DOMAIN
                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                     Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                     No.
                                                                                                                                                                                                                                                                                    1355
                                                                                                                                                                                                                              update)
                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                There are no restrictions ng as its content is in
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                                                                                                                                                                                                                                                                                                                                                                                                                                 1.
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THE POSTERIOR-MOST
                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                       in of
head and
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RESULT 9
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Best Local 9
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                                                                                                   MEDLINE-94139659; PubMed=7905822;
MEDLINE-94139659; PubMed=7905822;
Kuehnlein R.P., Frommer G., Friedrich M., Gonzalez-Gaitan M.,
Weber A., Wagner-Bernholz J.F., Gehring W.J., Jaeckle H., Schuh
"Spalt encodes an evolutionarily conserved zinc finger protein
"Spalt encodes an evolutionarily conserved zinc finger protein
"Spalt encodes an evolutionarily conserved zinc finger protein
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01-FEB-1995 (Rel. 31, Last seg
15-JUN-2002 (Rel. 41, Last ann
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InterPro; IPR000822; Znf_C2H2.
Pfam; PF00096; Zf.C2H2; 7.
PRINTS: PR00048; ZINCEINGER.
SMART; SM00355; ZnF_C2H2; 7.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 7.
                                                                  novel structure which provides homeotic gene tail region of the Drosophila embryo."; EMBO J. 13:168-179(1994).
                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                              NCBI_TaxID=7244;
                                                                                                                                                                                                                                                                                                                                           Drosophila virilis (Fruit fly).
Eukaryota; Metazoa; Arthropoda;
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                     FUNCTION: REQUIRED FOR THE ESTABLISHMENT HEAD AND THE ANTERIOR-MOST TAIL SEGMENTS
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DEVELOPMENTAL STAGE: FIRST EXPRESSED AT BLASTODERM
LATER IN RESTRICTED AERAS OF THE EMBRYONIC NERVOUS
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SUBCELLULAR LOCATION: Nuclear (Probable)
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01-OCT-1994 (Rel. 30, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Hydrogenase-2 operon protein hybG.
HYBG OR B2990 OR 24344 OR ECS3875.
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STRAIN=K12;
MEDLINE=97426617;
                                                           Menon N.K., Chatelus C.Y., Dervartanian M., We Shanmugam K.T., Peck H.D. Jr., Przybyla A.E., "Cloning, sequencing, and mutational analysis encoding Escherichia coli hydrogenase 2.";
                                                                                                        SEQUENCE FROM N.A.
STRAIN-K12 / TG1;
MEDLINE-94292472; PubMed-8021226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FlyBase; FBgn0013137; Dvir\salm.
InterPro; IPR000822; Znf_C2H2.
Pfam; PF00096; Zf-C2H2; 7.
                                                                                                                                                                                            Escherichia coli, and Escherichia coli 0157:H7.
                                                                                                                                                                                                        Escherichia
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PROSITE; PS50157; ZINC_FINGER_C2H2_2; 7.
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                          SEQUENCE FROM N.A
                                                                                                                                                         NCBI_TaxID-562,
                                                                                                                                                                       Escherichia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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nes 8; Conserv
                                                  Bacteriol.
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SUBCELLULAR LOCATION: Nuclear (Probable).
DEVELOPMENTAL STAGE: FIRST EXPRESSED AT BLASTODERM LATER IN RESTRICTED AERAS OF THE EMBRYONIC NERVOUS WELL AS IN THE DEVELOPING TRACHEA.
SIMILARITY: BELONGS TO THE SAL FAMILY OF C2H2-TYPE
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SM00355; ZnF_C2H2; 7.
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Conservative
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ID YGT2_YEAST
AC P53103;
DT 01-0CT-1996
DT 01-0CT-1996
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PROSITE; F
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MEDLINE-21074935; PubMed-11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; "Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12."; DNA Res. 8:11-22(2001).
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"The complete genome sequence science 277:1453-1474(1997).
   Hypothetical
                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001109; HupF_HypC. Pfam; PF01455; HupF_HypC; 1. PRINTS; PR00445; HUPFHYPC.
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EMBL; AE005529; AAG58127.1;
EMBL; AP002563; BAB37298.1;
EcoGene; EG11805; hybG.
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Mau B., Shao Y.;
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MEDLINE=21156231; PubMed=11258796;
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STRAIN=0157:H7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genome sequence of enterohaemorrhagic Nature 409:529-533(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.
                                                                                                                                                   7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: MAY HAVE A SPECIFIC ROLE IN THE MATURATION OF THE SUBUNITS OF HYD1 AND HYD2.
SIMILARITY: BELONGS TO THE HUPF/HYPC FAMILY.
                                                                                                                                                   GQVLAVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                    U09177;
U28377;
                                                                                                                                                                                                           Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                               PD003112;
                                                                                                                                                                                                                                                                                                PD003112; HupF_HypC; 1.; TIGR00074; hypC_hupF; PS01097; HUPF_HYPC; 1.
                                                                                                                                                                                                                                                                                  proteome.
                                                                                                                                                                                                                                                                     82
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   (Rel.
(Rel.
(Rel.
(Rel.
                                                                                                                                                                                                            Conservative
                                                                                                                                                   13
                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N.A.
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AAA69157.1; -.
                                                                           STANDARD;
 34,
34,
35,
kDa
                                                                                                                                                                                                                                                                     8808 MW;
                                                                                                                                                                                                                       0.8%;
Last sequence update)
Last annotation update)
protein in COX4-GTS1 in
                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kirkpatrick
                                                                                                                                                                                                                         Score 7; pred. No
                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                     8E9736BFC4EFD626 CRC64;
                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of Escherichia coli K-12.";
                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H.A.,
                                                                                                                                                                                                                         No.
                                                                         107
                                                                                                                                                                                                                         DB 1;
). 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli 0157:H7.";
                                                                         A
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 intergenic region
                                                                                                                                                                                                                                       Length
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                                                                                                                                                                                                         Gaps
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ADD DATE OF THE PROPERTY OF TH
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Y353_MYCPN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
       Hypothetical
SEQUENCE 1
                                                        SMART; SM00411; BHL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycoplasma pneumoniae Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X91489; CAA62792.1; -. EMBL; Z72704; CAA96894.1; -. SGD; S0003150; YGL182C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                  Nucleic
                                                                                                                                                                                                                                                                                                                                                                         "Complete sequence analysis of the pneumoniae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                              Himmelreich R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-ATCC 29342 / m129;
MEDLINE-97105885; PubMed-8948633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=2104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MPN529 OR MP313.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Sequencing of a 40.5 kb fragment chromosome VII from Saccharomyces Yeast 13:55-64(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-97197971; PubMed-9046087;
Coglievina M., Klima R., Bertani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-S288c / FY1679;
MEDLINE-97197971; Pubm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bruschi C.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84
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                                                                                                   AE000028; AAB95961.1;
                                                                                                                                                                                                                                                                                                                                                Acids Res.
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7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                          R.;
                                                                            IPR000119;
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107 AA; 1
       411; BHL; 1.
l protein; Complete
109 AA; 12410 MW;
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protein MG353
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                                                                         Bac_DNAbind
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          annotation
homolog (G1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                              Plagens H., Pirkl E., Li B.-C.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
proteome.
3FF862745F3C5316 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1D22E64BC819A499 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                              genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ion update)
(G12_orf109).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Delneri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
). 25;
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                                                                                                                                                                                                                                                                                                                                                                                           of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  left arm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zaccaria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          igh a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of.
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В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
                                                                                                    SPECIES=M.tuberculosis; STRAIN-CDC 1551 / Oshkosh; FleisChmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
                                                                                                                                                                                                                                  Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandram M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares S., Squares S., Squares S., Squares S., Squares Sulston J.E., Taylor K., Whitehead S., Barrell B.G., "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MP63_MYCTU STANDARD; PRT; 159 AA.
p97175; 008224;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Inmunogenic protein MP763/MPB63 precursor (Antigen kDa immunoprotective extracellular protein).
MP763 OR MPB63 OR MY1926C OR MY1977 OR MTCY09F9.38.
 SPECIES=M.tuberculosis;
                SEQUENCE OF 30-49
                                                                           "Whole genome comparison
                                                                                             Bishai W.;
                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                          Nature
                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES=M.tuberculosis; MEDLINE=98295987; PubMed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    extracellular proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES=M.tuberculosis; STRAIN=Erdmann; MEDLINE-97313166; PubMed=9169770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES=M.tuberculosis; STRAIN=H MEDLINE=97130011; PubMed=8975887
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and drug targets.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "High-level heterologous expression and secretion in rapidly growing nonpathogenic mycobacteria of four major Mycobacterium tuberculosis extracellular proteins considered to be leading vaccine candidates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MPT63, a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Harth G., Lee B.Y., Horwitz M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gennaro M.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Manca C.M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Actinomycetales; Corynebacterineae; NCBI_TaxID=1773, 1765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Actinobacteria; Actinobacteria (class);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Intect.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Molecular cloning, purification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium bovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 VATGVKE 28
                                                                                                                                                                                                                       ce genome sequence.
393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immun.
                                                                                                                                                                                         FROM N.A.
                                              (APR-2001)
                                                               strains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lyashchenko K., Wiker H.G., Usai D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antigen secreted by 65:16-23(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                65:2321-2328(1997).
                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=9634230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.08; F1
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                                              the
                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=H37Rv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-H37Rv;
                                                                           of.
                                              EMBL/GenBank/DDBJ
                                                                           Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 7; Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and serological characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacteriaceae; Mycobacterium
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                                              databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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                                                                           clinical
                                                                                                                                                                                                                                                                                                                                                                                  Harris
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                                                                           and
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                                                                                                          Α.,
                                                                                                                        S.L.,
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Eukaryota;
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P13403;
 by Toxoplasma gondii.";
Proc. Natl. Acad. Sci.
-!- SUBCELLULAR LOCATIO
                                                         SEQUENCE FROM N.A.
MEDLINE-90017513; PubMed-2798425;
Cesbron-Delauw M.F., Guy B., Torp
Cesbron J.Y., Charif H., Lepage P
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use by non-profit institutions as long a
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nagai S., Wiker H.G., Harboe M., Kinomoto M.; "Isolation and partial characterization of major protein antigens the culture fluid of Mycobacterium tuberculosis."; Infect. Immun. 59:372-382(1991).
                                                   Capron
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                                                                                                                          NCBI_TaxID=5811;
                                                                                                                                      Toxoplasma
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HOrwitz M.A., Lee B.W., Dillon B.J.,
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J; Z84498; CAB06500.1; -.
J; AE007052; AAK46249.1; -.
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or send a
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protein S7 gene of animals and human.";
(In) Plant Gene Register PGR98-203.
                                                                 Pfam; PF01251; Ribosomal_S7e; 1. ProDom; PD006276; Ribosomal_S7E; PR0SITE; PS00948; RIBOSOMAL_S7E;
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                                             Ribosomal protein. SEQUENCE 190 AA;
                                                                                                            EMBL; AF056316; AAD03501.1; EMBL; AF098519; AAC97947.1;
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Score 7; DB 1; Pred. No. 41; 0; Mismatches
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PIR; B23285; IVBOII.
HSSP; P01563; 2HIE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

Chung Y.G., Seidel G.E. Jr.;

"Cloning bovine interferon-tau genes and characterizing their

"cloning bovine interferon tau genes and characterizing their

transcriptional expression during early pregnancy.";

Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

-!- SUBCELLULAR LOCATION: Secreted.

-!- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
                                                                                                                                                                                                                                          SMART; SM00076; IFabd; PROSITE; PS00252; INTER
                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long a modified and this statement is not removed.
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                                                                                                                                                                                                                                                                     PRINTS; PR00266; INTERFERONAB. ProDom; PD000550; Interferon_a
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01-APR-1988 (Rel. 07, Last sequence update)
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"Topological analysis of the aerobic membrane-bound formate dehydrogenase of Escherichia coli.";

J. Bacteriol 180:6625-6634(1998).

-i- FUNCTION: ALLOWS TO USE FORMATE AS MAJOR ELECTRON DONOR DURING AEROBIC RESPIRATION. SUBUNIT GAMMA IS PROBABLY THE CYTOCHROME B556(FDO) COMPONENT OF THE FORMATE DEHYDROGENASE.

-i- SUBUNIT: FORMATE DEHYDROGENASE IS A MEMBRANE-BOUND COMPLEX, FOR BY SUBUNITS ALPHA, BETA AND GAMMA.
between the Swiss Institute of Bioinformathe European Bioinformatics Institute. The European Bioinformatics Institutions as long modified and this statement is not removed.
                                                                                                                      This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21156231; PubMed=11258796; Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoya Hayashi T., Makino K., Ohnishi M., Murata T., Tanaka M., Tobe 1 Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunac Kuhara S., Shiba T., Hattori M., Shinagawa H.; "Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic Acids
[2]
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01-OCT-1993
01-OCT-1993
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99069338; PubMed=9852007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch P. A., Blatter P. P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dehydrogenase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and a possible physiological role
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STRAIN-K12 / MG1655;
MEDLINE-93347969; PubMed-8346018;
Plunkett G. III, Burland V.D., Daniels D.
"Analysis of the Escherichia coli genome.
"Analysis of the By 2 minutes.";
"Engion from 87.2 to 89.2 minutes.";
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Escherichia coli 0157:H7.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                SIMILARITY: STRONG, TO FDNI.
                                                                                                                                                                                                      BY SUBUNITS
SUBCELLULAR
                                                                       SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel.
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27, Last sequence update)
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subunit) (Aerobic formate
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Tobe T.,
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Matches 7
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01-AUG-1992 (Rel. 23, Created)
01-BUG-1992 (Rel. 23, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Transcriptional regulatory protein fixj.
   InterPro;
InterPro;
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DOMAIN
                        PIR; S15167; S15167.
HSSP; P10958; 1DBW.
                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                     the
                                                                                                                                                                                                                                                              "Involvement of fixLJ in the regulation of nitrogen fixation Azorhizoblum caulinodans."; Mol. Microbiol. 5:665-673(1991).
                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                               Azorhizobium caulinodans.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
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Electron
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EMBL;
EMBL;
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                                                                                                                                                                                                                                                                                                              MEDLINE=91260451; PubMed=2046550;
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                       AND FIXK, REQUIRED FOR FIXN ACTIVATION.
SUBCELLULAR LOCATION: Cytoplasmic (Probable).
PTM: PHOSPHORYLATED BY FIXL (PROBABLE).
SIMILARITY: CONTAINS 1 RESPONSE REGULATORY DOMAIN.
                                                                                                                                                                                                                                     FUNCTION: FIXJ, WHEN ACTIVATED BY FIXL, INDUCES BOTH NIFA, REQUIRED FOR ACTIVATION OF CLASSICAL
                                                                                                                  European Bioinformatics Institute.
                                                                                                                                                                             SIMILARITY: CONTAINS 1 RESPONSE REGULATORY DOMAIN.
SIMILARITY: BELONGS TO THE LUXR/UHPA FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                     REGULATORS.
                                                                                                                SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict
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ene; EG11856; fdoI.
                                                X56658; CAA39980.1;
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  IPR000792;
IPR001789;
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SEQUENCE FROM N.A.
STRAIN-HHB / ATCC 27634;
MEDLINE-20250964; PubMed-10788522;
MEDLINE-20250964; PubMed-10788522; PubMed-107885
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DNA_BIND
SEQUENCE
                                                                                                                                                                                           EMBL; D63799; BAA33198.1; ALT_INIT.
InterPro; IPR002699; ATPSynt_Dsub.
Pfam; PF01813; ATP-synt_D; 1.
ProDom; PD004122; ATPSynt_Dsub; 1.
TIGRFAMS; TIGR00309; V_ATPase_subD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  thermophilus. Subunit structure and operon.";
J. Biol. Chem. 275:13955-13961(2000).
-i- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON GRADIENT ACROSS THE MEMBRANE.
-i- CATALYTIC ACTIVITY: ATP + H(2)0 + H(+)(In) = ADP + phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE: PS00622; HTH_LUXR_FAMILY; 1
PROSITE: PS50110; RESPONSE_REGULATORY; 1
Sensory transduction; Phosphorylation; Tra
DNA-binding; Activator; Nitrogen fixation.
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the European Bioinformatics Institute.
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Thermus thermophilus.
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Pfam; PF00196; GerE; 1.
PRINTS; PR00038; HTHLUXR.
ProDom; PD00039; Response_reg; 1.
ProDom; PD000307; HTH_LuxR; 1.
                                                                                                                                    Hydrolase;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: BELONGS TO THE V-ATPASE D SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "V-type H+-ATPase/synthase from a thermophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                197 ALLAGVA 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          721 ALLAGVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H(+)(Out)
   Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               211 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thermus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 727
                                                                                                                                 synthesis;
AA; 24677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.6.,
100.0%; F1
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                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
subunit D (EC 3.6.3.14) (V-type ATPase subunit D).
                                                                0.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                 Hydrogen ion transport.
MW; B666AE00DFE0B08B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 7; D
   0,
                                  Score 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHOSPHORYLATION (BY SIMILARITY).
H-T-H MOTIF (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESPONSE REGULATORY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          group; Deinococci; Thermales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E0F06B3EA4CD827D CRC64;
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                  No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                223
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                                                                DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                There are no restrictions on
                                                                1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Usage
   0;
                                                                Length 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            eubacterium, Thermus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADP + phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wakabayashi T.,
   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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Gaps
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KVPRLKA

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RESULT 21
COX2_ASCS!
ID COX2_A
AC P2486
DT 01-W
DT 15-U
DE CYTO
GN COII
OS ASCAI
OC ASCAI
OX NCBI,
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Best Local S
Matches 7
                                                                                                   P24882;
01-MAR-1992
01-NOV-1995
15-JUN-2002
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Ascarididae; Asc
NCBI_TaxID=6253
                        Mitochondrion .
Eukaryota; Metazoa; Nematoda;
                                                                                       Cytochrome c
                                                                                                                                                                              ASCSU
                                                                                                                                                                                                                                                                                                                                               InterPro: IPRO01454; Hlgnase/hydrlase.
Pfam; PF00702; Hydrolase; 1.
Carbohydrate metabolism; Hydrolase; Complete proteome.
SEOUTENCE 226 AA; 24560 MW; 83F95B10DBF53CB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                          Ascaris suum
                                                                                                                                                             COX2_ASCSU
                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE004329; AAF95765.1; -. TIGR; VC2624; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-El Tor N16961 / Serotype 01;
MEDLINE:20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                McDonald L., Utterback T., Salzberg S.L., Smith H.O., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cholerae
                                                                                                                                                                                                                                                                 241 AARAVGY 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 406:477-483(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-EL TOT N16961 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria;
NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vibrio cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phosphoglycolate phosphatase (EC GPH OR VC2624.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9KNV6;
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GPH_VIBCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUN-2002 (Rel.
15-JUN-2002 (Rel.
                                                                                                                                                                                                                                       29
                                                                                                                                                                                                                                                                                               Local Similarity
les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phosphate.
SIMILARITY: BELONGS TO THE CBBY/CBBZ/GPH/YIEH FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         an email to license@isb-sib.ch).
                                                                                                   (Rel.
                                                                                                                                                                                                                                                                                               Conservative
                                                        (Pig roundworm)
                                                                                     oxidase
                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                  21, Created)
32, Last sequence up
41, Last annotation
                                                                                    polypeptide
                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                           0.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last annotation update)

hatase (EC 3.1.3.18) (PGP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2-phosphoglycolate + H(2)0 = glycolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gamma subdivision; Vibrionaceae; Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence update)
                                                                                                                                                                                                                                                                                            0;
                                                       (Ascaris lumbricoides).
                                                                                                                                                                                                                                                                                                          Score 7; DB 1;
Pred. No. 49;
                        Chromadorea; Ascaridida; Ascaridoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                            Mismatches
                                                                                    ation update)
II (EC 1.9.3.1).
                                                                                                                 update)
                                                                                                                                                            232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           226 AA
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                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                     Length 226;
                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                           Gaps
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RSTA_ECOLI
ID RSTA_E
AC P52108
AC P52108
DT 01-0CT
DT 15-JUh
DE Transa
GN RSTA (
OS Eschei
OC Bactei
OC Bactei
OC NCBL_T
RN [1]
RN [1]
RP SEQUEI
                                                                                                                                                                                                                                                                                                                 В
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                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                Matches
                                                                                                P52108;
01-OCT-1996
01-OCT-1996
15-JUN-2002
                                     Bacteria; Proteobacteria; Escherichia.
                                                                      Transcriptional regulatory protein RSTA OR URPT OR B1608.
                                                                                                                                                                                                                                                                                                                                         METAL
METAL
                                                              Escherichia coli
                                                                                                                                                   RSTA_ECOLI
                                                                                                                                                                                                                                                                                                                            METAL
                                                                                                                                                                                                                                                                                                                                                                 METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                   ProDom; PD000131; Copper_CuA; 1.

PROSITE; PS00078; COX2; 1.

Oxidoreductase; Copper; Mitochondrion; Transmembrane; Inner membrane; Electron transport; Respiratory chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002429; Cyt_c_ox_2.
Pfam; PF00116; COX2; 1.
Pfam; PF02790; COX2_TM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genetics 130:471-498(1992).

-!- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. SUBUNIT 2 TRANSFERS THE ELECTRONS FROM CYTOCHROME C VIA ITS BINUCLEAR COPPER A CENTER TO THE BIMETALLIC CENTER OF THE CATALYTIC SUBUNIT 1.
                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; S26023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X54253; CAA38172.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Body wall muscle, and Egg;
MEDLINE=92201635; PubMed=1551572;
Okimoto R., Macfarlane J.L., Clary D.O., Wolstenholme D.R.;
"The mitochondrial genomes of two nematodes, Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001505; Copper_CuA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and Ascaris suum."
                                                                                                                                                                                                               208 SEMPVAL 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                           11 SEMPVAL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inner membrane.
SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE SUBUNIT 2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Integral membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            + 2 H(2)0
                                                                                                                                                                                                                                                              Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                              31
53
70
90
164
199
203
203
232 AA;
                                                                                               (Rel. 34, Created)
(Rel. 34, Last sequence up
(Rel. 41, Last annotation
                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S26023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Copper A
                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                            30
52
69
89
232
164
199
203
                                                                                                                                                                                                                                                                                                               26517 MW;
                                                                                                                                                                                                                                                                           0.8%;
                                                gamma
                                                                                                                                                                                                                                                                       Score 7; D
                                                                                                                                                                                                                                                              0;
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COPPER A
                                                                                                                                                                                                                                                                                                                                                             MITOCHONDRIAL INTERMEMBRANE COPPER A (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                 MITOCHONDRIAL MATRIX (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                            MITOCHONDRIAL
                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                               58F9B683FF9DA4C5 CRC64;
                                                subdivision;
                                                                                                                                                                                                                                                              Mismatches
                                                                                   ion update)
                                                                                                                                                242
                                                                                                                                                                                                                                                                   DB .
                                                                                                                                                                                                                                                                                                                            (PROBABLE)
                                                                                                                                                                                                                                                                                                                                        (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                   (PROBABLE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              as its content
                                                                                                                                                                                                                                                                                                                                                                                                                          INTERMEMBRANE (POTENTIAL)
                                                Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein.
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                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                       Length 232
                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mitochondrial
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                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a collaboration
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LDRSVDV

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                                                                                Query Match
Best Local S
Matches 7
                                                                                                                                                                     EccGene; EG13190; rstA.

InterPro; IPR001789; Response_reg.
InterPro; IPR001867; Trans_reg_C.
Pfam; PF00072; response_reg; 1.
Pfam; PF00486; trans_reg_C; 1.
ProDom; PD000039; Response_reg; 1.
ProDom; PD000039; Trans_reg_C; 1.
                                                                               MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                       EMBL;
EMBL;
HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97251357; PubMed=9097039;
Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
Aiba H., Baba T., Fujita K., Hayashi K., Kitakawa M.,
Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M.,
Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori
Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y.,
Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S.,
Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C.,
Yamamoto Y., Horiuchi T.;
                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 28.0\text{-}40.1 min region on the linkage m DNA Res. 3:363-377(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H:A., Goeden M.A., Rose D.J.,
                                                                                                                     Sensory transduction; Phosphorylation; DNA-binding; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-92356829; PubMed-1495392; Roecklein B.A., Kuempel P.L.;
                                                                                                                                               PROSITE; PS50110; RESPONSE_REGULATORY;
                                                                                                                                                              SMART; SM00448; REC;
                                                                                                                                                                                                                                                                                                                                                                                                                         between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "In vivo characterization
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mau B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
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334 LDRSVDV 340
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SIMILARITY: CONTAINS 1 RESPONSE REGULATORY DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: MEMBER OF THE TWO-COMPONENT REGULATORY SUBCELLULAR LOCATION: Cytoplasmic (Potential). PTM: PHOSPHORYLATED BY RSTB (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Microbiol.
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                                                                                                                                                                                                                                                                                    D90804; BAA15356.1; -.
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                          Conservative
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                       red. No. 52;
Mismatches
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52;
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CLDI_MOUSE
ID CLDI_MOUSE STANDARD;
PAC P56857; Q91ZZ1; Q91ZZ0; Q91ZY9;
DT 30-MAY-2000 (Rel. 39, Created)
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CLDI_HUMAN
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                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00822; PMP22_Claudin; 1. PROSITE; PS01346; CLAUDIN; 1. Tight junction; Transmembrane; A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genew; HGNC:2039; CLDN18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF221069; AAF26448.1; -. EMBL; AF349452; AAL15637.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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isoforms through alternative splicing.";
Mol. Cell. Biol. 21:7380-7390(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Niimi T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-2000 (Rel.
30-MAY-2000 (Rel.
15-JUN-2002 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P56856; Q96PH4; 30-MAY-2000 (Re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001832; Claudin
InterPro; IPR004031; PMP22_Cl
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                                                                                                                                                                                                       404 LOAVRAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: COMPONENT OF TIGHT JUNCTION (TJ) STRANDS.
SUBCELLULAR LOCATION: Integral membrane protein.
ALTERNATIVE PRODUCTS: 2 isoforms; Al (shown here) and A2;
produced by alternative splicing.
TISSUE SPECIFICITY: Concentrated at the cell-cell borders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           epithelial cells.
SIMILARITY: BELONGS TO THE CLAUDIN FAMILY.
                                                                                                                                                             LQAVRAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nagashima K., Ward J.M., .C., Kimura S.;
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41,
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Pred. No.
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SVFQYYEGLMRSCVRQSSGFTECRPYFTI -> MAVTACOGL
GFVVSLIGIAGIIAATCMDQWSTQDLYNNPVTAVENYQGLW
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EMBL; AF349450; AAL15635.1; --
EMBL; AF349451; AAL15636.1; --
EMBL; AF349453; AAL15638.1; --
MGD; MGI:1929209; Cldn18
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TRANSMEM 7
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InterPro: IPR004031; PMP22_Claudin.
Pfam; PF00822; PMP22_Claudin; 1.
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Mol. Cell. Biol. 21:7380-7390(2001).
-I- FUNCTION: COMPONENT OF TIGHT JUNCTION (TJ) STRANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      homeodomain transcription factor,
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Integral membrane protein.
ALTERNATIVE PRODUCTS: 4 isoforms; al.1 (shown here),
and A2.2; are produced by alternative splicing.
SIMILARITY: BELONGS TO THE CLAUDIN FAMILY.
                                                                                                                                                                                                                                                                                         LQAVRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  musculus
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)2 (Rel. 41, 1)2 (Rel. 41, 1)2 (Rel. 41, 1)2 (Rel. 41, 1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 264 AA;
                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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etazoa; Chordata;
theria; Rodentia;
                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transmembrane; Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLAUDIN;
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Last annotation updat
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AVFQYEGLWRSCVQQSSGFTECRPYFTI -> MSVTACQGL
GFVVSLIGFAGIIAATCMDQWSTQDLYNNPVTAVFNYQGLW
RSCVRESSGFTECRGYFTL (IN ISOFORM A2.1 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A2.2)
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                       update
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stomach-specific
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                                                                                                                                                                                                                                                                                                            RESULT
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Best Local S
Matches 7
                                           Masai E., Kata
Morohoshi N.;
"Cloning and s
                                                                                                                                                                                                                         01-AUG-1992
01-DEC-1992
01-NOV-1995
  "Cloning and sequencing of the geenzyme that cleaves beta-aryl eth
J. Bacteriol. 173:7950-7955(1991)
-i- FUNCTION: ABLE TO DEGRADE VAR
                                                                   MEDLINE=92078104; PubMed=1744051; Masai E., Katayama Y., Kawai S.,
                                                                                                 STRAIN-SYK-6;
                                                                                                                                                        Sphingomonas
                                                                                                                                                                  Pseudomonas paucimobilis
Bacteria; Proteobacteria;
                                                                                                           SEQUENCE FROM N.A.,
                                                                                                                                                                                                             Beta-etherase
                                                                                                                                          NCBI_TaxID=13689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00156; Pribosyltran; 1.

PROSITE; PS00103; PUR_PYR_PR_TRANSFER; FALSE_NEG.
DNA-binding; Transcription regulation; Repressor;
SEQUENCE 271 AA; 30361 MW; 04614AA24E1C4BCD CF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000836; PRTransferase.
InterPro; IPR002375; Pr/py_rp_transf.
Pfam; PF00156; Pribosyltran: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                               LIGE_PSEPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AJ222642; CAA10902.1; EMBL; AE006455; AAK06357.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES-L.1.lactis; STRAIN-IL1403; MEDLINE-21235186; PubMed-11337471; Bolotin A., Wincker P., Mauger S., Jai Weissenbach J., Ehrlich S.D., Sorokin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (AUG-1997) to -!- FUNCTION: CONTROLS T BIOSYNTHETIC GENES (-!- SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kilstrup M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lactococcus lactis (subsp. lactis) (Streptococcus lactis), an Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris) Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES=L.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome Res. 11:731~753(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. lactis IL1403.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                              722 LLAGVAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BIOSYNTHETIC GENES (By similarity).
SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE PHOSPHORIBOSYLTRANSFERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                   LLAGVAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a collab
een the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 7; Conser
                                                                                                                                                                                                       (Rel. 23 Created)
(Rel. 24, Last sequence update)
(Rel. 32, Last annotation update)
se (Beta-aryl ether cleaving enzym
                                                                                                                                                                                                                                                                                                                                                                                                    0.8%;
ilarity 100.0%;
Conservative
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 TO DEGRADE VARIOUS
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                                                                                                             SEQUENCE
                                                                                                                                                            (Sphingomonas paucimobilis).; alpha subdivision; Sphingomonadaceae;
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                            ether.";
                                                                                                                                                                                                                                                                              PRT;
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DIMERIC LIGNIN COMPOUNDS
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                                        Ω
                                                                                                                                                                                                         enzyme).
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                                      Pseudomonas paucimobilis
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                                                                                                                                                                                                                                                                                                                                                                                                                              Length 271;
                                                                   Yamasaki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete
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RESULT 27
YITT_BACSU
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Best Local S
Matches 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                Levine A., Vannier F., Roche B., Autret "A 10.3 kbp segment from nprB to argJ at Bacillus subtilis chromosome.";
                                                                                                                                                                                                                                                                                                                                                                                                              Shiga Y., Yamagata H., Udaka S.;
"Characterization of the gene encoding an intracellular proteinase inhibitor of Bacillus subtilis and its role in regulation of the major intracellular proteinase.";
J. Bacteriol. 175:7130-7137(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A43749; A43749.
InterPro; IPR004046; GST_Cterm.
InterPro; IPR004045; GST_Nterm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
MEDLINE-98044033; PubMed-9384377;
Kunst F., Ogasawara N., Moszer I.
                                                                                                                       Medina N., Vannier F., Roche B., Aut: "Sequencing of regions downstream of degrees) in Bacillus subtilis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M69107;
EMBL; D11473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities
                                          STRAIN-168;
                                                                                                                                                                               MEDLINE-98015415; PubMed-9353931;
                                                                                                                                                                                                                                                                                                                                MEDLINE=97177785; PubMed-9025291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID-1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein YITT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase; Lignin degradation; INIT_MET 0 0
                                                              SEQUENCE FROM N.A.
                                                                                                  Microbiology 143:3305-3308(1997)
                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                 Microbiology 143:175-177(1997).
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=168 / DB104;
MEDLINE-94042884; PubMed-8226659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              161 VPPTLEP 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    153 VPPTLEP 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity les 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Inner membrane-associated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF00043; GST_C; 1.
PF02798; GST_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            280 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA25878.1; -. BAA02032.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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Pred. No
                                                                                                                                           B., Autret S.,
tream of addA (
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  Albertini A.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  No.
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e 102 (
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and citG (289
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ARC PRINT REPORT OF THE PR

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RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S., Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., RA Choi S.K., Codani J.J., Pabret C., Ferrari E., Foulger D., RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D., RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D., RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D., RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D., Colim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G., RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G., RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C., RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C., RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M., Klein C., Medigue C., RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M., RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A. M., RA Parsecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S., RA Sato T., Schleich S., Schroeter R., Scoffone F., Takahashi H., Takemaru K., RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A., RA Yoshida K., Yoshikawa H., F., Zumstein E., Wedler H., Weitzenegger T., The Complete genome sequence of the Gram-positive bacterium Bacillus T., Schlings R., Scoffone Sequence of the Gram-positive bacterium Bacillus Subtilis.",
                                                RESULT 28
THTR_HUMAN
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AC
                                                                                                                      В
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                                                                                                                                                                                        Matches
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Best Local
THTR_HUMAN
Q16762;
15-JUL-1998
                                                                                                                                                                                                                                                          CONFLICT
SEQUENCE
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CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                              TRANSMEM TRANSMEM TRANSMEM
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EMBL; Y09476; CAA70630.1;
EMBL; Z79580; CAB01834.1;
EMBL; Z99109; CAB12952.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 390:249-256(1997).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: TO B.SUBTILIS YPJC AND YQFU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF02588; DUF161; 1.
Hypothetical protein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Subtilist; BG10850; yitT. InterPro; IPR003740; DUF161.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; A49921;
                                                                                                                  70 LNAAGLN :
                                                                                                                                                                                        Similarity 7; Conserv
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54
80
151
121
121
226
278
 (Rel.
                                                                                                                                                                                          Conservative
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                                  STANDARD;
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171
121
121
226
278
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100.0%; Pr/
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V -> D (IN REF.
V -> L (IN REF.
R -> T (IN REF.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                        V -> D (IN REF. 1).
V -> L (IN REF. 1).
R -> T (IN REF. 1).
4BF98B12B8DA59E7 C
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Mismatches
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MBL outstation -
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RA Clamp M. Smink L.J., Hunta A.R., Collins J.E., Brusklewich R., Beasre D.M.,
RA Bagguley C., Balley J., Barlow K.F., Bates K.N., Beasley O.P.,
RA BIrd C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
RA Burtill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
Clegy S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.
RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
RA Life G.R., Goward M.E., Graffam D.V., Griffiths M.N.D., Hall C.,
RA Hall R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S.,
RA Hall R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S.,
RA Hall R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S.,
RA Hall R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S.,
RA Martyn I.D., Mashreghi-Mchammadi M., Matthews L.H., McCann O.T.,
RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.,
RA Martyn I.D., Mashreghi-Mchammadi M., Matthews L.H., McCann O.T.,
RA Woldin M., Wall M., Skuce C.D., Smalley S., Smith M.L.,
RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
RA Williams S., L., Williams S.A., Williamson H., Williams T.E., Wilming L.,
RA Wilght C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
RA Wang O., Wang Y., Wang Z., White J., Wallier T.E., Wilming L.,
RA Wang O., Wang Y., Wang Z., White J., Wallier N., Shoan D., Song L.,
RA Wang O., Wang Y., Wang Z., White J., Williams D., Wu H., Yao Z.,
RA Mang O., Wang Y., Wang Z., White J., Williams D., Wu H., Yao Z.,
RA Mang O., Wang Y., Wang Z., White J., Williams D., Wu H., Yao Z.,
RA Mang O., Wang Y., Wang Z., White J., Williams D., Wu H., Yao Z.,
RA Mang O., Wang Y., Wang Z., White J., Williams D., Wu H., Yao Z.,
RA Mang O., Wang Y., Wang Z., White J., Williams D., Wu H., Yao Z.,
RA Mang O., Wang Y., Wang Z., White J., Williams D., Wu H., Yao Z.,
RA Mang O., Wang Y., Wang Z., White J., Williams P., Rawkins J.,
RA McCannon D., Demils G., Bentley D., Bentley D., Rohlfing T.,
RA McCannon D., Coca
                                                                                                                                                                                                         Wilkinson P., Bodenter...

Tilahun Y., Wright H.;

Tilahun Y., wright H.;
                                                                                                                                               Strausberg R.
                                                                                                                                                                   TISSUE~Uterus;
                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-97223398; PubMed=9070219;
Aita N., Ishii K., Akamatsu Y., Ogasawara Y., Tan
"Cloning and expression of human liver rhodanese
Biochem. Biophys. Res. Commun. 231:56-60(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-20057165;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HOMO sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thiosulfate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-9606;
ACTIVITY (BY SIMILARITY) CATALYTIC ACTIVITY: Thio SUBUNIT: MONOMER.
                                        mitted (JUI-2001) to the EMBL/GenBank/DDBJ databases. FUNCTION: FORMATION OF IRON-SULFUR COMPLEXES, CYANIDE DETOXIFICATION OR MODIFICATION OF SULFUR-CONTAINING ENZYMES OTHER THIOL COMPOUNDS, BESIDES CYANIDE, CAN ACT AS SULFUR ICACCEPTORS. ALSO HAS WEAK MERCAPTOPYRUVATE SULFURTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hunt A.R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sulfurtransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=10591208; R., Collins J.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata;
Primates;
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Last annotation update)
nsferase (EC 2.8.1.1) (Rhodanese).
             Thiosulfate +
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi;
             cyanide -
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                                          SULFURTRANSFERASE (MST)
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         sulfite
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           +
     thiocyanate
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RESULT 29
THTR_MOUSE
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                                                                                                                                                                                                               P52196;
01-OCT-1996;
30-MAY-2000
30-MAY-2000
                            recombinant protein expression.";
Biochem. Biophys. Res. Commun. 216:1101-1109(1995)
-!- FUNCTION: FORMATION OF IRON-SULFUR COMPLEXES A
DETOXIFICATION.
-!- CATALYTIC ACTIVI:
-!- SUBUNIT: MONOMER
                                                          SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE=Liver;
MEDLINE=96074596; PubMed=7488186;
Dooley T.P., Nair S.K., Garcia R.E., Courtney B.C.;
"Mouse rhodanese gene (Tst): cDNA cloning, sequencing,
                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                        Mammalia;
                                                                                                                                                                  Eukaryota;
                                                                                                                                                                               Mus musculus
                                                                                                                                                                                                      Thiosulfate
                                                                                                                                                                                                                                                                THTR_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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InterPro; IPR001307; Rhodanese.
Pfam; PF00581; Rhodanese; 2.
SMART; SM00450; RHOD; 2.
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                                                                                                                                                                                                                                                                                                                           256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                          VALAAYL 262
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DOMAIN: THE STRUCTURE CONSISTS OF 2 DOMAINS OF VERY SIMILAR CONFORMATION, SUGGESTING A COMMON EVOLUTIONARY ORIGIN. HOWEN THE SEQUENCES OF THE 2 DOMAINS ARE VERY DIFFERENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SM00450;
                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  an email to license@isb-sib.ch).
                                                                                                                                                      ; Metazoa; Chordata;
Eutheria; Rodentia;
                                                                                                                                                                                                                (Rel.
                                                                                                                                                                                                                                       (Rel.
                                                                                                                                                                                                    sulfurtransferase
                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143
159
186
                                                                                                                                                                                                                                                                                                                                                                                                                                              249
                                                                                                                                                                              (Mouse).
         ACTIVITY:
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                                                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RHOD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH10148.1; -.
                                                                                                                                                                                                               34, Created)
39, Last sequences
39, Last annotations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142
158
296
186
                                                                                                                                                                                                                                                                                                                                                                                                                                              249
                                                                                                                                                                                                                                                                                                                                                                                                                       33297
                                                                                                                                                                                                                                                                                                                                                                                  0.8%;
                                                                                                                                                                                              Last sequence update)
Last annotation update)
nsferase (EC 2.8.1.1) (Rhodanese).
    Thiosulfate + cyanide = sulfite + thiocyanate.
                                                                                                                                                                                                                                                                                                                                                                                                                      WW.
                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                             Score 7; Dr
                                                                                                                                                  Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                SUBSTRATE (THIOSULFATE) BINDING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBSTRATE (THIOSULFATE) BINDING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B DOMAIN.
MAY PLAY A ROLE IN
                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 62
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ВУ
                                                                                                                                                                                                                                                                                                                                                                                                                  872C52008AE8DC5B CRC64;
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                                                                                                                                                  Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                                                                                                                                                                           Length 296,
                               AND CYANIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBSTRATE BINDING
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                                                                                                                                                               Euteleostomi;
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                                                                 and
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RESULT 30
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Best Local
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MEDIINE-98295987; PubMed-9634230; Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harri Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Bavies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
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HSSP; P00586;
SWISS-2DPAGE;
                                                                                                                                                                                              30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
34 kDa antigenic protein homolog.
RW0954 OR MT0981 OR MTCY10D7.20C.
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ACT_SITE
                                                                                                               SEQUENCE FROM N.A.
STRAIN-H37RV;
                                                                                                                                                 Actinomycetales;
NCBI_TaxID=1773;
                                                                                                                                                                          Mycobacterium tuberculosis. Bacteria; Actinobacteria; I
                                                                                                                                                                                                                                                                          34KD_MYCTU
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InterPro; IPR001763; Rhodanese-like.
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TISSUE SPECIFICITY: FOUND IN NUMEROUS TISSUES.

DOMAIN: THE STRUCTURE CONSISTS OF DOMAINS OF VERY SIMILAR COMFORMATION, SUGGESTING A COMMON EVOLUTIONARY ORIGIN. HOWEVER, THE SEQUENCES OF THE 2 DOMAINS ARE VERY DIFFERENT.

SIMILARITY: BELONGS TO THE RHODANESE FAMILY.
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PS00683;
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ilarity 100.0%;
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TRANSMEM 42
TRANSMEM 77
                                                        Fuchs T., Malecova B., Linhart C., Sharan R., Khen M., Herwig R., Shmulevich D., Elkon R., Steinfath M., O'Bien J.K., Radelof U., Lehrach H., Olender Z., Gluesman G., Lancet D., Shamir R., "DEFOG: a practical scheme for deciphering families of genes."; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: PUTATIVE DOORANT RECEPTOR.

-i- SUBCELLULAR LOCATION: Integral membrane protein.

-i- SUBCELLULAR LOCATION: OF AMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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or send a
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
-!- SUBCELLULAR LOCATION: Integral membrane protein (Po
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-CDC 1551 / Oshkosh; Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Fleischmann R.D., Haland D., Eisen J.A., Carpenter L., Hickey E., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
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Q96RD3;
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                                                                                                                                                                                     SEQUENCE OF 70-287 FROM N.A
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15-JUN-2002 (Rel. 41, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Olfactory receptor 52E6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Deciphering the biology of complete genome sequence."; Nature 393:537-544(1998).
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42 62 POTENTIAL.

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303 AA; 30204 MW; 4FE18A0771
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Metazoa; Chordata; C
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"Genome sequence and analysis of the oral bacterium Fusobacterium nucleatum strain ATCC 25586.",
J. Bacteriol. 184:2005-2018(2002).
-1- FUNCTION: Exhibits a S-adenosyl-dependent methyltransferase activity (By similarity).
              the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                          15-JUN-2002 (Rel. 41, Last sequence update)
S-adenosyl-methyltransferase mraw (EC 2.1.1
MRAW OR FN1711.
                                                                                                                                                                                                 MEDLINE-21886394; PubMed-11889109;
                                                                                                                                                                                                                                                                                                 MRAW_FUSNN STANDARD;

08R6F5;

15-JUN-2002 (Rel. 41, Created)

15-JUN-2002 (Rel. 41, Last seq

15-JUN-2002 (Rel. 41, Last ann
                                                                                                                                                                                    Kapatral V., Anderson I., Ivanova N., Reznik G., Los T.,
                                                                                                                                                                                                                                                     Fusobacterium nucleatum (subsp. nuclea
Bacteria; Fusobacteria; Fusobacterium.
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   01-FEB-1994 (Rel. 28, I
16-OCT-2001 (Rel. 40, I
Octaprenyl-diphosphate
                                          01-FEB-1991
                                                         P19641;
                                                                   ISPB_
                                                                                                                                                                                                                                             InterPro; IPR000683; GFO_IDH_MOCA_C.
InterPro; IPR004104; GFO_IDH_MOCA_C.
Pfam; PF01408; GFO_IDH_MOCA; 1.
Pfam; PF02894; GFO_IDH_MOCA_C; 1.
                                                                                                                                                                                                                            Oxidoreductase; NAD. SEQUENCE 317 AA;
                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1996
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P49307;
01-FEB-1996
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                                                                                                                                                                                                                                                                                                                                                                                                              ROSSBACH S., Kulpa D.A., ROSSBACH U., de Bruijn F.J.;
"Molecular and genetic characterization of the rhizopine catabolism
(mocABRC) genes of Rhizobium mellioti L5-30.";
MOL Gen. Genet. 245:11-24(1994)
-1- FUNCTION: COULD CATALYZE THE NADH-DEPENDENT DEHYDROGENASE REACTION
INVOLVED IN RHIZOPINE (L-3-O-METHYL-SCYLLO-INOSAMINE) CATABOLISM.
                                                                                                                                                                                                                                                                                                  EMBL; X78503; CAA55269.1;
                                                                                                                                                   752 GSSGLVS 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=95147842; PubMed=7845353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RHIME
                                                                                                                              220 GSSGLVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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(Rel. 17, Created)
(Rel. 28, Last sequence update)
(Rel. 40, Last annotation updat
diphosphate synthase (EC 2.5.1.-
                                                                                                                                                                            Conservative
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(Rel. 33, Last sequence up)
(Rel. 40, Last annotation
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(Octaprenyl pyrophosphate

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Blochem. Blophys. Res. Commun. 202:340-345(1994).
Blochem. Blophys. Res. Commun. 202:340-345(1994).
-i- FUNCTION: SUPPLIES OCTAPRENVL DIPHOSPHATE, THE PRECURSO:
-i- FUNCTION: SUPPLIES OF THE ISOPRENOID QUINONES UBIQUINONE AND ME:
-i- SIMILARITY: BELONGS TO THE FPP/GGPP SYNTHETASES FAMILY.
                                                                                                                                                                                                                                EMBL; D13267; -; NOT ANNOTATED_CDS.
EMBL; U18997; AAA57988.1; -
EMBL; AE000399; AAC75219.1; -
EMBL; X68873; CAA48735.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                          the
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Nakagawa T., Kawamukai M., Matsuda H.;
"The identification of Escherichia coli ispB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Choi Y.-L., Nishida T., Kawamukai M., Utsumi R., Sakai H., K
"Cloning and sequencing of an Escherichia coli gene, nlp, hi
homologous to the ner genes of bacteriophages Mu and D108.";
J. Bacteriol. 171:5222-5225(1989).
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"The complete genome sequence Science 277:1453-1474(1997).
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MEDLINE=97426617; PubMed=9278503;
Blattner F.R. Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Gloning and nucleotide sequencing of the genes, ribosomal proteins L21 and L27 of Escherichia co. DNA Seq. 4:59-67(1993).
                                                                                                                                                                             Pfam;
                                                                                                                                                                                                         EcoGene;
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                                                                                                                                                                                          InterPro;
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MEDLINE=94146411; PubMed=8312607;
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10: EGI0017; ispB.

Pro; IPR00092; Polyprenyl_synt.

PF00348; polyprenyl_synt; 1.

ITE; PS00444; POLYPRENYL_SYNTHET_2; 1.

ITE; PS00723; POLYPRENYL_SYNTHET_1; 1.

ITE; PS00723; POLYPRENYL SYNTHET_1; 1.

Tenne biosynthesis; Transferase; Complete proteome.

15217 MW; 08AD7AE7AC230EF8 CRC64;
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a coli.";
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ID E13K_TOBAC

STANDARD;

PRT; 331 AA.

AC P52398;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-JUL-1999 (Rel. 34, Last annotation update)

DT 15-JUL-1999 (Rel. 34, Last annotation update)

DT 16-JUL-1999 (Rel. 34, Last annotation update)

DT 16-JUL-1999 (Rel. 34, Last annotation update)

DT 16-JUL-1996 (Rel. 34, Last sequence update)

DT 16-JUL-1996 (Rel. 34, Created)

DT 16-JUL-1996 (Rel. 34, Last sequence update)

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Pfam; PF00332; Glyco_hydro_17; 1.
PROSITE; PS00587; GLYCOSYL_HYDROL F1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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SIGNAL
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Plant Physiol. 96:390-397(1991).
-!- FUNCTION: IS THOUGHT TO BE AN IMPORTANT PLANT DEFENSE-RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-cv. Xanthi NC; TIS Ward E.R., Payne G.B., MC Sharkey K.C., Beck J.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOD_RES
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INDUCTION: BY VIRAL INFECTION.
SIMILARITY: BELONGS TO FAMILY 17 OF GLYCOSYL HYDROLASES
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TISSUE SPECIFICITY: IS EXPRESSED PRIMARILY IN EPIDERMAL CELL
HEALTHY PLANT, AND FOLLOWING INDUCTION BY ETHYLENE, ACCUMULAS
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PRODUCT AGAINST FUNGAL PATHOGENS.
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Glycosidase; Signal; Multigene
potenvial.
27 331 GLUCAN ENDO-1
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"Crystallographic and blochemical analyses of Haemophilus influenzae Fe(3+)-binding protein. Blochemistry 40:15631-15637(2001).

-I- FUNCTION: THIS PROTEIN MAY BE A CENTRAL CC ACOULSTION SYSTEM.

-I- SUBCELLULAR LOCATION: Periplasmic.

-I- SUBCELLULAR LOCATION: Periplasmic.

-I- SIMILARITY: BELONGS TO THE BACTERIAL EXTRA
                                                                                                                                         Bruns C.M., Anderson D.S., Vaughan McRee D.E., Mietzner T.A.,
                                                                                                                                                               Bruns
                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (1.75 ANGSTROMS) OF 24-332.
MEDLINE-21614394; PubMed-11747438;
                                                                                                                                                                                                                                     Mietzner T.A., McRee D.E.;
"Structure of Haemophilus influenzae Fe(+3)-binding
                                                                                                                                                                                                                                                                                                                           Gray C., Fountoulakis M.; "Two-dimensional map of the proteome of Haemophilus Electrophoresis 21:411-429(2000).
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 24-31.
MEDLINE=20137488; Pubv
                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS)
MEDLINE-98025060; PubMed-9360608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-Rd / KW20 / ATCC 51907;

MEDLINE-95350630; PubMed-7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F. Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M. McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weldman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                   convergent
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Identification of two iron-repressed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-NTHI TNIUD;
MEDLINE-95012644; PubMed-7927717;
MEDLINE-95012644; PubMed-7927717;
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01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Iron-utilization periplasmic protein precursor binding protein) (FBP) (Iron-regulated 40 kDa p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Whole-genome random sequencing and assembly of Haemophilus influenzae
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Bacteria; Proteobacteria;
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        CAUTION:
                    PROTEIN FAMILY
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                                                                                                                                                                                                                 evolution within a superfamily t. Biol. 4:919-924(1997).
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RESULT 37
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the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                               Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burl Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose Mau B., Shao Y.;
                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                           Science
                                                                                                                                                      MEDLINE=97426617; PubMed=9278503;
                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN=K12 / MG1655;
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16-OCT-2001 (Rel.
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EMBL; S72674; AAB32110.1;
PIR; A41833; A41833.
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BP_bacterial_1; 1.

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transport; Periplasmic; s
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                                                                                                Escherichia coli K-12.";
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Heng H.H.Q., Kolakowski L.F. Jr., Lynch K.R., George S.R.;
"Cloning and chromosomal mapping of four putative novel human
                                                                                                                                                                                                                                                                                                                                                                                                               Genew; HGNC:4476; GPR21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G-protein-coupled receptor genes."; Gene 187:75-81(1997).
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Mammalia; Eutheria;
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nes 7; Conser
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TISSUE SPECIFICITY: NOT DETECTED IN THE BRAIN REGIONS THALAMUS,
PUTAMEN, CAUDATE, FRONTAL CORTEX, PONS, HYPOTHALAMUS, HIPPOCAMP
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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2 (Rel. 41, Last annotation update)
protein-coupled receptor GPR21.
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347 AA;
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(Rel. 35, Last sequence up
(Rel. 41, Last annotation
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receptor;

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Primates;
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1 POTENTIAL.
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s; Pred. No. 72;
0; Mismatches
                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL PROTEIN YPFG; 1E75666CE3E066FF CRC64;
                 EXTRACELLULAR (POTENTIAL)
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
                                                                                                         CYTOPLASMIC 4 (POTENTIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                         (POTENTIAL).
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72;
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                                                                                                                             (POTENTIAL).
  (POTENTIAL)
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RESULT 39
HRCA_CAUCR
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Best Local
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P54305;
01-OCT-1996
                                                                                                                                                                                                                                                                                        Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B., DeBoy R.T., Dodson R.J., Durin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K., Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O., Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.; "Complete genome sequence of Caulobacter crescentus."; "Complete genome sequence of Caulobacter crescentus."; Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

-I- FUNCTION: NEGATIVE REGULATOR OF CLASS I HEAT SHOCK GENES (GRPE-DRAK-DRAJ AND GROELS OPERONS). PREVENTS HEAT-SHOCK INDUCTION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
CARBOHYD
EMBL; U33324; AAB01515.1; -.
EMBL; AE005689; AAK22140.1;
TIGR; CC0153; -.
                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
DOMAIN
                                                           InterPro; IPR002571; HrcA.
Pfam; PF01628; HrcA; 1.
                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                           Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E., Eisen J., Heldelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 involved in negatively regulating heat-inducible transcription, and
the chaperone gene grpE.";
J. Bacteriol. 178:1829-1841(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=CB15N / NA1000;
MEDLINE=96178944; PubMed=8606155;
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16-0CT-2001
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                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-21173698;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=155892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HRCA OR CC0153.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gomes S.L., Shapiro L.;
Identification of a Caulobacter crescentus operon encoding
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                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE HRCA FAMILY.
                                                                                                                                                                                                                                                                                 THESE OPERONS.
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(Rel. 34, Last sequence up
(Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            crescentus
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CYTOPLASMIC (POTENTIAL).

N'LINKED (GLCNAC. . .) (POTENTIAL).

N'LINKED (GLCNAC. . .) (POTENTIAL).

N'S 5369DFC216E9EEC4 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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Pred. No.
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RESULT 40
PCE_TACTR
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                                                                                                                                InterPro: IPR001314; Chymotrypsin. InterPro: IPR001254; Ser_protease_Try. Pfam; Pr00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN. SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS00134; TRYPSIN_DOM; 1.
PROSITE; PS00135; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local
                 MOD_RES
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CHAIN
                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                              DOMAIN
                                                                         CHAIN
                                                                                                         SIGNAL
                                                                                                                  Glycoprotein.
                                                                                                                               Hydrolase;
                                                                                                                                                                                                                           EMBL; M58366; AAA30094.1; -.
PIR; A23689; A23689, HSSP; P00763; 1DPO.
MEROPS; S01.221; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Muta T., Hashimoto R., Miyata T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Hemocyte;
MEDLINE-91093088; PubMed-2266134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Proclotting enzyme precursor (EC 3.4.21.86).
Tachypleus tridentatus (Japanese horseshoe crab).
Eukaryota: Metazoa: Arthropoda: Chelicerata: Merostomata: Xiphosura:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND DISULFIDE BONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCE_TACTR
P21902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=6853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              838 GGQVLAV 844
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nes 7; Conserv
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                                                                                                                          protease;
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29
127
375
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PROCLOGIANCE
SERINE PROTEASE.

SERINE PROTEASE.

PYRROLIDONE CARBOXYLIC ACID.

CHARGE RELAY SYSTEM (BY SIMILARITY).

CHARGE RELAY SYSTEM (BY SIMILARITY).

CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                                    Zymogen; Signal; Hemolymph clotting;
                                                                    PROCLOTTING PROCLOTTING
                                                                                         POTENTIAL
                                                                                                 25 (POTENTIAL).
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                                                                ENZYME HEAVY CHAIN.
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ilarity 100.0%;
Conservative
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84
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311
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351
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235
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                                                        0;
                                                                                  N-LINKED (GLCNAC. ..).
N-LINKED (GLCNAC. ..).
N-LINKED (GLCNAC. ..).
; 94209E514DFCF8FB CRC64;
                                                                                                                                     INTERCHAIN
                                                       Mismatches
                                                              DB 1;
5. 77;
                                                                    Length 375;
                                                      0; Indels
                                                      0;
                                                      Gaps
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Q8zs53 anabaena sp Q9hk17 thermoplasm Q8ti39 methanosarc Q9kp31 vibrio chol

methanosarc
gallus gall
pasteurella
yersinia pe
neisseria m

rickettsia

synechocyst salmonella

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Minimum DB
Maximum DB
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                                                                                                                                                Score
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     protein search, using sw model
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Match
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Gapop 60.0 , Gapext 60.0
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sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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sp_bacteriap:*
sp_archeap:*
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    Q8ZB95
Q8XEL5
Q9I0U1
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Q9R802
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Q98JV3
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              Q9r802 salmonella
Q9ck26 pasteurella
Q9rph7 mycobacteri
P95086 mycobacteri
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Q98jv3 rhizobium l
Q98kh9 rhizobium l
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Q8y4c5 listeria mo
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Q9zb14 mycobacteri
P72239 pseudomonas
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Q9HSM2
7 Q9HSM2
7 Q8U3R1
7 Q8U3R1
7 Q9M9H3
8 Q915D8
8 Q98G25
9 Q25405
9 Q8XX44
9 Q949H0
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Jerop
       Ogcpw7 mus musculu
Qgiaa6 gallus gall
Qgbg7 xylella fas
O86212 enterococcu
Qglva5 arabidopsis
O97jh2 clostridium
O8xg83 salmonella
O9rvu8 deinococcus
O97t44 streptococc
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025405 lymnaea sta
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0949h0 hordeum vul
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Q8trel methanosarc
Q9pvi8 gallus gall
Q9clv3 pasteurella
Q8z102 yersinia pe
Q9jsv0 neisseria m
Q98552 paramecium
Q9up45 homo sapien
Q96yv4 sulfolobus
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Q8tvh6 methanopyru
Q9hgm2 schizosacch
Q9hsp4 halobacteri
Q8u3r1 pyrococcus
Q9m9h3 arabidopsis
Q91568 pseudomonas
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Q48697 arabidopsis
Q45283 bacillus li
Q8w6c9 vibrio phag
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Q9pd36 xylella fas
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0929x1
0929x1
0947p8
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2 archaeoglob 5 gallus gall 8 solanum suc 2 rhizobium l 3 agrobacteri 5 rhizobium m 6 listeria in 6 listeria mo 9 porphyra te 7 bacillus su 0 neisseria m

Result No.

Q9mhu3 parascaris Q9mhv3 baylisascar Q9mhv2 baylisascar

pyrococcus
arabidopsis
pseudomonas
rhizobium 1

Q8tzj9 pyrococcus

100 110 111 113 113 114

	157 158 159 160 161 162	153 154	150 151	148 149	146 147	144 145	142 143	140 141	138 139	136 137	134 135	132 133	130 131	128 129	126 127	124	122	120	118	116	114	112 113	110 111	108	106 107	104	103	101	100	986	96	999	92	90
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RESULT 1
Q8ZB95
ID Q8ZB
Q8ZB
AC Q8ZB
DT 01-y
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                                                                      RX MEDLINE-21470413; PubMed=11586360;
RA MEDLINE-21470413; PubMed=11586360;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Parkhill J., Wren B.W., Thomson N.R., Churcher C., Mungall K.L.,
RA Prentice M.B., Sebalhia M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holtroyd S., Jagels K., Karlyshev A.V.,
RA Feltwell T., Hamlin N., Holtroyd S., Jagels K., Karlyshev A.V.,
RA Feltwell T., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RT Menome Sequence of Yersinia pestis, the causative agent of plague.";
DR RIL Nature 413:523-527(2001).
DR EMBL, AJ414157; CAC92753.1; --
DR ROSITE; PS00213; LIPOCALIN; UNKNOWN I.

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Q1-MAR-2002
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                                                 Hypothetical protein; Complete proteome.
SEQUENCE 578 AA; 64405 MW; 69AD3780BFDC20F1 CRC64;
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08vm06 streptococc
09sx29 arabidopsis
09ruc5 deinococcus
09ruc5 deinococcus
09ksh8 vibrio chol
09a192 streptococc
08ypg8 anabaena sp
03059 escherichia
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Q93816 streptococc
Q91813 arabidopsis
Q8xrt5 ralstonia s
Q9hqi0 halobacteri
Q9f9j1 comamonas s
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Q9c7p9 arabidopsis
Q9a0f1 streptococc
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Query Match
Best Local Similarity
Matches 11; Conserv
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EMBL; AE008906; AAL23229.1; .

EMBL; AL627283; CAD06889.1; .

Interpro; IPR000184; Bac_surfag_D15.
Interpro; IPR000566; Lipocln_cytFABP.
Pfam; PF01103; Bac_surface_Ag; 1.

PROSITE; PS00213; LIPOCALIN; UNKNOWN_1.
Hypothetical protein; Complete proteome SEQUENCE 577 AA; 64765 MW; FBA4A190
  Q910U1;
Q910U1;
01-MAR-2001
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SPECIES=S.typhimurium, STRAIN=LT2 / SGSC1412 / ATCC 700720;

SPECIES=S.typhimurium, STRAIN=LT2 / SGSC1412 / ATCC 700720;

MEDLINE=21534948; pubMed=11677609;

MCCLelland M., Sanderson K.E., Spieth J., Clifton S.W., Latre: Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Li Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvann L., Stone K., Wilson R.K., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;

Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIES-S. typhi; STRAIN-CT18; MEDLINE-21534947; PubMed-11677608;
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01-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete genome sequence of Salmonella enterica serovar Typhimurium
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NCBI_TaxID=602,
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N., Mulvaney E.,
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        STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PUBMed=11677609;
MCCLelland M., Sanderson K.E., Spietl
Courtney L., Porwollik S., Ali J., D
                                                                                                                                                                                         Submitted
                                                                                                                                                                                                                 Valdivia
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Nature 406:959-964(2000).
EMBL; AE004682; AA605991.1;
Hypothetical protein; Complete proteome.
SEQUENCE 579 AA; 63739 MW; 23467005C836FBBF CRC64;
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MEDLINE-20437337; Pubmed-10984043;
Stover C.K. Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.
Garber R.L., Goltry L., Tolentino E., Westbrock Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saier M.H., Hancock R.E.M., Lory S., Olson M.V.;
"Complete Geography of the Complete Complete
                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                         SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                     "Macrophage-dependent induction of a type III secretion system and its Mol. Microbiol. 30:175-188(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 277:2007-2011(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Fluorescence-based
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Valdivia R.H., Monack D.M.,
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the Salmonella pathogenicity island
s role in intracellular survival.";
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Hensel M., Shea J.E., Waterman R., Mundy R., Nikolaus T., Banks G.,
Vazquez-Torres A., Gleeson C., Fang F.C., Holden D.W.;
"Genes encoding putative effector proteins of the type III secretion
system of Salmonella pathogenicity island 2 are required for bacterial
virulence and proliferation in macrophages.";
Mol. Microbiol. 30:163-174(1998).
EMBL, AJ224892; CAA12191.1; -
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MEDLINE=21145866;
May B.J., Zhang Q.
                                     SEQUENCE FROM N.A. STRAIN=PM70;
                                                                                                                 Bacteria; P
Pasteurella
                                                                                                                                                                      Hypothetical PM1809.
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EMBL; AF020808; AAC28885.1;
EMBL; AE008761; AAL20328.1;
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Ryan E., Sun H., Floren
Ryan R., Wilson R.
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Zhang Q.,
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PubMed=11248100;
., Li L.L., Paust
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Whittam T.S.,
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Kapur V.;
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RESULT
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ID RPH7
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STRAIN-H37RV;
MEDLING-98295987; PubMed-9634230;
COle S.T., Brosch R., Parkhill J., Garnier T., Chur
Cordon S.V., Eiglmeier K., Gas S., Barry C.E. III,
Gordon S.V., Brasham D., Brown D., Chillingworth T.,
                                                                                                                                                                                                                                                                                                                                                P95086;
01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein Rv3072c.
RV3072C OR MT3157 OR MTCY22D7.09.
                                                                                                                                                                                                                                                       Mycobacterium tuberculosis.

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae
Bacteriales; Corynebacterineae; Mycobacteriaceae;
NCBI_TaxID=1773;
                                                                                                                                                                                        SEQUENCE FROM N.A.
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Griffin IV T.J., Parsons L., Leschziner A.E.,
Derbyshire K.M., Grindley N.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "In vitro transposition of tn552: a tool mutagenesis.";
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Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
EMBL; AE006218; AAK03893.1; -.
InterPro; IPR000184; Bac_SurfAg_D15.
InterPro; IPR001092; HLH_basic.
Pfam; PF01103; Bac_SurfAce_Ag; 1.
PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
HYPOthetical protein; Complete proteome.
HYPOTHORICE 586 AA; 67106 MW; 00895174DED58283 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic Acids Res. 27:3859-3865(1999).
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llarity 100.0%;
Conservative (
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13,
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Pred. No. 8.5
0; Mismatches
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                   Churcher C., III, Tekaia F. T., Connor R.
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                                                                                     Harris
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Best Local
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TIGR; MT3157; -..
TIDErCLLIST; RV3072c; -.
Tuberculist; Rv3072c; -.
InterPro; IPR002103; Bac_luciferas;
InterPro; IPR00296; bac_luciferase; 1.
Pfam; PP00296; bac_luciferase; 1.
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01-OCT-2001
01-OCT-2001
01-MAR-2002
                                                                                                     EMBL; AP002998; BAB49062.1; -. Hypothetical protein; Complete SEQUENCE 235 AA; 26023 MW;
                                                                                                                                                                                Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
                                                                                                                                           Mesorhizobium loti.";
DNA Res. 7:331-338(2000).
                                                                                                                                                                                                                                   MEDLINE=21082930; PubMed=11214968; Kaneko T., Nakamura Y., Sato S., Asamizu
                                                                                                                                                                                                                                                                  STRAIN-MAFF303099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers C., Statton J.E., Taylor K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from complete genome sequence."; Nature 393:537-544(1998).
                                                                                                                                                                      "Complete genome structure of the
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                         Phyllobacteriaceae;
NCBI_TaxID=381;
                                                                                                                                                                                                                                                                                                                                      Bacteria;
                                                                                                                                                                                                                                                                                                                                                   Rhizobium
                                                                                                                                                                                                                                                                                                                                                                 Hypothetical MLR1763.
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Submitted (APR-2001) to the
EMBL; 283865; CAB06251.1; -.
EMBL; AB007133; AAK47493.1;
TIGR; MT3157; -
                           238
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STRAIN-CDC 1551 / OSHKOSH;
Fleischmann R.D., Alland D.,
 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           895 RVDVATGV 902
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ALVAARAV 231
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8; Conserv
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Proteobacteria; alpha subdivision;
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(TrEMBLrel. 18, 1
2 (TrEMBLrel. 20, 1
                                                   Conservative
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Mesorhizobium.
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Pred. No
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DB2C4A2DA6D19FC6
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5073A9EE87C0359D CRC64;
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Murphy L.,
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RESULT 11
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DNA Res. 7:331-338(2000).

EMBL; AP003000; BAB49857.1; -.

InterPro; IPR001683; GFO_IDH_MocA.

InterPro; IPR002161; GFO_IDH_MocA_C.

InterPro; IPR002016; Peroxidase.

Pfam; PF01408; GFO_IDH_MocA_C; 1.

PROSITE; PS00435; PEROXIDASE_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                            Q927W8;
Q927W8;
01-DEC-2001
01-DEC-2001
Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A., Baquero F., Berche P., Bloecker H., Brandt P., Chakrabotty T., Charabit A., Chetouani F., Couve E., de Daruwar A., Dehoux P., Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget C., Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P., Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson I., Jones L.-M., Keerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G., Mordsiak G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell F., Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
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01-OCT-2001 (TrEMBLrel.
01-OCT-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                 SEQUENCE FROM N.A. STRAIN-CLIP 11262 PubMed=11679669;
                                                                                                                                                                                                      LISTETIACEAE; Listeria.
NCBI_TaxID=1642;
                                                                                                                                                                                                                                      Bacteria; Firmicutes;
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01-DEC-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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Bacteria; Proteobacteria; alpha subdivision;
Phyllobacteriaceae; Mesorhizobium.
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nes 8; Conserv
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OR LIN2669.
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               B., Perez-Diaz J.-C., Purcell R.
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lo. 51;
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EMBL, AL596173; CAC97985.1; -. Listilist; LIN02669; -. InterPro; IPR001023; Hsp70.
InterPro; IPR001023; Hsp70.
InterPro; IPR004753; MrcB_Mrl.
PRINTS; PR01652; SHAPPEROTEIN.
ProDom; PD000089; Hsp70; 1.
TIGRPAMS; TIGR00904; mrcB; 1.
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Q8Y4C5;
Q1-MAR-2002
01-MAR-2002
01-JUN-2002
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Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
Entian K.-D., Fshhi H., Garcia-del Portillo F., Garrido P.,
Gautier L., Goebel W., Gomez-Dopez N., Hain T., Hauf J., Jackson D.,
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
Mordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Remmel B., Rose M., Schlueter T., Simoss N., Tierrez A.,
Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
"Comparative genomics of Listeria species.";
                                                                                                                                                                                                                                                                      ListiList; LMO02525; ...
InterPro; IPR001023; Hsp70.
InterPro; IPR004753; MreB_Mrl.
PRINTS; PR01652; SHAPEPROTEIN.
ProDom; PD000089; Hsp70; 1.
                                                                                                                                                                                                                                                                                                                                                                                                           "Comparative genomics of Listeria Science 294:849-852(2001).
EMBL; AL591983; CAD00603.1; -.
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MBL OR LMO2525.
                                                                                                                                                                                                     Complete proteome. SEQUENCE 331 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=EGD-E / SEROVAR 1/2A;
MEDLINE=21537279; PubMed=11679669;
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38 GQVLAVGT 45
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    Query Match
Best Local Similarity
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P72239
P72239;
01-FEB-1997
                                                                     InterPro; IPR000794; Ketoacyl-synt.
Pfam; PF00109; ketoacyl-synt; 1.
Pfam; PF02801; ketoacyl-synt_C; 1.
SEQUENCE 379 AA; 39691 MW; 6297
                                                                                                                                                                       EMBL; U56980; AAB41300.1; -. HSSP; P73283; 1E5M.
                                                                                                                                                                                                                    STRAIN-GLYCINEA; MEDLINE-97149205; PubMed-8996103; MEDLINE-97149205; PubMed-8996103; Penfold C.N., Bender C.L., Turner J.G.; "Characterisation of genees involved in lacid, the polyketide component of the place in 183:167-173(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas syringae (pv. Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1997
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-21128732; PubMed-11234002;
Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Mungall K., Basham D., Brown D., Chillingworth T., Fraser A., Hamlin N.,
Murphy S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Quall M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CFA-beta-ketoacylsynthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Massive gene decay in the leprosy Nature 409:1007-1011(2001).
EMBL; AL585159; CAA22708.1; -.
EMBL; AL583918; CAC29807.1; -.
Leproma, ML0299; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Pseudomonas
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Pfam; PF01266; DAO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1999 (TrEMBLrel. 10, Created)
01-JUN-2002 (TrEMBLrel. 10, Last sequence update)
Hypothetical 36.3 kDa protein (potation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GVRWASPV 174
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8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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kDa protein (Putative oxidoreductase).
    100.0%;
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                           0.98;
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gamma subdivision;
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Last annotation update)
Score 8;
Pred. No.
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                                                                  629745BCE98DA0B1 CRC64;
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E8D64FB7F817658B CRC64;
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DB 2;
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5. 54;
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                   Length 379;
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Q9KYD1
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Best Local
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  Q8V5A8;
01-MAR-2002
                                              Q8V5A8
                                                                                                                                                                                                                                                                                                                              "Complete genome sequence of the model actinomyc coelicolor A3(2).";
Nature 417:141-147(2002).
EMBL; AL356812; CAB92561.1; -.
InterPro; IPR000005; HTHAIRC.
PROSITE; PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1.
SEQUENCE 383 AA; 37020 MW; 9FFEFD7E45827D4E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-A3(2) / M145;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09KYD1
09KYD1;
01-0CT-2000
01-0CT-2000
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Tawaren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hopwood D.A.;
                                                                                                                                                                                                        721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "A set of ordered cosmids and a detailed genetic and the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=A3(2);
Thomson N.R.,
                                                                                                                                                            170 ALLAGVAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Redenbach M., Kieser H.M., Denapaite D., Kinashi H., Hopwood D.A.;
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                                                                                          16
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                                                                                                                                                                                                      ALLAGVAV 728
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8; Conserv
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(MAY-2000) t
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(TrEMBLrel.
                                                                                                                                                                                                                                                Conservative
                                           PRELIMINARY;
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AY-2000) to
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20,
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15,
21,
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Pred. No
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EMBL/GenBank/DDBJ databa
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                                                                                                                                                                                                                                                                  No.
                                         452
                                                                                                                                                                                                                                                                  DB 16;
5. 60;
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                                         B
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                                                                                                                                                                                                                                                                                     Length 383;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     physical map
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                                                                                                                                                                                                                                           0,
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Best Local
  076799;
076799;
01-NOV-1998
01-NOV-1998
01-MAR-2002
                                                                                                                                                                                                                                                                              STRAIN=A3(2) / M145;

Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,

Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,

Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,

Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,

Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,

Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,

Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,

Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.

Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                  Streptomyces coelicolor.

Streptomyces coelicolor.

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Bacteria; Firmicutes; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                      "Complete genome sequence of the model coelicolor A3(2),";
Nature 417:141-147(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein SC06331.
SC06331 OR SC10H5.07.
                                                                                                                                                                                                        Hypothetical SEQUENCE 4
                                                                                                                                                                                                                            EMBL; AL031232; CAA20279.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               086499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome organization of Casphalia extranea densovirus (CIteravirus.",
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF375296; AAL56545.1;
SEQUENCE 452 AA; 52387 MW; BOFBAA9129C148C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Tijssen P., Fediere G., Li Y., Zad
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Viruses; ssDNA viruses; Parvov
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01-MAR-2002
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                                                                                                                                 PVALAAYL
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469 AA; 52166 MW;
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Last sequence update)
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Last annotation update)
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Pred. No
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STRAIN=C2A / ATCC 35395 / DSM 2834;

STRAIN=C2A / ATCC 35395 / DSM 2834;

REDLINE-21929760; PubMed=11932238;

RETLINE-21929760; PubMed=11932238;

REPLINE-21929760; PubMed=11932238;

REPLINE-
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Best Local
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Best Local
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01-JUN-2002
01-JUN-2002
01-JUN-2002
                                                                                                                                                                                                                                                             Genome Res. 12:532-542(2002)
EMBL; AE011149; AAM07661.1;
                                                                                                                                                                                                                                                                                            and physiological diversity.";
Genome Res. 12:532-542(2002).
                                                                                                                                                                                                        SEQUENCE
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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-1- SIMILARITY: BELONGS TO THE CY
EMBL; AF083945; AAC33297.1; --
ElyBase; FBgn0025418; Dmet\Cyp9b3
404 LQAVRALS 411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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NCE 506 AA; 58555 MW; 246B
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8; Conserv
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0067; p450; 1.
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                                                                                    Conservative
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                                                                                                                                                                                                        AA; 5562
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Last annotation updat
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Pred. No.
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                                                                                                                                                                                                     A07C705CBCA80278 CRC64;
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                                                                                                             DB 17;
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Best Local
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Q8ZS53;
Q1 MAR-2002 (TrEMBLrel. 201-MAR-2002 (TREMBLrel. 201-MA
                      Plasmid;
SEQUENCE
                                                                                                                                                            Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sas Watanabe A., Iriguchi M., Ishikawa A., Kawashima Kishida Y., Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yasuda M., Tabata S.;
"Complete genomic sequence of the filamentous nit cyanobacterium Anabaena sp. strain PCC 7120.";
                                                                                                                                          cyanobacterium Anabaena sp. DNA Res. 8:205-213(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anabaena sp. (strain PCC Plasmid pCC7120beta. Bacteria; Cyanobacteria;
                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE-21595285; PubMed-11759840;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-20406833; PubMed-10952301;
Heldelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwineldelberg J.F., Eisen J.A., Nelson W.C., Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam Gill S.R., Nelson K.E., Rain T.D., Tettelin H., Diragoi I., Bass S., Qin H., Dragoi I., McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Ve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID-103690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical ALL7659.
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01-OCT-2000
01-JUN-2002
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InterPro; IPR000566; Lipocin_cytFABP.
Pfam; PF01103; Bac_surface_Ag; 1.
PROSITE; PS00213; LIPOCALIN; UNKNOWN_1.
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STRAIN-EL TOR N16961 / SEROTYPE 01;
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        AP003602; BAB77302.1; -.
id; Hypothetical protein;
NCE 731 AA; 83004 MW;
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8; Conserv
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al protein VC2548.
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n All7659.
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5644 MW; E96946FB85F1C426 CRC64;
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                                                                                                                                                                                                                                                                                         Matsuno A., Muraki A.,
Takazawa M., Yamada M.
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Lin H., Richardson D.,
Qin H., Dragoi I., Sellers P.
D., Nierman W.C., White O.,
Mekalanos J.J., Venter J.C.,
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T., Kimura T.,
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RESULT 23
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Best Local Similarity
Matches 8; Conserv
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InterPro; IPR004362; MGS_like.
Pfam; PF00289; CPSase_L_chain; 2
Pfam; PF02786; CPSase_L_D2; 1.
Pfam; PF02787; CPSase_L_D3; 1.
Pfam; PF02142; MGS; 1.
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Q9HK17;
01-MAR-2001 (TrEMBLrel. 16, C:
01-MAR-2001 (TrEMBLrel. 16, L;
01-UN-2002 (TrEMBLrel. 21, L;
                                                 Q9VKH2;
01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
  MEDLINE=20196006; PubMed=10731132; Adams M.D., Celniker S.E., Holt R.A.,
                                                                                                       SALM protein.
SALM OR CG6464.
                                 SEQUENCE FROM N.A.
                                                                                                                                                                    Q9VKH2
                                                                                                                                                                                                                                                                                                  Complete proteome. SEQUENCE 1047 AA
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STRAIN-DSM 1728;
MEDLINE=20479972; PubMed=11029001;
Ruepp A., Graml W., Santos-Martine,
Ruepp A., Graml W., Stocker;
                                                                                                                                                                                                                                                                                                                     PRINTS; PR00098; CPSASE.
PROSITE; PS00867; CPSASE_2;
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HSSP; P00968; LJDB.
                                                                                                                                                                                                                                         626
                                                                                                                                                                                                                                                                                                                                                                                                                                     acidophilum.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baume: "The genome sequence of the thermoacidophilic scavenger".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Archaea; Euryarchaeota; Thermopla Thermoplasmataceae; Thermoplasma. NCBI_TaxID=2303;
                                                                                                                                                                                                                    941 KGVKLYAT
                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 407:508-513(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thermoplasma acidophilum.
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                                                                                                                                                                                                                                                                      Similarity
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C.A.,
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                                                                                                                                                                                                                                                                            Length 1047;
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 Gocayne J.D.,
                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Baumeister
                                                                                                                                                                                                                                                                                                                                                                                                                                                   K.K., Volker C., Baumeister W.;
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                                                                     Muscomorpha;
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RESULT 24
048697
RRN OCCOORDINATION
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RA Sutton G.G., Wortman J.R., Yandell M.D., Ehang O., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Henderson S.N.,
RA HARIL J.F., Agbayani A., An H.-J., Andrews-Ffannkoch C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Ffannkoch C.R., Beldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Charry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Chriy J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Wei M.-H., Ibeywam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li., Lingy Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Reinert K., Remington K., Sinpson M., Skupski M.P., Smith T.,
RA Sylekka R., Tector C., Tunner R., Venteer E., Wang A.H., Wang X.,
RA Harris N.M., Wassarman D.A., Weinsteon M., Skupski M.P., Smith T.,
RA Hang Z.-Y., Massarman D.A., Weinstock G.M., Weissenbach J.,
RA Hang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Hang X.H., Zhong F.N., Zhong W., Zhang O., Zhang G., Zhang 
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01-JUN-1998 (TrEMBLrel. (
01-JUN-1998 (TrEMBLrel. (
01-JUN-2001 (TrEMBLrel. ]
F3I6.24 protein.
                                                                                                                                                                                                                                                    048697
                                                 Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                   F316.24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00028; ZĪNC_FINGER_C2H2_1; 7.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 7.
DNA-binding; Metal-binding; Zinc-finger.
SEQUENCE 1373 AA; 151014 MW; A6D857870F645ACC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00096; zf-C2H2; 7. SMART; SM00355; ZnF_C2H2; 7.
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George R.A., Lew
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InterPro; IPR000822; znf_C2
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is S.E.,
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Richards S., A
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Last sequence update)
Last annotation updat
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o. 1.9e+02;
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                                                                       core eudicots; Rosidae;
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Best Local
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Q8W6C9;
01-MAR-2002
01-MAR-2002
01-MAR-2002
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Q45283;
Q1-NOV-1996
                                                                                                                                                                                                                                                                    CHAIN
NON_TER
SEQUENCE
SEQUENCE FROM N.A.
Basu N., Kar S., Ghosh R.K.;
"Molecular analysis of filamentous phage VSK of Vibrio cholerae 0139:
                                                                                                                                                                                                                                                                                                   Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-CV. COLUMBIA; Federspiel N.A., Palm C.J., Conway A.B., Kurtz D.B., Conway A.R., Au M., Araujo R., Buehler E., Dewar K., Feng J., Kim C., Li Y., Oji O., Osborne B.I., Shinn P., Sun H., Toriumi M., Vysotskala V.S., Yu G., Ecker J., Theologis A., Davis R.W.; Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                              AMYL
                                                                         ORF62.
                                                                                                                                                                                                                                                                                                                                plasmid construction.";
Gene 96:37-41(1990).
                                          NCBI_TaxID=181604;
                                                    Viruses;
                                                             Vibrio phage
                                                                                    Memb4
                                                                                                                                                                                                                                                                                                                                                              Jorgensen P.L., Hansen C.
                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=91092499; PubMed=2265757;
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART;
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                                                                                                                                                                                                                                                                                                                      EMBL; M62637; AAA22232.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus licheniformis
                                                                                                                                                                                                      166 KRLYARL 172
                                                                                                                                                                                                                                                                                                                                                 Torgensen P.L., Hansen C.K., Poulsen G.B., Diderichsen B.;
Tn vio genetic engineering: homologous recombination as a tool
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            843 RELLEQLL 850
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CE 1417 AA;
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8; Conserv
                                                    hage VSK.
ssDNA viruses;
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2 (TrEMBLrel. 20,
2 (TrEMBLrel. 20,
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                                                                                                                                    PRELIMINARY;
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33
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33
                                                                                                                                                                                                                                                                     3711 MW;
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100.0%; Pr
0;
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157750 MW;
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                                                    Inoviridae;
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08, Last annotation update)
(Fragment).
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Last sequence update)
Last annotation update)
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Pred. No.
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                                                                                                                                                                                                                                       No.
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5. 69;
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). 2e+02;
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Best Local
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Q9PD36;
Q1-OCT-2000
01-OCT-2000
01-MAR-2002
Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M., Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S., Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S., Bueno M.R.P., Camargo A.A., Camargo L.E., Carraro D.M., Carrer H., Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M., Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H., Faccincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
                                                                          MEDLINE-20365717; PubMed-10910347;
                                                                                           STRAIN-9A5C
                                                                                                                                    Xylella.
                                                                                                                                                                   Hypothetical
XF1543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               euraryota; Viridiplantae; Stru
Spermatophyta; Magnoliophyta;
eurosids I; Fabales: Entre
                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                           Bacteria; Proteobacteria;
                                                                                                                                                        Xylella fastidiosa
                                                                                                                                                                                                                                                                                                                                                                                  NON_TER
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                                                                                                                         NCBI_TaxID-2371;
                                                                                                                                                                                                                                                                                                                                                                                                              Prueil L., Mittler R.;
"Dehydrin in retama retam.";
Submitted (CCT-2001) to the EMBL/GenBank/DDBJ
EMBL; AF439276; AAL32035.1;
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InterPro; IPR000167; Dehydrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spermatophyta; Magnoliophyta; Embryophyta; Tracheophyta; eurosids I; Fabales; Fabaceae; Papilionoideae; Genisteae; Retama.
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00257; dehydrin; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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01-MAR-2002
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Submitted (NOV-2001) to the
EMBL; AF453500; AAL49745.1;
SEQUENCE 62 AA; 7221 MW;
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les 7; Conser
                                                                                                                                                                                                                                                                                      EVVVPPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FROM
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                                                                                                                                                                                                                                                                                                                                                                        66 AA;
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7354 MW;
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5.1.3e+02;
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Matches
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Tabata S.;
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P74009;
01-FEB-1997
01-FEB-1997
01-MAR-2002
                                                                                                                                                                  Synechocystis sp. strain PCCbmus. 11. Jey-
entire genome and assignment of potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S., Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A., de Oliveira R.C., de Oliveira R.C., Palmieri D.A., Paris A., Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B., Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M., de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E., da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr., da Silva A.C.R., da Silva S.M., Jr., de Souza A.A., de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H., Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L., Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
                                                                                                                   Hypothetical protein; CoseQUENCE 72 AA; 8400
                                                                                                                              EMBL; D90911; BAA18080.1; -.
Hypothetical protein; Complete proteome
                                                                                                                                                                                                                                                                         Miyajima
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=97061201; PubMed=8905231;
Kaneko T., Sato S., Kotani H., Ta
                                                                                                                                                                                     "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the
                                                                                                                                                                                                                                                          Hosouchi
                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1148;
                                                                                                                                                                                                                                                                                                                                                            Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales;
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Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
HO P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
Krieger J.E., Kuramae E.E., Laigret F., Lambals M.R., Leite L.C.C.,
Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
Menck C.F.M., Miracca B.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
                             216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein; Complete proteome. SEQUENCE 66 AA; 6871 MW; 8DA1217E63550F41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The genome sequence of the plant pathogen xylella fastidiosa.";
Nature 406:151-159(2000).
EMBL; ABF84352.1;
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                                                                                                                                                                3:109-136(1996)
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7 (TrEMBLrel.
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                                                                      DB 16; L;
). 1.4e+02;
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RESULT Q8XGJ5

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RESULT 31
Q8TRE
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DE MA123
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01-JUN-2002
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Methanosarcina acetivorans.
Archaea; Euryarchaeota; Methanococci;
Methanosarcinaceae; Methanosarcina.
NCBI_TaxID=2214;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
Nature 413:848-852(2001).
EMBL; AE008844; AAL22017.1; -
EMBL; AE008847; CAD02975.1; -
InterPro; IPR001109; HupF_HypC.
Pfam; PF01455; HupF_HypC: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Parkhill J. Dougan G. James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
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Q8XGJ5;
01-MAR-2002
01-MAR-2002
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                                                                                        Molybdenum-pterin
                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO0445; HUPFHYPC.
PRODOM; PD003112; HupF; HypC; 1.
TIGREAMS; TIGR00074; hypC_hupF;
PROSITE; PS01097; HUPF_HYPC; 1.
                                                                                                                                                                                                                                                                                                                                                             Complete proteome. SEQUENCE 82 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hydrogenase-2 operon protein (Hydrogenase-2 component protein). HYBG OR STM1143 OR STM3314. Salmonella typhimurium, and Salmonella typhi.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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100.0%; Pr
0;
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                                           Methanosarcinales;
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N., Mulvaney E.,
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RESULT 32
Q9PVI8
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O9PVI8; O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-MAY-2000 (TrEMBLrel. 21, Last annotation update)
Regulator of G-protein signalling 12 (Fragment).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Galliformes; Phasianidae; Phasianinae;
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NON_TER
SEQUENCE
                                                                                                                                              PRINTS; PR01301; RGSPROTEIN.
ProDom; PD001580; Reg_of_pr0
SMART; SM00315; RGS; 1.
PROSITE; PS50132; RGS; 1.
                                                                                                                                                                                                                                   -!- SIMILARITY: CONTAINS 1 RGS EMBL; AF090086; AAF00029.1; -. HSSP; P49799; 1AGR.
                                                                                                                                                                                                                                                                          Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                    Schiff M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P., FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A., Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R., Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W., Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M., Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K., Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C., Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I., Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E., Metcalf W.W., Birren B., Swanson R.V., Zinder S.H., Lander E., Metcalf W.W., Birren B.,
                                                                                                                                                                                                         Pfam; PF00615; RGS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and physiological diversity.";
Genome Res. 12:532-542(2002).
EMBL; AE010791; AAM04658.1; -.
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STRAIN=C2A / ATCC 35395 / DSM 2834;
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                                                                                                                                                                                                                                                                                                       Mechanisms of desensitization of
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                        NHVPAHD 46
NHVPAHD
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                                                   Similarity 100 7; Conservative
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                                                                                                         85 AA;
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100.0%; Pr
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100.0%; Pred. No. 1.6e+02;
tive 0; Mismatches 0;
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No. 1.6e+02;
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WEDLINE-21470413; PubMed-11586360;

WADDLINE-21470413; PubMed-11586360;

AP Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,

AP Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,

AP ARCHILLING, Sebaihia M., James K.D., Churcher C., Mungall K.L.,

AP Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,

AR Chillingworth T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,

AR Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,

AR Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,

AR Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.,

"Genome sequence of Yersinia pestis, the causative agent of plague.";

RI Nature 413:523-527(2001).

DR EMBL; Ad414144 (CAC89571.1; -.

KW Flagella; Hypothetical protein; Complete proteome.

KW Flagella; Hypothetical protein; Complete proteome.
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Q9CLV3;
01-JUN-2001
01-JUN-2001
01-DEC-2001
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Bacteria; Proteobacteria;
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                                                                                                          77
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                                                                                                          AVARAIL 83
                                                                                                                                                            AVARAIL 539
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1 (TrEMBLrel. 17, I
1 (TrEMBLrel. 19, I
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(TrEMBLrel. 20, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
agellar regulatory protein.
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100.0%; Pr
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Last annotation update)
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0; Mismatches
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Pred. No.
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1.7e+02;
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0. 1.7e+02;
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                                                                                                                                                                                                                                                                 Length 88,
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RESULT
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Nature 404:502-506(2000).

R EMBL, AL162758; CAB85336.1;

R Hypothetical protein; Complete proteome.
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                                        [3]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=20478054; PubMed=11021991;
Sun L., Gurnon J.R., Adams B.J., Graves M.
Sun L., Gurnon of a beta-1,3-glucanase
                         Virology
[4]
                                                                                                                                           MEDLINE=2001336; PubMed=10544099; MEDLINE=2001336; PubMed=10544099; Kaiser A., Vollmert M., Tholl D., Graves M.V., Lisec A.D., Nickerson K.W., Van Etten J.L.; "Chlorella virus PBCV-1 encodes a functional ho
SEQUENCE FROM N.A. Van Etten J.L.;
                                                                                                                                                                                                               Kutish G.F., Li Y., Lu Z., Furuta M., Rock "Analysis of 76 kb of the chlorella virus positions 182 to 258."; Virology 223:303-317(1996).
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Q98552; Ol-FEB-1997 (TrEMBLrel. 02;
Ol-FEB-1997 (TrEMBLrel. 02;
Ol-DEC-2001 (TrEMBLrel. 19;
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Q9JSV0;
01-OCT-2000
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MEDLINE=96400190; PubMed=8806566;
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Viruses; dsDNA viruses, no RNA stage;
                                                                                                                       Virology
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MEDLINE-20222556; PubMed-10761919;
Parkhill J., Achtman M., James K.D.,
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La (Tremblrel. 19, La
La protein NMA2123.
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100.0%; Pr
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Last annotation updat
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Phycodnaviridae; Chlorovirus.
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                                                                                                                                                                   Gurnon J.R., Xing W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 91;
                                                                                                                                                                                                                                          Van Etten J.L.; 330-kb genome:
                                                         Etten J.L.;
by chlorella
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Q96YV4
Q96YV4;
01-DEC-2001
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Q9UP45;
Q9UP45;
Q1-MAY-2000 (TIEMBLrel. 13, Created)
Q1-MAY-2000 (TIEMBLrel. 13, Last sequence update)
Q1-MAY-2000 (TIEMBLrel. 13, Last annotation update)
Q1-MAY-2000 (TIEMBLREL. 13, Last annotation update)
Type XIII collagen (Fragment).
HOMO Saplens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrat:
Mammalia; Eutharia; Primates; Catarrhini; Hominid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (DEC-2000) to the EMBL; U42580.
                                                                                                                                                                                                                                            Collagen.
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Graves M.V., Van Etten
Submitted (DEC-1998) to
                                                                                                                                                                                                                                                                                         human homologue.
Matrix Biol. 18:
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                                                                                                                                                                                                                                                                                                                                                    Kvist A.P., Latvanlehto A., Sund M., H
Palotie A., Beier D., Pihlajaniemi T.;
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MEDLINE=99357014; PubMed=10429945;
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7; Conserv
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(MAY-1997)
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95 AA; 11069 MW;
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18:261-274(1999).
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NO. 1.8e+02;
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Q92GX1;
01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                       MEDLINE-21442074; PubMed-11557893;
Ogata H., Audic S., Renesto-Audiffren
Samson D., Roux V., Cossart P., Weisse
                                                                                                                                                                TIGRFAMS; TIGR01044; rplV_bact; 1.
PROSITE; PS00464; RIBOSOMAL_L22; UNKNOWN_1.
Ribosomal protein; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-JUN-2002 (TrEMBLrel. 21, 50% ribosomal protein L22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete genome sequence of an aerobic thermoacidophilic Crenarchaeon, Sulfolobus tokodaii strain7.";
DNA Res. 8:123-140(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S., Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y., Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A., Oshima T., Kikuchi H.;
                                                                                                                                                                                                                          Pfam; PF00237; Ribosomal_L22; 1.
ProDom; PD001032; Ribosomal_L22; 1.
                                                                                                                                                                                                                                                              Science 293:2093-2098(2001).
EMBL; AE008652; AAL03539.1; -.
InterPro; IPR001063; Ribosomal_L22.
                                                                                                                                                                                                                                                                                                                   Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V., Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M., Raoult D., "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN=MALISH 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; alp
Rickettsiaceae; Rickettsieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rickettsia conorii.
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Archaea; Crenarchaeota;
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119 AA;
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13253 MW; 5BE636CA907C7DA8 CRC64;
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eae; Rickettsia.
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                                                                       Score 7; DB 1; Pred. No. 2.2 0; Mismatches
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Last annotation update)
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C2FC9E804E1AC83C CRC64;
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                                                                                         DB 16; Lo
5. 2.2e+02;
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RESULT 40
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RC STRAIN-VC-16 / DSM 4304 / ATCC 49558;

RX MEDLINE-98049343; PubMed-9389475;

RX MEDLINE-98049343; PubMed-9389475;

RX Klenk H.-P. Clayton R.A., Tomb J.-F., White O., Nelson K.E.,

RA Klenk H.-P. Clayton R.A., Tomb J.-F., White O., Nelson K.E.,

RA Klenk H.-P. Clayton R.A., Tomb J.-F., White O., Nelson K.E.,

RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

Gill S.,

RA Richardson D.L., McMenney K., Adams M.D., Loftus B.,

RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,

RA Peterson S., Reich C.I., McKeil L.K., Badger J.H., Glodek A., Zhou L.,

Peterson S., Reich C.I., McKeil L.K., Badger J.H., Glodek A., Zhou L.,

RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,

RA Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,

RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,

RA Wenter J.C.;

RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,

RA Venter J.C.;

"The complete genome sequence of the hyperthermophilic, sulphate-

RT reducing archaeon Archaeoglobus fulgidus.";

RL Nature 390:364-370(1997),

DR EMBL, AE000997; AAB89718.1;

-. OR TIGR, AF1530;

-. OR TIGR, AF1530
                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 7
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SEQUENCE 119 AA; 14025 MW; 7F75DA993E80C15C CRC64;
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O1-JAN-1998 (TrEMBLrel. 05, Created)
O1-JAN-1998 (TrEMBLrel. 05, Last sequence update)
O1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein AF1530.
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Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
NCBI_TaxID=2234;
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nes 7; Conserv
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Llarity 100.0%; Pred. No. 2.;
Conservative 0; Mismatches
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phila mela	ABB64927	22	1600	3.1	148.5	45
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Porphorymonas ging	AAY34369	20	899	٠	154	3
as	AAY34495	20	891	3.3	154	12
Drosophila melanog	ABB63911	22	2016	٠	54	11
an diagn	ABG21666	22	1249	٠	57	40
Cellulose synthase	AAR45002	14	1319	3.4	159.5	39
luenzae b	AAR53754	15	797	•	61	88
Ь	AAR53756	15	797		59	37
H. influenzae b Ea	AAR53755	15	797	3.6	7]	36
1a	ABB58843	22	2748	٠	173.5	35
	AAY44391	21	813		176.5	34
. catarrhalis BA	AAY44390	21	813	٠	176.5	ü
influenza	AAR53757	15	792	٠	178	32
	AAR53758	15	793		184.5	31
Ler	AAW71477	19	847	4.0	188.5	30
H. pylori outer me	<b>~</b>	20	925	4.1	194.5	29
H. pylori ORF 05ep	AAW55729	18	925	4.1	194.5	28
Novel human diagno	55	22	371	4.4	206	27
H. pylori HPS120 p	AAB46311	22	916	4.4	206.5	26
	AAY74861	21	615	4.5	215	25
	AAY99625	21	587	4.5	215	24
	AAY99624	21	609	4.6	219	23
	AAY99623	21	609	4.6	219	22
Neisseria meningit	AAY74862	21	615	4.7	220	21
Porphorymonas ging	AAY34379	20	803		224.5	20
Porphorymonas ging	AAY34506	20	775		224.5	19
Novel human diagno	ABG17710	22	474		235.5	18
_	AAG78603	22	896		238.5	17
acid	AAY84947	21	797	5.4	253	16
seria meningi	AAB23788	22	797	•	259	15
eria m	78	22	797	•	259	14
id	AAB84746	22	797	5 5	259	13
o acid	7	22	797	5.5	259	12
Neisseria meningit	AAU04451	22	797		259	1

## ALIGNMENTS

RESULT 1
AAY95987
ID AAY9
XX

AAY95987 standard; Protein; 919

8

05-DEC-2000 AAY95987;

Moraxella catarrhalis BASB081 protein. (first entry)

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PA
                                                                                            Y F T
                                                                                                                                           Key
                                                                                                                                                                                                            BASB081; infection; otitis media; pneumonia; sinusitis; inflammation; therapy; antibacterial; antiinflammatory;
                   26-FEB-1999;
                                        23-FEB-2000
                                                           08-SEP-2000.
                                                                                                              Misc-difference
                                                                                                                                                                                                    diagnosis
(SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                               W0200052842-AJ
                                                                                                                                  Protein
                                                                                                                                                     Peptide
                                                                                                                                                                                 Moraxella catarrhalis.
                                       2000WO-EP01468
                    99GB-0004559
                                                                                                              365
                                                                                                                                  /label= Signal_peptide
31..919
                                                                                                                                                     Location/Qualifiers
1..30
                                                                                                  /note= "Ile in sequence of AAY95988"
                                                                                                                     'label= Mature_protein
                                                                                                                                                                                                               vaccine;
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Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptide or polynucleotide, and optionally at least I other M. Catarrhalis antigen. A method for diagnosing a M. catarrhalis infection involves identifying a BASBO81 polypeptide, or an antibody that is immunospecific for it, in a sample. A therapeutic composition useful in treating M. catarrhalis diseases in humans comprises an antibody directed against a BASBO81 polypeptide. The disease can be a bacterial infection, e.g. otitis media in infants and children, pneumonia in elderlies, sinusitis, nosocomial infections and invasive diseases, chronic otitis media with hearing loss, fluid accumulation in the middle ear, auditive nerve damage, inflammation of the middle ear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein. It shows 99.9% homology in the mature region to a sequence (see AAY95988) deduced from a PCR product. The invention provides BASB081 polypeptides, polypucleotides, expression vectors, host cells, and a process for producing a BASB081 polypeptide. Also provided are vaccine compositions comprising a BASB081.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                               421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence homology to Neisseria meningitidis omp85 outer membrane protein. It shows 99.9% homology in the mature region to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New BASB081 polypeptides from Moraxella catarrhalis and polynucleotides encoding the polypeptides used for treating infections, or as a vaccine for preventing infections, especially those caused by M. catarrhalis -
                                                                                                                           421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is that of the Moraxella Mc2391 (ATCC 43617) BASBO81 protein, which is
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mes 919; Conserv
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                   EFSASNLIQDKLNLVAAKARHLYDMPDDRVLAINHDDGVNRSILGRISDAVSAVARAILP
                                                                NMVNTEIVFPEREQIQNDQVSFEQSSSSRTEPAQVDESTLEPVIETVELTDGILMDISPI
                                                                                                                                                                                         FDEVVFFTIDPKTNQLTTDPDKLPVKRELLEQLLTVNNGEAYNLQAVRALSNDLIATRYF
                                                                                                                                                                                                                                                                                        LLIGDVFHHGKYETKKNLIENASAEHGYFDGRWLDRSVDVILPDNTADVSLIYDTGTQYR 360
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FDEVVFFTIDPKTNQLTTDPDKLPVKRELLEQLLTVNMGEAYNLQAVRALSNDLIATRYF
                                                                                                                                                                                                                                                            LLIGDVFHHGKYETKKNLIENASAEHGYFDGRWLDRSVDVILPDNTADVSLIYDTGTQYR
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)B; AAA50536.
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ilarity 100.0%;
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Pred. No. 6.5e-317;
; Mismatches 0;
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The present sequence

is that of the

Moraxella catarrhalis strain

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RESULT 2
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                                 New BASB081 polypeptides from Moraxella catarrhalis and polynucleotides encoding the polypeptides used for treating infections, or as a vaccine for preventing infections, especially those caused by M. catarrhalis -
                   Claim 1;
                                                                                 N-PSDB;
                                                                                  WPI; 2000-587296/55
N-PSDB; AAA50537.
                                                                                                                                      (SMIK ) SMITHKLINE
                                                                                                                                                                                23-FEB-2000;
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                                                                                                                                                                                                                           WO200052042-A1
                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                        Moraxella catarrhalis
                                                                                                                                                                                                                                                                                                            diagnosis
                                                                                                                                                                                                                                                                                                                     BASB081; infection; inflammation; therap
                                                                                                                                                           26-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                 AAY95988;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GVKEEGNPIKLHFFIGTPF
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                 Page 61; 97pp;
                                                                                                                                                                                2000WO-EP01468
                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                     ction; otitis media; pneumonia; sinusitis;
therapy; antibacterial; antiinflammatory;
                                                                                                                                                           99GB-0004559
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                                                                                                                                                                                                                                           /note= "Val in sequence of AAY95987"
                                                                                                                                      BEECHAM BIOLOGICALS
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amino acid sequence homology to Neisseria meningitidis omp85 outer membrane protein. The sequence was deduced from PCR-amplified DNA (see AAA50537), and shows 99.9% homology to the mature region of a BASB081 gene translation product (see AAY95987). The invention provides BASB081 polypeptides, polynucleotides, expression vectors, bost cells, and a process for producing a BASB081 polypeptide. Also provided are vaccine compositions comprising a BASB081 polypeptide cor polynucleotide, and optionally at least 1 other M. catarrhalis antigen. A method for diagnosing a M. catarrhalis infection involves identifying a BASB081 polypeptide, or an antibody that is immunospecific for it, in a sample. A therapeutic composition cuseful in treating M. catarrhalis diseases in humans comprises an antibody directed against a BASB081 polypeptide. The disease can be a bacterial infection, e.g. otitis media in infants and children, contained the middle ear, sudditive nerve damage, delayed cof the middle ear.
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YRLDKLKTQAPPETWQDLPVDFVNGKPSQEALLAGVAVHKTVADNLVNPMRGYRQRYSLE
                                                                                                                                              QQNNPANTINHVPAHDTAINQAKAGNPPVLLTPEQIQARLNAAGLNAKPQSQALDVVNFD
                                                                                   YATKPLSHPLNDQLRATLGYQQEVFGHSTNGFDLSTRTLEHEISRSIIQNGGWNRTYSLR
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                                                             YATKPLSHPLNDQLRATLGYQQEVFGHSTNGFDLSTRTLEHEISRSIIQNGGWNRTYSLR
                                                                                                                                                                                                                                 LAINHDDGVNRSILGRISDAVSAVARAILPDESENEVIDLPERTALANRKTPADVYQSKK
                                                                                                                                                                                                                                                         LAINHDDGVNRSILGRISDAVSAVARAILPDESENEVIDLPERTALANRKTPADVYQSKK
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Pred. No. 7e-307;
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        The present sequence is that of outer membrane protein BASB067 of Haemophilus influenzae strain Rd KW20. BASB067 is a surface expressed protein that is recognised by the immune system. It shows 23% identity to the protective surface antigen DIS of H. influenzae and has a similar secondary structure. Its N-terminal domain is predicted to contain a mixture of alpha-helix and beta-strands, and could be used as a vaccine antigen. The C-terminal domain is predicted to form a beta-barrel composed of anti-parallel, amphipathic beta-strands. The external loops of the beta-barrels of integral outer membrane proteins frequently contain immunodominant B-cell epitopes, making the C-terminal domain of BASB067 a strong candidate vaccine antigen. The
                                                                                                                                                                                                       used
                                                                                                                                                                                                                    BASB067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haemophilus
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                                                                                                                                                                                                                                                                                Ruelle J,
                                                                                                                                                                                                                                                                                                                                   09-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KGFTNDTKIGAGVGVRWASPVGQVRVDVATGVKEEGNPIKLHFFIGTPF 919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YRLDKLKTQAPPETWQDLPVDFVNGKPSQEALLAGVAVHKTVADNLVNPMRGYRQRYSLE
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                                                                                                                                                                                                     polypeptide
r diagnosing
                                                                                                                                                                                                                                            AAA50269
                                                                                                                                                                            Page 78-80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             screening; infection; diagnosis; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           membrane protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "N-terminal 237..578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= Signal_peptide
23..578
/label= Mature_protein
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                                                                                                                                                                                                    polynucleotide from Haemophilus influenzae treating H. influenzae infections -
                                                                                                                                                                            English.
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materials
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RESULT 4
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Haemophilus influenza ntHi strain 289 BASB067 protein
                                     07-NOV-2000
                                                                     AAY95821;
                                                                                                 AAY95821 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     production of BASB067 polypeptides and polynucleotides, for use especially in therapeutic and prophylactic vaccines. It also relates to methods for using such polypeptides and polynucleotides in the prevention and treatment of microbial diseases, in diagostic assays for detecting diseases associated with microbial infections, and assays for detecting expression or activity of BASB067 polypucleotides. Antibodies raised against BASB067 can be used to treat humans with H. influenzae disease.
                                                                                                                                                                             541 GVRWASPVGAIKFDIATPIRDKDNSKNIQFYIG 573
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                                                                                                                                                                                                             GVRWASPVGQVRVDVATGVKEEGNPIKLHFFIG 916
                                                                                                                                                                                                                                                                                                               KVQASSAWVRTYAEN---
                                                                                                                                                                                                                                          YKKIAPKNRNGKLYGGSRLLTTSLEYQYQVYPNWWAATFADSGLAADNYTAKELRYGTGV
                                                                                                                                                                                                                                                                     HDSLSPISDKGYLTGGQVLAVGTAEYNYEFMKDLRLAVFGDIGNAYDKGFTNDTKIGAGV 883
                                                                                                                                                                                                                                                                                                                                      IARAGISGVYSFGDNAYGSNRAHOMTGGIQAGYIWSDNFNHVPYRLRFFAGGDQSIRGYA 823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QIGWTKPWINSRGHSLRSNLYLSAPKQTLEATYRMPLLKNPLNYYYDFAVGWE----GEK 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PDESENEVIDLPERTALANRKTPADVYQSKKVPLYVFVASDKPRDGQIGLGWGSDTGTRL 599
                                                                                                                                                                                                                                                                                                                                                                      -----ITDKTL---LLYPTVGFTRTRLRGGSFATWGDVQKITFDLSKRIWLSESSFI
                                                                                                                                                                                                                                                                                                                                                                                                             QEALLAGVAVHKTVADNLVNPMRGYR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                        EN--DTNTRVLTLSALRYWNNAHGWQYFGGLRMRYDSF-TQAD-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VTKFEHNLINRDGYQAGAELRLSEDKKGVK-LYATKPLSHPLNDQLRATLGYQQEVFGHS 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----LVQPNVN----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REDEVVEETIDEKTNQLTTDEDKLEVKRELLEQLLTVNMGEAYNLQAVRALSNDLIATRY 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-KDGVLVEHQTYDDYKTAISRLALNRGYFDGNFKISRLEISPETHQAWWRMLFDSGVRY 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLLIGDVFHHGKYETKKNLIENASAEHGYFDGRWLDRSVDVILPDNTADVSLIYDTGTQY 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IEFSASNLIQDKLNLVAAKARHLYDMPDDRVLAINHDDGVNRSILGRISDAVSAVARAIL 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RVFGYYESSVRFERKQRQGKRDLLIAHVTPGEPTKIAGTDVQIEGEAAQDENFNALRKNL 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142;
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                                 (first entry)
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                                                                                                                                                                                                                                                                                                          ----HRVVARAEIGYLHTKGIEKIPPTLRFFAGGDRSVRGYG
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Pred. No. 1.2e-21;
5; Mismatches 235
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DP DP

190 HYGNITE

RFDEVVFFTIDPKTNQLTTDPDKLPVKRELLEQLLTVNMGEAYNLQAVRALSNDLIATRY 419

-SHSQIRDDYLNNILNIKSGDPYLMNNLSDLTSDFSSSNW

P-KEGVLVEHQTYDDYKTAISRLALNRGYFDGNFKISRLEISPETHQAWWRMLFDSGVRY

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                                                                                                                                                                                                 The present sequence is that of outer membrane protein BASB067 of CHaemophilus influenzae non-typeable (NtHi) strain 289. BASB067 is CC a surface expressed protein that is recognised by the immune system. CC It shows homology to the protective surface antigen D15 of CH. influenzae and has a similar secondary structure. Its CH. influenzae and has a similar secondary structure of alpha-helix CC and beta-strands, and could be used as a vaccine antigen. The CC creminal domain is predicted to form a beta-barrel composed of CC anti-parallel, amphipathic beta-strands. The external loops of CC anti-parallel, amphipathic beta-strands Trequently CC contain immunodominant B-cell epitopes, making the C-terminal CC domain of BASB067 a strong candidate vaccine antigen. The CC contain immunodominant B-cell epitopes, making the C-terminal CC domain of BASB067 a strong candidate vaccine antigen. The CC especially in therapeutic and polynucleotides for the production of BASB067 polypeptides and polynucleotides. It also CC especially in therapeutic and prophylactic vaccines. It also CC especially in therapeutic and prophylactic vaccines, in diagostic and seases for detecting diseases associated with microbial infections, and appears of a detecting diseases associated with microbial infections,
                                                                                                                       Matches
                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                          polypeptides or polynucleotides. Antibodies raised against the mature portion of this BASB067 polypeptide can be used to treat
                                                                                                                                                                                                                                                                  and assays for detecting expression or activity of BASB067 polypeptides or polynucleotides. Antibodies raised against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 81-82; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   {\tt BASB067} polypeptide and polynucleotide from Haemophilus influenzae are used for diagnosing and treating H. influenzae infections -
                                                                                                                                                                                                                                     humans with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-515059/46.
N-PSDB; AAA50270.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASB067; outer membrane prantibacterial; screening;
                                                                          243 RAVGYYDIDLSIIRNS-IGEVDVIIHDL--GEPVYIDYRAVEVRGEGADDKAFTTVADEV 299
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                                     71 RVFGYYESSVRFERKQRQGKRDLLIAHVTPGEPTKIAGTDVQIEGEAAQDENFDALRKNL 130
                                                                                                 Max
Local v
PLLIGDVFHHGKYETKKNLIENASAEHGYFDGRWLDRSVDVILPDNTADVSLIYDTGTQY 359
                                                                                                                                     Similarity
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                                                                                                                   Conservative 106;
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                                                                                                                                   Score 427.5; DB Pred. No. 5e-21;
                                                                                                                   Mismatches
                                                                                                                                                    DB 21;
                                                                                                                   235;
                                                                                                                 Indels 211;
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N-PSDB; AAS07278

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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B antigen; pharynx; meningitis; infection; baculovirus; yeast.
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence represents a Neisseria meningitidis serogroup A 85 kDa antigenic protein. Neisseria meningitidis colonises the pharynx, causing meningitis and, occasionally, septicaemia in the absence of meningitis. This antigenic protein is useful in the manufacture of a medicament for treating or preventing infection due to Neisseria bacteria, such as meningitis and septicaemia. It is also useful as a diagnostic reagent for detecting the presence of Neisseria bacteria or antibodies raised against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neisseria, and as a reagent for raising the antibodies. The Nei
nucleotide sequences can be expressed in a variety of different
expression systems, for example, mammalian cells, baculoviruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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     506
                                                                           450
                                                                                                             611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pacteria and yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 66-68; 92pp; English
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                                                                                                                                                                                                                                                 LYDMPDD-----RVLAINHDDGVNRSILGRISDAVSAVARAILPDESENEVIDLPE
 YKTTTA----GGGVRMGIPVTEYDRVNFGLAAEHLTVNTYNKAPKRYADFIRKYGKTDGA
                                   HEISRSIIQNGGWNRTYSLRYRLDKLKTQAPPE----TWQDLP---VDFVN--GK-PSQ
                                                                       FGTGKSAALRASRSK--TTLNGSLSFTDPYFTADGVSLGY--DIYGKAFDPRKASTSVKQ
                                                                                                         DGYQAGAELRLSEDKKGVKLYATKPLSHPLNDQLRATLGYQQEVFGHSTNGFDLSTRTLE
                                                                                                                                                NMSLTERST -
                                                                                                                                                                             RTALANRKTPADVYQSKKVPLYVFVASDKPRDGQIGL--GWGSDTGTRLVTKFEHNLINR
                                                                                                                                                                                                                    MESAPYDTSKLQRSKERVELLGYFDNVQ----
                                                                                                                                                                                                                                                                                          ----EISVQPLPNAGTKTVDFVLHIEPGRKIYVNEIHITGNNKTRDE--VVRRELRQ
                                                                                                                                                                                                                                                                                                                                                              LEKLLTMKPGKWYERQQMTAVLG---------EIQNRMGSAGYAYS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GNOVYSDRKLMR------QMSLTEGGIWTWLTRSDRFDRQKFAQDMEKVTDFYQNNGYF
                                                                                                                                                                                                                                                                                                                            TEPAQVDESTLEPVIETVELTDGILMDISP-----IEFSASNLIQDKLNLVAAKARH
                                                                                                                                                                                                                                                                                                                                                                                                                                         DFRILDTDIQTNEDKTRQTIKITVHEGGRFRWGKV---SIEGDTNE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FNQATLNQAVAGLKEEYLGRGKLNIQITPKVTKLARNRVDIDITIDEGKSAKITDIEFE- 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DGRWLDRSVDVILPDNTADVSLIYDTGTQYRFDEVVFFTIDPKTNQLTTDPDKLPVKREL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MD---LNGSIPRLRQ------TALVAARAVGYYDIDLSIIRNSIGEVDVIIHDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDA---IKKNLESFGLAQSQY 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARLFNDGVNKVP----RLKAKFYQSSQSGETSAIGSSHQKTEPYANIKAALED--ITQESA 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPLAFADFTIQDIRVEGLQRTEPSTVFNYLPVKVGDTYN------DTHGSAIIKSLY 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   792 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5,6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 265.5; DB 22; Pred. No. 1.1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                           -GSLDLSAGWVQDTG--LVMSAGVSQDNL
                                                                                                                                                                                                                  -----FDAVPLAGTPDK-----VDL--
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       The present sequence represents a Neisseria gonorrheae protein. The protein is used to produce the compositions of the invention. The specification describes a composition, comprising a Neisseria meningitidis serogroup B outer membrane preparation and an immunogenic component. The immunogenic component is protein disclosed in W099/57280, W099/36544, W099/24578, W099/6791, W097/28273, W096/29412, W095/03413, W099/31132, W099/58683, W099/55873, and/or N. meningitidis protein PorA, TbpB, PilC, OpA, or Omp85. The composition is used for making TbpA, TbpB, PilC, OpA, or Omp85. The composition is used for making
                                                                                                                                                                            Composition for treating or preventing infection to, detecting, or for raising antibodies against Neisserial bacteria, comprises an N. meningitidis serogroup B outer membrane preparation and an immunogenic
                                                                                                                                        Disclosure; Page 65-67;
                                                                                                                                                                                                            Composition
                                                                                                                                                                                                                                                                                                                                    17-JAN-2000;
09-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein
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DB; AAH42129.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SFGDNAYGSNRAHQMTG-----
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                                                                                                                                                                                                                                                                             Rappuoli R,
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treating or preventing
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infection due to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bacteria; a diagnostic reagent for detecting the presence of Neisserial bacteria or of antibodies raised against Neisserial bacteria; and/or a reagent which can raise antibodies against Neisserial bacteria. It may also be used as a vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116 TPLSLEELFAQESTEMGINPND-----YIPEYQGEQPNSEVVVPPTLEPEKPGLIKRLY 169
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E--EGNPIKLHFFIGTPF
                                 GSVWDGRTYTAAENGNNKSVYSENAHKSTFTNELRYSAGGAVTWLSPLGPMKFSYAYPLK
                                                                                                   SVRGYESGTLGP----KVYDEYGEKISYGGNKKANVSAELLFPMPGAKDARTVRLSLFADA
                                                                                                                                   SIRGYAHDSLSPISDKGYLTGGQVLAVG---TAEYNYEFM-----KDLRLAVFGDI
                                                                                                                                                                                                       SFGDNAYGSNRAHQMTG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MESAPYDTSKLQRSKERVELLGYFDNVQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DFRILDTDIQTNEDKTRQTIKITVHEGGRFRWGKV---SIEGDTNE------VPKAE
                                                                                                                                                                                                                                                                                                                                                                          FGTGKSAALRASRSK--TTLNGSLSFTDPYFTADGVSLGY--DIYGKAFDPRKASTSVKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----EISVQPLPNAGTKTVDFVLHIEPGRKIYVNEIHITGNNKTRDE--VVRRELRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TEPAQVDESTLEPVIETVELTDGILMDISP-----IEFSASNLIQDKLNLVAAKARH
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                                                                   -- NAYDKGFTNDTKIGAGVGVRWASPVGQVRVDVATGVK
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Pred. No. 1.1e-09;
9; Mismatches 352
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                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                        The present invention describes an immunogenic composition (I) comprising a Neisseria antigen and an adjuvant composition comprising an oligonucleotide comprising at least I CG motif. Also described is an adjuvant composition (II) comprising an oligonucleotide which comprises at least I CG motif and a complete Freund's adjuvant (CFA), where the oligonucleotide preferably comprises at least one phosphorothicate bond. AAA92359 to AAA92385 represent specifically claimed oligonucleotides of the present invention. (I) is useful for stimulating an immune response in a mammal, preferably a human, against Neisseria infection, preferably Neisseria meningitidis infection and in the manufacture of a medicament for inducing a protective immune response in a mammal. The present sequence represents the claimed Neisseria gonorrheae amino acid sequence disclosed in GB-9928197.4, which is given in the present invention.
                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 22; Page 32; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunogenic composition useful for stimulating an immune response in mammal against Neisseria infection, comprises Neisseria antigen and adjuvant composition comprising an oligonucleotide with a CG motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Grandi G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CG motif; complete Freund's adjuvant; phosphorothioate; immunogenic; Neisseria antigen; Neisseria meningitidis; Neisseria gonorrhoeae; bactericidal; antibacterial; vaccine; immunostimulatory; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB23786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria gonorrheae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neisseria gonorrheae amino
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270 GEPVYIDYRAVEVRGEGADDKAFTTVADEVPLLIGDVFHHGKYETKKNLIENASAEHGYF
                                                                                                                                                                                           116 TPLSLEELFAQESTEMGINPND-----YIPEYQGEQPNSEVVVPPTLEPEKPGLIKRLY 169
                                      124
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                                                                                                                                                                                                                                                Local Similarity
                                FNQATLNQAVAGLKEEYLGRGKLNIQITPKVTKLARNRVDIDITIDEGKSAKITDIEFE-
                                                                                                                                                             SPLAFADFTIQDIRVEGLQRTEPSTVFNYLPVKVGDTYN-----DTHGSAIIKSLY 66
                                                                                                ATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDA---IKKNLESFGLAQSQY 123
                                                                                                                              ARLFNDGVNKVP---RLKAKFYQSSQSGETSAIGSSHQKTEPYANIKAALED--ITQESA 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-015529/02
                                                                     MD---LNGSIPRLRQ------
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                                                                                                                                                                                                                             Score 265.5; DB 22;
Pred. No. 1.1e-09;
9; Mismatches 352;
                                                                TALVAARAVGYYDIDLSIIRNSIGEVDVIIHDL 269
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                                                                                                                  meningococcal infection;
                                                                                                                               Outer membrane protein;
                                                                                                                                                             Amino
                                                                                                                                                                                      21-AUG-2000
                                                                                                                                                                                                                                         AAY84946 standard; Protein;
                                                 Peptide
                                                                                          Neisseria
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                                                                                                                                                                                                                                                                                                            KKPEDEIORFOFOLGTTF 792
                                                                                                                                                                                                                                                                                                                                                                  GSVWDGRTYTAAENGNNKSVYSENAHKSTFTNELRYSAGGAVTWLSPLGPMKFSYAYPLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIRGYAHDSLSPISDKGYLTGGQVLAVG---TAEYNYEFM-----KDLRLAVFGDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SFGDNAYGSNRAHQMTG--------GIQAGYIWSDNFNHVPYRLRFFAGGDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DGSFKGLLYKGTYGWGRNKTDSASWPTRGY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EALLAGVAVHKTV-----ADNLVNPMRGYRQRYSLEVGSSGLVSDANMAIARAGISGVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YKTTTA----GGGVRMGIPVTEYDRVNFGLAAEHLTVNTYNKAPKRYADFIRKYGKTDGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HEISRSIIQNGGWNRTYSLRYRLDKLKTQAPPE----TWQDLP---VDFVN--GK-PSQ 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FGTGKSAALRASRSK--TTLNGSLSFTDPYFTADGVSLGY--DIYGKAFDPRKASTSVKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DGYQAGAELRLSEDKKGVKLYATKPLSHPLNDQLRATLGYQQEVFGHSTNGFDLSTRTLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RTALANRKTPADVYQSKKVPLYVFVASDKPRDGQIGL--GWGSDTGTRLVTKFEHNLINR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MESAPYDTSKLQRSKERVELLGYFDNVQ------FDAVPLAGTPDK-----VDL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LYDMPDD------RVLAINHDDGVNRSILGRISDAVSAVARAILPDESENEVIDLPE 552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----EISVQPLPNAGTKTVDFVLHIEPGRKIYVNEIHITGNNKTRDE--VVRRELRQ
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                                                                                                                                                             acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----YSATHNQTWFFPLSKTFTLMLGGEVGIAGGY---GRTKEIPFFENFYGGGLG
                                                                                         gonorrheae
                                                                                                                                                           sequence of
                                                                                                                                                                                     (first entry)
                                                            Location/Qualifiers
                                    /note=
                                                                                                                                                                                                                                                                                                                                                                                           -----NAYDKGFTNDTKIGAGVGVRWASPVGQVRVDVATGVK
                                  "signal peptide"
                                                                                                                                                          outer membrane
                                                                                                                            omp85; gonococcal infection; symptomatic
                                                                                                                  protective
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                                                                                                                  immune
                                                                                                                                                          protein (omp)
                                                                                                                  response; vaccine.
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                                                                                                                               disease;
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Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Fig 2; 98pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated outer membrane protein 85 of Neisseria gonorrhoeae meningitidis useful for vaccine, therapeutic and diagnostic compositions for gonococcal or meningococcal infections \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB;
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MESAPYDTSKLQRSKERVELLGYFDNVQ-----FDAVPLAGTPDK-----VDL--
                                                                                                                                                                                                                               TEPAQVDESTLEPVIETVELTDGILMDISP-----IEFSASNLIQDKLNLVAAKARH
                                                                                                                                                                                                                                                                                                                         LEQLLTVNMGEAYNLQAVRALSNDLIATRYFNMVNTEIVFPEREQIQNDQVSFEQSSSSR 449
                                                                                                                                                                                                                                                                                                                                                                                DFRILDTDIQTNEDKTRQTIKITVHEGGRFRWGKV---SIEGDTNE-----VPKAE 283
                                                                                                                                                                                                                                                                                                                                                                                                                             DGRWLDRSVDVILPDNTADVSLIYDTGTQYRFDEVVFFTIDPKTNQLTTDPDKLPVKREL 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GNQVYSDRKLMR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATLNQAVAGLKEEY----LGRGKLNIQITPKVTKLARNRVDIDITIDEGKSAKITDIEFE-
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                                                                                                                                                                                                                                                                                    LEKLLTMKPGKWYERQQMTAVLG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      resent invention may also be used in the screening chemical compounds such as drugs or vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.5%;
20.6%;
                                                                                                                           RVLAINHDDGVNRSILGRISDAVSAVARAILPDESENEVIDLPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 259.5; DE
Pred. No. 3e-09;
9; Mismatches 3
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Novel 85 kDa antigen fr
gonorrhoeae, useful in
                                                                                                                                29-NOV-1999;
09-MAR-2000;
            Novel 85 kDa
                                     N-PSDB; AAS07277.
                                                WPI; 2001-381289/40.
                                                                        Giuliani MM,
                                                                                               (CHIR-)
                                                                                                                                                                    28-NOV-2000; 2000WO-IB01851
                                                                                                                                                                                           31-MAY-2001.
                                                                                                                                                                                                                   WO200138350-A2
                                                                                                                                                                                                                                                     Binding-site
                                                                                                                                                                                                                                                                            Protein
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bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU03957 standard;
                                                                                                                                                                                                                                                                                                   Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSVWDGRTYTAAENGNNKSVYSENAHKSTFTNELRYSAGGAVTWLSPLGPMKFIYAYPLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G-----NAYDKGFTNDTKIGAGVGVRWASPVGQVRVDVATGVK 903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SVRGYESGTLGP----KVYDEYGEKISYGGNKKANVSAELLFPMPGAKDARTVRLSLFADA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIRGYAHDSLSPISDKGYLTGGQVLAVG---TAEYNYEFM------KDLRLAVFGDI 865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------YSATHNQTWFFPLSKTFTLMLGGEVGIAGGY---GRTKEIPFFENFYGGGLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SFGDNAYGSNRAHQMTG------GIQAGYIWSDNFNHVPYRLRFFAGGDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EALLAGVAVHKTV-----ADNLVNPMRGYRQRYSLEVGSSGLVSDANMAIARAGISGVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YKTTTA----GGGVRMGIPVTEYDRVNFGLAAEHLTVNTYNKAPKRYADFIKQYGKTDGA 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FGTGKSAALRASRSK--TTLNGSLSFTDPYFTADGVSLGY--DIYGKAFDPRKASTSVKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DGSFKGLLYKGTVGWGRNKTDSALWPTRGY------LTGVNAEIALPGSKLQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DGYQAGAELRLSEDKKGVKLYATKPLSHPLNDQLRATLGYQQEVFGHSTNGFDLSTRTLE
                                                                                              CHIRON SPA.
STATENS INST
                                                                                                                                                                                                                                                                                                                                                                                               meningitidis serogroup B antigenic protein.
                                                                                                                                                                                                                                                                                                                                                             infection;
                                                                                                                                                                                                                                                                                                                                                                       B antigen;
                                                                                                                                 99GB-0028197.
2000GB-0005698.
                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                        Pizza M,
                                                                                                                                                                                                                                                   /note= "Mature N. meningitidis serogroup B antigen" 715..722
                                                                                                                                                                                                                                                                                     /note= "Signal
                                                                                                                                                                                                                                           /note=
                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein;
from Neisseria meningitidis and Neisseria in the manufacture of a medicament for tre
                                                                                                                                                                                                                                                                                                                                                            pharynx; meningitis; septicaemia; mammalian cell;
baculovirus; yeast.
                                                                                               FOLKEHELSE
                                                                                                                                                                                                                                       "ATP/GTP-binding site motif A (P-loop)"
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                                                                     Rappuoli
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Best Local Sin
Matches 191;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence represents a Neisseria meningitidis serogroup B 85 kDa antigenic protein. Neisseria meningitidis colonises the pharynx, causing meningitis and, occasionally, septicaemia in the absence of meningitis. This antigenic protein is useful in the manufacture of a medicament for treating or preventing infection due to Neisseria bacteria, such as meningitis and septicaemia. It is also useful as a diagnostic reagent for detecting the presence of Neisseria bacteria or antibodies raised against Neisseria, and as a reagent for raising the antibodies. The Neisserial nucleotide sequences can be expressed in a variety of different expression systems, for example, mammalian cells, baculoviruses, plants,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                              N--GK-PSQEALLAGVAVHKTV-----
                                                                                                                                                                                         RKASTSIKQYKTTTA----GAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHYADFI
  ALPGSKLQY - -
                                               ARAGISGVYSFGDNAYGSNRAHQMTG-----
                                                                                            KKYGKTDGTDGSFKGWLYKGTVGWGRNKTDSALWPTRGY
                                                                                                                                                                                                                                         FDLSTRTLEHEISRSIIQNGGWNR-----TYSLRYRLDKLKTQAPPETWQDLP----VDFV 713
                                                                                                                                                                                                                                                                                        SAGVSQDNLFGTGKSAALRASRSK--TTLNGSLSFTDPYFTADGVSLGY--DVYGKAFDP 496
                                                                                                                                                                                                                                                                                                                                     KFEHNLINRDGYQAGAELRLSEDKKGVKLYATKPLSHPLNDQLRATLGYQQEVFGHSTNG
                                                                                                                                                                                                                                                                                                                                                                                                                                  ENEVIDLPERTALANRKTPADVYQSKKVPLYVFVASDKPRDGQIGL--GWGSDTGTRLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -VVRRELRQMESAPYDTSKLQRSKERVELLGYFDNVQ-----FDAVPLAGTPDK- 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAGYAYS-----EISVQPLPNAETKTVDFVLHIEPGRKIYVNEIHITGNNKTRDE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SFEQSSSSRTEPAQVDESTLEPVIETVELTDGILMDISP-----IEFSASNLIQDKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----VPKAELEKLLTMKPGKWYERQQMTAVLG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NASAEHGYFDGRWLDRSVDVILPDNTADVSLIYDTGTQYRFDEVVFFTIDPKTNQLTTDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GNQVYSDRKLMR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GEPVYIDYRAVEVRGEGADDKAFTTVADEVPLLIGDV-----FHHGKYETKKNLIE 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FNQATLNQAVAGLKEEYLGRGKLNIQITPKVTKLARNRVDIDITIDEGKSAKITDIEFE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARLFNDGVNKVP---RLKAKFYQSSQSGETSAIGSSHQKTEPYANIKAALED--ITQESA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPLALADFTIQDIRVEGLQRTEPSTVFNYLPVKVGDTYN-----DTHGSAIIKSLY 66
                                                                                                                                                                                                                                                                                                                                                                                          ----VDL--NMSLTERST----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NLVAAKARHLYDMPDD------RVLAINHDDGVNRSILGRISDAVSAVARAILPDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DKLPVKRELLEQLLTVNMGEAYNLQAVRALSNDLIATRYFNMVNTEIVFPEREQIQNDQV 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DFYQNNGYFDFRILDTDIQTNEDKTKQTIKITVHEGGRFRWGKV---SIEGDTNE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDA---IKKNLESFGLAQSQY 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative 121;
---YSATHNQTWFFPLSKTFTLMLGGEVGIAGGY---GRTKEIPFF
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Pred. No. 3.2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                            -ADNLVNPMRGYRQRYSLEVGSSGLVSDANMAI 764
                                                                                                                                                                                                                                                                                                                                                                                       ---------GSLDLSAGWVQDTG--LVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    342;
                                             -GIQAGYIWSDNFNHVPYR 808
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648
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B
                                             The sequence represents a Neisseria gonorrhoeae 85 kDa antigenic protein. N. gonorrhoeae is closely related to N. meningitidis, which colonises the pharynx, causing meningitis and, occasionally, septicaemia in the absence of meningitis. This antigenic protein is useful in the manufacture of a medicament for treating or preventing infection due to Neisseria bacteria, such as meningitis and septicaemia. It is also useful as a diagnostic reagent for detecting the presence of Neisseria bacteria or antibodies raised against Neisseria, and as a reagent for raising the antibodies. The Neisserial nucleotide sequences can be expressed in a variety of different expression systems for example members.
Sequence
                                                                                                                                                                                           Claim 1; Page 37-39;
                                                                                                                                                                                                                                 Novel 85 kDa antigen from Neisseria meningitidis and Neisseria gonorrhoeae, useful in the manufacture of a medicament for treating
                                                                                                                                                                                                                                                                                                                                               (CHIR-)
(STAT-)
                                                                                                                                                                                                                     preventing Neisserial bacteria infection
                                                                                                                                                                                                                                                                                         WPI; 2001-381289/40
                                                                                                                                                                                                                                                                                                                     Giuliani MM,
                                                                                                                                                                                                                                                                                                                                                                                         09-MAR-2000; 2000GB-0005698
                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-MAY-2001
                         baculoviruses,
                                                                                                                                                                                                                                                                                                                                                                                                      29-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                               28-NOV-2000; 2000WO-IB01851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200138350-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLGPMKFSYAYPLKKKPEDEIQRFQFQLGTTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PVGQVRVDVATGVKE---EGNPIKLHFFIGTPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VRLSLFADAGSVWDGKTYDDNSSSATGGRVQNIYGAGNTHKSTFTNELRYSAGGAVTWLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LRLAVFGDIGNAYD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENFYGGGLGSVRGYESGTLGP----KVYDEYGEKISYGGNKKANVSAELLFPMPGAKDART 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LRFFAGGDQSIRGYAHDSLSPISDKGYLTGGQVLAVG---TAEYNYEFM------KD 856
                      of different expression systems, firuses, plants, bacteria and yeast.
                                                                                                                                                                                                                                                                                                                                               CHIRON SPA.
STATENS INS
                                                                                                                                                                                                                                                                             AAS07279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gonorrhoeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein; pharynx;
infection; baculo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gonorrhoeae antigenic protein
 797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                     Pizza M,
AA
                                                                                                                                                                                                                                                                                                                                                                                                      99GB-0028197
                                                                                                                                                                                                                                                                                                                                                 INST FOLKEHELSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Signal 22..797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein;
                                                                                                                                                                                         92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             baculovirus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Mature N. gonorrhoeae antigen"
                                                                                                                                                                                                                                                                                                                    Rappuoli R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           meningitis; septicaemia; mammalian cell;
virus; yeast; Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptide'
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                                                                                                                                                                                                                                                                                                                    Holst J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    919
                                        for
                                      example,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -KGFTNDTKIGAGVGVRWAS 889
                                        mammalian cells
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Best Local Similarity
Matches 191; Conserv
                AAU04451;
                                                      AAU04451 standard;
                                                                                                                                                                                             PVGQVRVDVATGVKE---EGNPIKLHFFIGTPF
                                                                                                                                                                                                                                                                                                                                                  LRFFAGGDQSIRGYAHDSLSPISDKGYLTGGQVLAVG---TAEYNYEFM------KD 856
                                                                                                                                                                                                                               VRLSLFADAGSVWDGKTYDDNSSSATGGRVQNIYGAGNTHKSTFTNELRYSAGGAVTWLS
                                                                                                                                                                                                                                                                             LRLAVFGDIGNAYD-----
                                                                                                                                                                                                                                                                                                            ENFYGGGLGSVRGYESGTLGP----KVYDEYGEKISYGGNKKANVSAELLFPMPGAKDART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N--GK-PSOEALLAGVAVHKTV------ADNLVNPMRGYRQRYSLEVGSSGLVSDANMAI 764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KFEHNLINRDGYQAGAELRLSEDKKGVKLYATKPLSHPLNDQLRATLGYQQEVFGHSTNG
                                                                                                                                                     PLGPMKFSYAYPLKKKPEDEIQRFQFQLGTTF 797
                                                                                                                                                                                                                                                                                                                                                                                                     ALPGSKLQY
                                                                                                                                                                                                                                                                                                                                                                                                                                         ARAGISGVYSFGDNAYGSNRAHQMTG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KKYGKTDGTDGSFKGWLYKGTYGWGRNKTDSALWPTRGY------LTGVNAEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RKASTSIKQYKTTTA----GAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHYADFI 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FDLSTRTLEHEISRSIIQNGGWNR-----TYSLRYRLDKLKTQAPPETWQDLP---VDFV 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SAGVSQDNLFGTGKSAALRASRSK--TTLNGSLSFTDPYFTADGVSLGY--DVYGKAFDP 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENEVIDLPERTALANRKTPADVYQSKKVPLYVFVASDKPRDGQIGL--GWGSDTGTRLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAGYAYS-----EISVQPLPNAETKTVDFVLHIEPGRKIYVNEIHITGNNKTRDE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----VDL--NMSLTERST----------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ·VVRRELRQMESAPYDTSKLQRSKERVELLGYFDNVQ------FDAVPLAGTPDK- 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DKLPVKRELLEOLLTVNMGEAYNLQAVRALSNDLIATRYFNMVNTEIVFPEREQIQNDQV 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NLVAAKARHLYDMPDD-----RVLAINHDDGVNRSILGRISDAVSAVARAILPDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SFEOSSSSRTEPAQVDESTLEPVIETVELTDGILMDISP----IEFSASNLIQDKL 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----VPKAELEKLLTMKPGKWYERQQMTAVLG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NASAEHGYFDGRWLDRSVDVILPDNTADVSLIYDTGTQYRFDEVVFFTIDPKTNQLTTDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GEPVYIDYRAVEVRGEGADDKAFTTVADEVPLLIGDV-----FHHGKYETKKNLIE 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FNQATLNQAVAGLKEEYLGRGKLNIQITPKVTKLARNRVDIDITIDEGKSAKITDIEFE- 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARLFNDGVNKVP---RLKAKFYQSSQSGETSAIGSSHQKTEPYANIKAALED--ITQESA 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPLALADFT IQDIRVEGLQRTEPSTVFNYLPVKVGDTYN-----DTHGSAIIKSLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TPLSLEELFAQESTEMGINPND-----YIPEYQGEQPNSEVVVPPTLEPEKPGLIKRLY 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DFYQNNGYFDFRILDTDIQTNEDKTKQTIKITVHEGGRFRWGKV---SIEGDTNE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GNQVYSDRKLMR-------QMSLTEGGIWTWLTRSNQFNEQKFAQDMEKVT 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MD---LNGSIPRLRQ------TALVAARAVGYYDIDLSIIRNSIGEVDVIIHDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDA---IKKNLESFGLAQSQY 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative 121;
                                                      Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20.5%; Pred. No. 3.2e-09; ative 121; Mismatches 342;
                                                                                                                                                                                                                                                                                                                                                                                            -YSATHNQTWFFPLSKTFTLMLGGEVGIAGGY---GRTKEIPFF 648
                                                      797
                                                    ⋛
                                                                                                                                                                                             919
                                                                                                                                                                                                                                                                         -----KGFTNDTKIGAGVGVRWAS 889
                                                                                                                                                                                                                                                                                                                                                                                                                                      ------GIQAGYIWSDNFNHVPYR 808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -GSLDLSAGWVQDTG--LVM
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                                                                                                                                                                                                                                                                                     Qγ
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                             Matches 191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence represents a Neisseria meningitidis serogroup A 85 kDa antigenic protein. Neisseria meningitidis colonises the pharynx, causing meningitis and, occasionally, septicaemia in the absence of meningitis. This antigenic protein is useful in the manufacture of a medicament for treating or preventing infection due to Neisseria bacteria, such as meningitis and septicaemia. It is also useful as a diagnostic reagent for detecting the presence of Neisseria bacteria or antibodies raised against Neisseria, and as a reagent for raising the antibodies. The Neisserial nucleotide sequences can be expressed in a variety of different expression systems, for example, mammalian cells, baculoviruses, plants,
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: There are two versions of this sequence displayed in specification (see AAU03958).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 39-40; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bacteria and yeast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel 85 kDa antigen from Neisseria meningitidis and Neisseria gonorrhoeae, useful in the manufacture of a medicament for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Giuliani MM,
      183
                                                                                                                                                                                                         170
                                                                                                                                                                                                                                                                                       116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             preventing Neisserial bacteria infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-MAR-2000; 2000GB-0005698
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein
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bacterial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-OCT-2001
                                                                                                                                                                    67
                                                                                                                                                                                                                                                 16
                                                                                                                                                                                                                                                                             TPLSLEELFAQESTEMGINPND-----YIPEYQGEQPNSEVVVPPTLEPEKPGLIKRLY 169
      GNOVYSDRKLMR - -
                                     GEPVYIDYRAVEVRGEGADDKAFTTVADEVPLLIGDV----FHHGKYETKKNLIE 320
                                                                           FNQATLNQAVAGLKEEYLGRGKLNIQITPKVTKLARNRVDIDITIDEGKSAKITDIEFE- 182
                                                                                                                     MD---LNGSIPRLRQ-----
                                                                                                                                                           ATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDA---IKKNLESFGLAQSQY 123
                                                                                                                                                                                                 ARLFNDGVNKVP----RLKAKFYQSSQSGETSAIGSSHQKTEPYANIKAALED--ITQESA 224
                                                                                                                                                                                                                                         SPLALADFTIQDIRVEGLQRTEPSTVFNYLPVKVGDTYN------DTHGSAIIKSLY 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001-381289/40
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infection;
                                                                                                                                                                                                                                                                                                                                                                                                             797 AA;
                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99GB-0028197
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                                                                                                                                                                                                                                                                                                                       5.5%; Score 259; DB 22; 20.5%; Pred. No. 3.2e-09; tive 121; Mismatches 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pharynx; meningitis; septicaemia; mammalian
baculovirus; yeast.
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                                                                                                                   -TALVAARAVGYYDIDLSIIRNSIGEVDVIIHDL 269
-QMSLTEGGIWTWLTRSNQFNEQKFAQDMEKVT 226
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                                                     Protein
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                                                                                Peptide
                                                                                                                         Neisseria
                                                                                                                                                              Serogroup
                                                                                                                                                                                      Amino acid sequence of a Neisseria serogroup B protein
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                                                                                                                                                                                                                                                                      AAB84744 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                        PLGPMKFSYAYPLKKKPEDEIQRFQFQLGTTF
                                                                                                                                                                                                                                                                                                                                                                  PVGQVRVDVATGVKE--EGNPIKLHFFIGTPF 919
                                                                                                                                                                                                                                                                                                                                                                                             VRLSLFADAGSVWDGKTYDDNSSSATGGRVQNIYGAGNTHKSTFTNELRYSAGGAVTWLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LRFFAGGDQSIRGYAHDSLSPISDKGYLTGGQVLAVG---TAEYNYEFM-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KKYGKTDGTDGSFKGWLYKGTVGWGRNKTDSALWPTRGY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N--GK-PSQEALLAGVAVHKTV-----ADNLVNPMRGYRQRYSLEVGSSGLVSDANMAI 764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SAGVSQDNLFGTGKSAALRASRSK--TTLNGSLSFTDPYFTADGVSLGY--DVYGKAFDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENEVIDLPERTALANRKTPADVYQSKKVPLYVFVASDKPRDGQIGL--GWGSDTGTRLVT 601
                                                                                                                                                                                                                                                                                                                                                                                                                       ENFYGGGLGSVRGYESGTLGP----KVYDEYGEKISYGGNKKANVSAELLFPMPGAKDART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALPGSKLQY-----YSATHNQTWFFPLSKTFTLMLGGEVGIAGGY---GRTKEIPFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARAGISGVYSFGDNAYGSNRAHQMTG------GIQAGYIWSDNFNHVPYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RKASTSIKQYKTTTA----GAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHYADFI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SFEQSSSSRTEPAQVDESTLEPVIETVELTDGILMDISP-----IEFSASNLIQDKL 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DKLPVKRELLEQLLTVNMGEAYNLQAVRALSNDLIATRYFNMVNTEIVFPEREQIQNDQV 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FDLSTRTLEHEISRSIIQNGGWNR----TYSLRYRLDKLKTQAPPETWQDLP---VDFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -VVRRELRQMESAPYDTSKLQRSKERVELLGYFDNVQ-----FDAVPLAGTPDK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NLVAAKARHLYDMPDD-----RVLAINHDDGVNRSILGRISDAVSAVARAILPDES 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAGYAYS-----EISVQPLPNAETKTVDFVLHIEPGRKIYVNEIHITGNNKTRDE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DFYQNNGYFDFRILDTDIQTNEDKTKQTIKITVHEGGRFRWGKV----SIEGDTNE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----VPKAELEKLLTMKPGKWYERQQMTAVLG----
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                                                                                                                       meningitidis
                                                                                                                                                              protein;
                                                                                                                                                                                                                   (first entry)
                                                  /note= "signal peptide" 22..797
                                                                                           Location/Qualifiers
                                                                                                                                                            outer membrane protein;
                                       "mature protein'
                                                                                                                                                                                                                                                                         797
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                                                                                                                                                              Neisserial infection;
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Best Local Similarity Zv...
191; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     specification describes a composition, comprising a Neisseria meningitidis serogroup B outer membrane preparation and an immunogenic component. The immunogenic component is protein disclosed in W099/57280, W099/36544, W099/24578, W099/66791, W097/28273, W099/29412, W095/03413, W099/31132, W099/58683, W099/5873, and/or N. meningitidis protein PorA, TbpB, PilC, OpA, or Omp85. The composition is used for making a medicament for treating or preventing infection due to Neisserial bacteria; a diagnostic reagent for detecting the presence of Neisserial bacteria; a diagnostic reagent for detecting the presence of Neisserial bacteria or of antibodies raised against Neisserial bacteria; and/or a reagent which can raise antibodies against Neisserial bacteria. It may also be used as a vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Composition for treating or preventing infection to, detecting, or for raising antibodies against Neisserial bacteria, comprises an N. meningitidis serogroup B outer membrane preparation and an immunogenic component.
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N-PSDB; AAH42128.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             67
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                                     NLVAAKARHLYDMPDD------RVLAINHDDGVNRSILGRISDAVSAVARAILPDES
 -VVRRELRQMESAPYDTSKLQRSKERVELLGYFDNVQ----
                                                                                                              SFEQSSSSRTEPAQVDESTLEPVIETVELTDGILMDISP-----IEFSASNLIQDKL 492
                                                                                                                                                                                       DKLPVKRELLEQLLTVNMGEAYNLQAVRALSNDLIATRYFNMVNTEIVFPEREQIQNDQV
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                                                                                                                                                                                                                                                                                                                                            GEPVYIDYRAVEVRGEGADDKAFTTVADEVPLLIGDV-----FHHGKYETKKNLIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDA---IKKNLESFGLAQSQY 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARLFNDGVNKVP---RLKAKFYQSSQSGETSAIGSSHQKTEPYANIKAALED--ITQESA 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPLALADFTIQDIRVEGLQRTEPSTVFNYLPVKVGDTYN-----DTHGSAIIKSLY 66
                                                                                                                                                   ----VPKAELEKLLTMKPGKWYERQQMTAVLG------
                                                                                                                                                                                                                              DFYQNNGYFDFRILDTDIQTNEDKTKQTIKITVHEGGRFRWGKV---SIEGDTNE----
                                                                                                                                                                                                                                                                                                         GNQVYSDRKLMR--------QMSLTEGGIWTWLTRSNQFNEQKFAQDMEKVT
                                                                                                                                                                                                                                                                                                                                                                                FNQATLNQAVAGLKEEYLGRGKLNIQITPKVTKLARNRVDIDITIDEGKSAKITDIEFE- 182
                                                                                                                                                                                                                                                                                                                                                                                                                   MD---LNGSIPRLRQ-----TALVAARAVGYYDIDLSIIRNSIGEVDVIIHDL
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2000GB-0005699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 259; DB 22;
Pred. No. 3.2e-09;
1; Mismatches 342;
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RESULT 13
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Composition for treating or preventing infection to, detecting, or raising antibodies against Neisserial bacteria, comprises an N. meningitidis serogroup B outer membrane preparation and an immunoge
                                                        N-PSDB; AAH42130.
                                                                   WPI; 2001-451895/48
                                                                                          Pizza M,
                                                                                                                                         17-JAN-2000;
09-MAR-2000;
                                                                                                                 (CHIR-) CHIRON SPA
                                                                                                                                                                          17-JAN-2001; 2001WO-IB00166
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                                                                                                                                                                                                                                                              Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VRLSLFADACSVWDGKTYDDNSSSATGGRVQNIYGAGNTHKSTFTNELRYSAGGAVTWLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENFYGGGLGSVRGYESGTLGP----KVYDEYGEKISYGGNKKANVSAELLFPMPGAKDART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LRFFAGGDQSIRGYAHDSLSPISDKGYLTGGQVLAVG---TAEYNYEFM-----KD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALPGSKLQY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARAGISGVYSFGDNAYGSNRAHQMTG------GIQAGYIWSDNFNHVPYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KKYGKTDGTDGSFKGWLYKGTVGWGRNKTDSALWPTRGY-----LTGVNAEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RKASTSIKQYKTTTA----GAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHYADFI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAGVSQDNLFGTGKSAALRASRSK--TTLNGSLSFTDPYFTADGVSLGY--DVYGKAFDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KFEHNLINRDGYQAGAELRLSEDKKGVKLYATKPLSHPLNDQLRATLGYQQEVFGHSTNG 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENEVIDLPERTALANRKTPADVYQSKKVPLYVFVASDKPRDGQIGL--GWGSDTGTRLVT 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----VDL--NMSLTERST------------GSLDLSAGWVQDTG--LVM
                                                                                         Rappuoli R,
                                                                                                                                                                                                                                                                                                                       meningitidis
                                                                                                                                                                                                                                                                                                                                                                           sequence of a Neisseria serogroup A protein
                                                                                                                                         2000GB-0001067
2000GB-0005699
                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                              /note= "signal peptide" 22..797
                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                         Giuliani
                                                                                                                                                                                                                                               "mature protein'
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA
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                                                                                                                                                                                                                                                                                                                                                      protein; Neisserial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a Neisseria serogroup A protein. The protein is used to produce the compositions of the invention. The specification describes a composition, comprising a Neisseria meningitidis serogroup B outer membrane preparation and an immunogenic component. The immunogenic component is protein disclosed in W099/57280, W099/36144, W099/24578, W099/6791, W097/28273, W095/29412, W095/03413, W099/31132, W099/36883, W099/56791, W097/28273, W099/5412, W099/58883, W099/55873, and/or N. meningitidis protein PorA, Theating to Component in the composition is used for making a medicament for treating or preventing infection due to Neisserial bacteria; a diagnostic reagent for detecting the presence of Neisserial bacteria or of antibodies raised against Neisserial bacteria; and/or a reagent which can raise antibodies against Neisserial bacteria. It may
 765
                                                                                                                                                                                                                                                                412 ---- VDL--NMSLTERST---
                                                                                                                                                                                                                                                                                                                                                                                                                      314
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                             KKYGKTDGTDGSFKGWLYKGTVGWGRNKTDSALWPTRGY------LTGVNAEI
                                                                N--GK-PSQEALLAGVAVHKTV-----ADNLVNPMRGYRQRYSLEVGSSGLVSDANMAI 764
                                                                                                       RKASTSIKQYKTTTA----GAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHYADFI
ARAGISGVYSFGDNAYGSNRAHQMTG
                                                                                                                                        FDLSTRTLEHEISRSIIQNGGWNR-----TYSLRYRLDKLKTQAPPETWQDLP---VDFV
                                                                                                                                                                                 SAGVSQDNLFGTGKSAALRASRSK--TTLNGSLSFTDPYFTADGVSLGY--DVYGKAFDP
                                                                                                                                                                                                                   KFEHNLINRDGYQAGAELRLSEDKKGVKLYATKPLSHPLNDQLRATLGYQQEVFGHSTNG
                                                                                                                                                                                                                                                                                             ENEVIDLPERTALANRKTPADVYQSKKVPLYVFVASDKPRDGQIGL--GWGSDTGTRLVT
                                                                                                                                                                                                                                                                                                                                                                       NLVAAKARHLYDMPDD------RVLAINHDDGVNRSILGRISDAVSAVARAILPDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DKLPVKRELLEQLLTVNMGEAYNLQAVRALSNDLIATRYFNMVNTEIVFPEREQIQNDQV 440
                                                                                                                                                                                                                                                                                                                                  -VVRRELRQMESAPYDTSKLQRSKERVELLGYFDNVQ-----FDAVPLAGTPDK- 411
                                                                                                                                                                                                                                                                                                                                                                                                                    SAGYAYS-
                                                                                                                                                                                                                                                                                                                                                                                                                                    SFEQSSSSRTEPAQVDESTLEPVIETVELTDGILMDISP------IEFSASNLIQDKL 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GEPVYIDYRAVEVRGEGADDKAFTTVADEVPLLIGDV-----FHHGKYETKKNLIE 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----VPKAELEKLLTMKPGKWYERQQMTAVLG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDA---IKKNLESFGLAQSQY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPLALADFTIQDIRVEGLQRTEPSTVFNYLPVKVGDTYN------DTHGSAIIKSLY 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                be used as a vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  191;
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                                                                                                                                                                                                                                                                                                                                                                                                              ----EISVQPLPNAETKTVDFVLHIEPGRKIYVNEIHITGNNKTRDE-
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1; Mismatches
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Pred. No. 3.2e-09;
                                                                                                                                                                                                                                                            -GSLDLSAGWVQDTG--LVM
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-GIQAGYIWSDNFNHVPYR

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Matches 191
                                                                                                adjuvant composition (II) comprising an oligonucleotide which comprises at least 1 CG motif and a complete Frend's adjuvant (CFA), where the oligonucleotide preferably comprises at least one hosphorothicate bond. AAA92359 to AAA92385 represent specifically claimed oligonucleotides of the present invention. (I) is useful for stimulating an immune response in a mammal, preferably a human, against Neisseria infection, preferably Neisseria meningitidis infection and in the manufacture of a medicament for inducing a protective immune response in a mammal. The present sequence represents the claimed Neisseria meningitidis serogroup B amino acid sequence disclosed in GB-9928197.4, which is given in the present
                                                                                                                                                                                                                                              The present invention describes an immunogenic composition (I) comprising a Neisseria antigen and an adjuvant composition comprising an oligonucleotide comprising at least 1 CG motif. Also described is an
                                                                                                                                                                                                                                                                                                                                  Immunogenic composition useful for stimulating an immune response in mammal against Neisseria infection, comprises Neisseria antigen and adjuvant composition comprising an oligonucleotide with a CG motif -
                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
                                                            Sequence
                                                                                                                                                                                                                                                                                                            Claim 22;
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               Score 259;
Pred. No. 3.
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meningitidis; Neisseria gonorrhoeae;
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               DB 22;
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                            Length 797;
278;
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                                                                                                                                                                                                                                                                            N--GK-PSQEALLAGVAVHKTV-----ADNLVNPMRGYRQRYSLEVGSSGLVSDANMAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TPLSLEELFAQESTEMGINPND-----YIPEYQGEQPNSEVVVPPTLEPEKPGLIKRLY
PLGPMKFSYAYPLKKKPEDEIQRFQFQLGTTF
                                                                                                LRLAVFGDIGNAYD-----
                                                                                                                                                            LRFFAGGDQSIRGYAHDSLSPISDKGYLTGGQVLAVG---TAEYNYEFM----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DKLPVKRELLEQLLTVNMGEAYNLQAVRALSNDLIATRYFNMVNTEIVFPEREQIQNDQV 440
                               PVGQVRVDVATGVKE--EGNPIKLHFFIGTPF
                                                             VRLSLFADAGSVWDGKTYDDNSSSATGGRVQNIYGAGNTHKSTFTNELRYSAGGAVTWLS
                                                                                                                            ENFYGGGLGSVRGYESGTLGP----KVYDEYGEKISYGGNKKANVSAELLFPMPGAKDART
                                                                                                                                                                                             ALPGSKLQY----
                                                                                                                                                                                                                           ARAGISGVYSFGDNAYGSNRAHQMTG-------GIQAGYIWSDNFNHVPYR
                                                                                                                                                                                                                                                          KKYGKTDGTDGSFKGWLYKGTVGWGRNKTDSALWPTRGY------LTGVNAEI
                                                                                                                                                                                                                                                                                                                        RKASTSIKQYKTTTA----GAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHYADFI 552
                                                                                                                                                                                                                                                                                                                                                    FDLSTRTLEHEISRSIIQNGGWNR-----TYSLRYRLDKLKTQAPPETWQDLP---VDFV
                                                                                                                                                                                                                                                                                                                                                                                       SAGVSQDNLFGTGKSAALRASRSK--TTLNGSLSFTDPYFTADGVSLGY--DVYGKAFDP
                                                                                                                                                                                                                                                                                                                                                                                                                     KFEHNLINRDGYQAGAELRLSEDKKGVKLYATKPLSHPLNDQLRATLGYQQEVFGHSTNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENEVIDLPERTALANRKTPADVYQSKKVPLYVFVASDKPRDGQIGL--GWGSDTGTRLVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SFEQSSSSRTEPAQVDESTLEPVIETVELTDGILMDISP-----IEFSASNLIQDKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DFYQNNGYFDFRILDTDIQTNEDKTKQTIKITVHEGGRFRWGKV---SIEGDTNE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NASAEHGYFDGRWLDRSVDVILPDNTADVSLIYDTGTQYRFDEVVFFTIDPKTNQLTTDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GNQVYSDRKLMR--------QMSLTEGGIWTWLTRSNQFNEQKFAQDMEKVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MD---LNGSIPRLRQ----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ARLFNDGVNKVP---RLKAKFYQSSQSGETSAIGSSHQKTEPYANIKAALED--ITQESA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    -VDL--NMSLTERST------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -VPKAELEKLLTMKPGKWYERQQMTAVLG----
                                                                                                                                                                                           ----YSATHNQTWFFPLSKTFTLMLGGEVGIAGGY---GRTKEIPFF
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                                                                                              --------KGFTNDTKIGAGVGVRWAS
                                 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                    -GSLDLSAGWVQDTG--LVM
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Best Local S
Matches 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  comprising a Neisseria antigen and an adjuvant composition comprising an obligonucleotide comprising at least 1 CG motif. Also described is an adjuvant composition (II) comprising an obligonucleotide which comprises at least 1 CG motif and a complete Freund's adjuvant (CFA), where the obligonucleotide preferably comprises at least one phosphorothicate bond. AAA92359 to AAA92385 represent specifically claimed obligonucleotides of the present invention. (I) is useful for stimulating an immune response in a mammal, preferably a human, against Neisseria infection, preferably Reisseria meningitidis infection and in the manufacture of a medicament for inducing a protective immune response in a mammal. The present sequence represents the claimed Neisseria meningitidis serogroup A amino acid sequence disclosed in GB-9928197.4, which is given in the present
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunogenic composition useful for stimulating an immune response in mammal against Neisseria infection, comprises Neisseria antigen and a adjuvant composition comprising an oligonucleotide with a CG motif -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes an immunogenic composition (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 22;
                    381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Grandi G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CG motif; complete Freund's adjuvant; phosphorothioate; immunogenic; Neisseria antigen; Neisseria meningitidis; Neisseria gonorrhoeae; bactericidal; antibacterial; vaccine; immunostimulatory; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CHIR-) CHIRON SPA
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                                                                                                                                                                                                                                                                                                                                      116 TPLSLEELFAQESTEMGINPND-----YIPEYQGEQPNSEVVVPPTLEPEKPGLIKRLY 169
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             DKLPVKRELLEQLLTVNMGEAYNLQAVRALSNDLIATRYFNMVNTEIVFPEREQIQNDQV
                                                                                                                   GNQVYSDRKLMR
                                            DFYQNNGYFDFRILDTDIQTNEDKTKQTIKITVHEGGRFRWGKV---SIEGDTNE----
                                                                          NASAEHGYFDGRWLDRSVDVILPDNTADVSLIYDTGTQYRFDEVVFFTIDPKTNQLTTDP
                                                                                                                                           GEPVYIDYRAVEVRGEGADDKAFTTVADEVPLLIGDV-----FHHGKYETKKNLIE
                                                                                                                                                                             FNQATLNQAVAGLKEEYLGRGKLNIQITPKVTKLARNRVDIDITIDEGKSAKITDIEFE-
                                                                                                                                                                                                             MD---LNGSIPRLRQ---
                                                                                                                                                                                                                                                                       ARLFNDGVNKVP---RLKAKFYQSSQSGETSAIGSSHQKTEPYANIKAALED--ITQESA 224
                                                                                                                                                                                                                                         ATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDA---IKKNLESFGLAQSQY 123
                                                                                                                                                                                                                                                                                                           SPLALADFTIQDIRVEGLQRTEPSTVFNYLPVKVGDTYN----
                                                                                                                                                                                                                                                                                                                                                                                 191;
                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page 33; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                meningitidis serogroup A amino acid sequence
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Pred. No. 3.2e
21; Mismatches
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                                                                                                                                                                                                          ~TALVAARAVGYYDIDLSIIRNSIGEVDVIIHDL
                                                                                                            -QMSLTEGGIWTWLTRSNQFNEQKFAQDMEKVT
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3.2e-09;
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                                                                                                                                                                                                                                                                                      LRFFAGGDQSIRGYAHDSLSPISDKGYLTGGQVLAVG---TAEYNYEFM-----KD
                                                                                                                                      PLGPMKFSYAYPLKKKPEDEIQRFQFQLGTTF
                                                                                                                                                                   PVGQVRVDVATGVKE--EGNPIKLHFFIGTPF
                                                                                                                                                                                                                                LRLAVFGDIGNAYD-----
                                                                                                                                                                                                                                                                                                                           ALPGSKLQY----
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                                                                                                                                                                                                 VRLSLFADAGSVWDGKTYDDNSSSATGGRVQNIYGAGNTHKSTFTNELRYSAGGAVTWLS
                                                                                                                                                                                                                                                                                                                                                                                   KKYGKTDGTDGSFKGWLYKGTVGWGRNKTDSALWPTRGY------LTGVNAEI
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                                                                                                                                                                                                                                                                                                                                                        ARAGISGVYSFGDNAYGSNRAHQMTG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SAGVSQDNLFGTGKSAALRASRSK--TTLNGSLSFTDPYFTADGVSLGY--DVYGKAFDP 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KFEHNLINRDGYQAGAELRLSEDKKGVKLYATKPLSHPLNDQLRATLGYQQEVFGHSTNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -VVRRELRQMESAPYDTSKLQRSKERVELLGYFDNVQ-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----VPKAELEKLLTMKPGKWYERQQMTAVLG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----VDL--NMSLTERST-----
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----EISVQPLPNAETKTVDFVLHIEPGRKIYVNEIHITGNNKTRDE-
                                                            Protein;
                                                                                                                                                                                                                                                                                                                        -YSATHNOTWFFPLSKTFTLMLGGEVGIAGGY---GRTKEIPFF
                                                              797
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------GSLDLSAGWVQDTG--LVM
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                                                                                                                                                                                                                                                                                                                                                      -----GIQAGYIWSDNFNHVPYR
                                                                                                                                                                                                                              -- KGFTNDTKIGAGVGVRWAS
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RESULT 16
AAY84947
ID AAY84
XX AAY84
XX AAY84
XX AMino
DT 21-AU
XX Outer
KW Outer
KW menin
XX MO200
XX WO200
XX PD 27-AF
XX 22-OC
XX 22-OC
XX Y UWK
XX UUGd
XX UUGG
XX
                                                             N-PSDB; AAA15156
                                                                                                                                                                                                                                                                                                                                                                                                                                  22-OCT-1998;
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                                                                                                                                                                                                                                                                                                                   (UYMO-) UNIV MONTANA
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Neisseria meningitidis meningococcal infection; Outer membrane protein; omp85; Amino acid sequence of outer membrane protein (omp)

omp85; gonococcal infection; symptomatic disease; protective immune response; vaccine.

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Best Local Sir
Matches 190;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 41; Page 89-92; 98pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated outer membrane protein 85 of Neisseria gonorrhoeae and meningitidis useful for vaccine, therapeutic and diagnostic compositions for gonococcal or meningococcal infections
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KKYGKTDGTDGSFKGWLYKGTVGWGRNKTDSALWPTRGY-----
                                                       N--GK-PSQEALLAGVAVHKTV-----ADNLVNPMRGYRQRYSLEVGSSGLVSDANMAI 764
                                                                                                                                                                                                                                                                                       KFEHNLINRDGYQAGAELRLSEDKKGVKLYATKPLSHPLNDQLRATLGYQQEVFGHSTNG
                                                                                                                                                                                                                                                                                                                                                                                                           ENEVIDLPERTALANRKTPADVYQSKKVPLYVFVASDKPRDGQIGL--GWGSDTGTRLVT 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NLVAAKARHLYDMPDD------RVLAINHDDGVNRSILGRISDAVSAVARAILPDES 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPLAFADFTIQDIRVEGLQRTEPSTVFNYLPVKVGDTYN-----DTHGSAIIKSLY 66
                                                                                                                 RKASTSIKQYKTTTA----GAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHYADFI
                                                                                                                                                                        FDLSTRTLEHEISRSIIQNGGWNR-----TYSLRYRLDKLKTQAPPETWQDLP---VDFV 713
                                                                                                                                                                                                                                   SAGVSQDNLFGTGKSAALRASRSK--TTLNGSLSFTDPYFTADGVSLGY--DVYGKAFDP 496
                                                                                                                                                                                                                                                                                                                                                             ----VDL--NMSLTERST----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SAGYAYS-----EISVQPLPNAETKTVDFVLHIEPGRKIYVNEIHITGNNKTRDE- 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SFEQSSSSRTEPAQVDESTLEPVIETVELTDGILMDISP-----IEFSASNLIQDKL 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----VPKAELEKLLTMKPGKWYERQQMTAVLG-----EIQNRMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DKLPVKRELLEQLLTVNMGEAYNLQAVRALSNDLIATRYFNMVNTEIVFPEREQIQNDQV 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DFYQNNGYFDFRILDTDIQTNEDKTKQTIKITVHEGGRFRWGKV---SIEGDTNE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GEPVYIDYRAVEVRGEGADDKAFTTVADEVPLLIGDV-----FHHGKYETKKNLIE 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -VVRRELRQMESAPYDTSKLQRSKERVELLGYFDNVQ-----FDAVPLAGTPDK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NASAEHGYFDGRWLDRSVDVILPDNTADVSLIYDTGTQYRFDEVVFFTIDPKTNQLTTDP 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GNQVYSDRKLMR-------QMSLTEGGIWTWLTRSNQFNEQKFAQDMEKVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FNQATLNQAVAGLKEEYLGRGKLNIQITPKVTKLARNRVDIDITIDEGKSAKITDIEFE- 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MD---LNGSIPRLRQ------TALVAARAVGYYDIDLSIIRNSIGEVDVIIHDL 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDA---IKKNLESFGLAQSQY 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARLFNDGVNKVP----RLKAKFYQSSQSGETSAIGSSHQKTEPYANIKAALED--ITQESA 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.4%; Score 253; DB 21; 20.4%; Pred. No. 8.4e-09; tive 121; Mismatches 343;
                                                                                                                                                                                                                                                                                                                                                       -GSLDLSAGWVQDTG--LVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 797;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 278;
-LTGVNAEI
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ARLFNDGVNKVPRLKAKFYQSSQSGETSAIGSSHQKTEPYANIKAALEDITQESAM 225	169 Y	ρ 2
	66	Db
MSVIEETTPLSLEELFAQESTEMGINPNDYIPEYQGEQPNSEVVVPPTLEPEKPGLIKRL 168	109	QΥ
NAASKDDPSIVYLPPQINGSSNDEBLQTELPMLLATALKNKIGEQSPPLGLD 108	24	B 2
O)	Query Ma Best Loc Matches	?
	Q Sequence 896 AA;	SQ
ence is		3 G G
des isolated polynucleotides encoding 1 or Omp100 protein of Lawsonia ces can be used in vaccines for the pr		8888
:		XX PS
intracellularis polynucleotide and encoded protein, used to awsonia intracellularis infection .	Lawsonia prevent L	X P P
67.	R WPI; 2001-592540/67.	X DR
OD INC.	(PFIZ ) PFIZER PROD	X X
US-0160922.	22-OCT-1999; 99US-	X PR
JP-0320736.	F 20-OCT-2000; 2000JP-03	X P S
	D 26-JUN-2001.	X PD
	N JP2001169787-A.	XX
lularis.	)S Lawsonia intracellular X	20 X
YefW; ABC1; Omp100; Lawsonia intracellularis infection;	HtrA; PonA; HypC; vaccine.	XXX
lularis protein SEQ ID NO: 5.	)E Lawsonia intracellularis	XEX
st entry)	20-NOV-2001 (first	× D :
	C AAG78603;	Y A S
; Protein; 896 AA.	SULT 17 578603 AAG78603 standard;	AA RE
PLGPMKFRYAYPLKKKPEDBIQRFQFQLGTTF 797	766	В
VKEEGNPIKLHFFIGTPF 919	890	Qy
VRLSLFADAGSVWDGKTYDDNSSSATGGRVQNIYGAGNTHKSTFTNELRYSAGGAVTWLS 765	706	Db
YDKGFTNDTKIGAGVGVRWAS 889	857	Qy
;   ; NKKANVSAELLFPMPGAKDART	649	Дb
LRFFAGGDQSIRGYAHDSLSPISDKGYLTGGQVLAVGTAEYNYEFMKD 856	809	δ
ARAGISGVYSFGDNAYGSNRAHQMTG	765 600	Db Qy

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                                 Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                      Novel human diagnostic protein #17701.
                                                                                                                             18-FEB-2002
                                                                                                                                                                                    ABG17710 standard; Protein; 474
                                                                                                                                                                                                                                                                           864
                                                                                                                                                                                                                                                                                                           891
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  392
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                                                                                                                                                                                                                                                                         MGDLR 868
                                                                                                                                                                                                                                                                                                                                                                                              ---SRSKNHIIHWRTRAGAAYKNSKKPVPVFDRFFIGGIDSIRGYDTEDLAPKDPRFGDE
                                                                                                                                                                                                                                                                                                                               IGGDRMAFLNLEYIWTFQPELGLALVPFYDIGFQTDSVQTSNPFSKLKQSYGLELRWRSP
                                                                                                                                                                                                                                                                                                                                                              TGGQVLAVGTAEYNYEFMKDLRLAV--FGDIGNAYDKGFTND----TKIGAGVGVRWASP
                                                                                                                                                                                                                                                                                                                                                                                                                            NAYGSNRAHOMTGGIQAGYIWSDNFNHVPYRLRFFAGGDQSIRGYAHDSLSPISDK-GYL 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRKKTYGDTIRLFHPI-----GEYSSIFVGYRIDQYRLYDIPSTAPRSYLDY-QGKN 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----STRTLEHEISRSIIQNGGWNRTYSLRYRLDKLKTQAPPETWQDLPVDFVNGKP
                                                                                                                                                                                                                                                                                                       VGQVR 895
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ISSVVSGGFTFDST--DSRERPSKGHTAKLIVEYGGGGLGGNDNFFKPIAELQGFYSI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SQEALLAGVAVHKTVADNLVNPMRGYRQRYSLEVGSSGLVSDANMAIARAGISGVYSFGD 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -GYILSIEGFISSKSSSLDLSFTNPRVYDTD------FGFSNNIYTLRDEWDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DGYQAGAELRLSEDKKGVKLYATKPLSHPLNDQLRATLGYQQEVFGHSTNGFDL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIDVTFLIDKKQKVFLRRIIVEGNTRTRDNVILRELRLADGDLFNGQHLRRSNECLNRLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------QSKKVPLYVFVASDKPRDGQIGLGWGSDTGTRLVTK---FEHNLINR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----VIDLPERTAL-----ANRKTPADVY----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DKLNLVAAKARHLYDMPDDRVLAINHDDGVNRSILGRISDAVSAVARAILPDESENE---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DQVSFEQSSSSRTEPAQVDESTLEP-----VIETVELTDGILMDISPIEFSASNLIQ 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QLLTVNMGEAYNLQAVRALSNDLIATRYFNMVNTEIVFPER------EQIQN 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LDRSV--DVILPDNTADVSLIYDTGTQYRFDEVVFFTIDPKTNQLTTDPDKLPVKRELLE 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --NGLIKK-NTIADVRIHGLKVLDPDVILTRLTINKGDHTDHAKINAEIKKIWELG--YF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---SVISDRLLSQDIQKITDLYRKEGYYLAE--VNYEIKEKENTSSA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDYRA-VEVRGEGADDKAFTTVADEVPLLIGDVFHHGKYETKKNLIENASAEHGYFDGRW 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SDVSASIEESGEG----RLLVFTVQEKPKITDVVVQGSKAVSIDNILAAMSSKKG-----
                                                                                                                        (first entry)
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DXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess blodiversity
CC and to produce other types of data and products dependent on DNA and
CC diagnostic amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local :
                                                                    AAY34506
                                  25-AUG-1999
                                                                                                    AAY34506 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                215
                                                                                                                                                                                                                                  913 FFIG 916
                                                                                                                                                                                                                                                               158 GKWWGAVFVDSGEAVSDIRRSDFKTGTGVGVRWESPVGPIKLDFAVPVADKDEHG---LQ
                                                                                                                                                                                                                                                                                                                                                                                  795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 20; SEQ ID No 48069; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-639362/73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAR-2001; 2001WO-US08631
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                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 45.2 hes 56; Conservative
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                                                                                                                                                                                              FYIG
                                                                                                                                                                                                                                                                                               KDLRLAVFGDIGNAYDKGFTNDTKIGAGVGVRWASPVGQVRVDVATGV--KEEGNPIKLH 912
                                                                                                                                                                                                                                                                                                                                     GWIETGDFDKVPPDLRFFAGGDRSIRGYKYKSIAPKYANGDLKGASKLITGSLEYQYNVT 157
                                                                                                                                                                                                                                                                                                                                                        GYIWSDNFNHVPYRLRFFAGGDQSIRGYAHDSLSPISDKGYLTGGQVLAVGTAEYNYEFM 854
                                                                                                                                                                                                218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        474 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                               5.0%; Score 235.5; DB 2
45.2%; Pred. No. 6.5e-08;
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Porphorymonas gingivalis protein PG45

(first entry)

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10-DEC-1997;
31-DEC-1997;
31-DEC-1997;
31-DEC-1998;
10-MAR-1998;
09-APR-1998;
03-APR-1998;
05-MAY-1998;
22-MAY-1998;
29-JUL-1998;
                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gingivitis
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Ross E
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                                                                                                                                                                                                                            109
                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                            PLLIGDVFHHGKYETKKNLIENASAEHGYFDGRWLDRSVDVILPDN-TADVSLIYDTGTQ 358
     DVYQSKK---
                                                                         GESPTDSLEVEDMKVLYYRKMPVRPKILAKRFRFFSGNLYRQK-----
                                                                                                                                             NDLIATRYFNMVNTEIVFPEREQIQNDQVSFEQSSSSRTEPA----QVDESTL-----
                                             RVLAINHDDGVNRSILGRISDAVSAVARAILPDESENEVIDLPERTAL----ANRKTPA
                                                                                                                      RD----NGYYYFRPQDIIYEADTLLVRGAVCLRAKLSEDTPPQAMRPWRIGKRTAVLLGMN
                                                                                                                                                                                               YRFDEVVFFTIDPKINQLTTDPDKLPVKRELLEQLLTVNMGEAYNL-----
                                                                                                                                                                                                                    PVFISQV----KSDSRAKVATNILREHGYFDAK-VKSSVTTLKKDSLKAKISYTVDMASP 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BC,
                        -----DDETTRKSLARLG-AFSVIDLNFLQRDSISGLLDVRLLTTLDKPWDASLET--
                                                                                            -EPVIETVELTD-GIL----MDISP-----IEFSASNLIQDKLNLVAAKARHLYDMPDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Barr IG,
Rothel LJ,
                                                                                                                                                                                                                                                                                                                                                 gingivitis
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97AU-0001839.
97AU-0001182.
98AU-0002546.
98AU-0002264.
98AU-0003128.
98AU-0003128.
98AU-0003338.
98AU-0004517.
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-VPLYVFVASDKPRDGQIGLGW---GS---DTGTRLVTKFEHNLINRDG
                                                                                                                                                                                                                                                                      4.7%; Score 224.5; DB 20; 20.6%; Pred. No. 7.4e-07; tive 90; Mismatches 290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hocking DM, Webb EA;
                                                                                                                                                                     -STFPDSILAYRQTPS---LIRKGDQFNLAKLHEERQTISALL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English
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RESULT 20
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31-DEC-1997;
30-JAN-1998;
10-MAR-1998;
09-APR-1998;
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22-MAY-1998;
29-JUL-1998;
                                               Agius CT,
Ross BC,
                   N-PSDB; AAX91597
                            WPI; 1999-385613/32
                                                                                                                             23-APR-1998
                                                                                                                                                                                      04-AUG-1998;
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                                                                                                                                                                                                                                                                                      Porphorymonas gingivalis; vaccine; antigenic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KLKTQAPPETWQDLPVDFVNGKPSQEALLAGVAVHKTVADNLVN-PMRGY-----RQRYS 748
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                                              Barr IG,
Rothel LJ,
                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                              98AU-0002911.
98AU-0003128.
98AU-0003338.
98AU-0003654.
98AU-0004917.
                                                                                                                                                                                                                                                                  gingivalis
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97AU-0000839.
97AU-0001182.
                                                                                                                                                                                                                                                                                                                  gingivalis protein
                                                                                                                                              98AU-0001546
98AU-0002264
                                                                                                                                                                                                         98WO-AU01023
                                                                                                                                                                                                                                                                                                                                                                             Protein;
                                               Hocking D
Webb EA;
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Antigenic Porphorymonas gingivalis peptides

for preventing

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAX91536 to AAX91801 encode two hundred and sixty six antigenic
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LHLPYNTGKKGYYNIPRFKDAIGFHLAVGYPF 803
                                    VK - - - - - EEG - - -
                                                                  AVFLDAGNVWLLREDSSRPGGALSEVGSVSNFLNSIALGTGVGLRYDLAFLVVRVDVGFG
                                                                                                         AVEGDIGNAY - - - - -
                                                                                                                                      SEQFYVGGANSIRAFTVRSIGPGRFNPDSDNQYSYLDQVGEFKLEANVEYRGKLFGDLHA
                                                                                                                                                                         RLRFFAGGDQSIRGYAHDSL----SPISDKGYL---TGGQVLAVGTAEYNYEFMKDLRL 859
                                                                                                                                                                                                                                              LEVGSSGLVSDANMAIA-RAGISGVYSFGDNAYGSNRAHQMTGGIQAGYIWSDNFNHVPY
                                                                                                                                                                                                                                                                                 SVSEKSPHHLWMQFGLSEAGNLLNLIYLAAGKKYSDT--KNFVGVPFSQFIKATGELRYS
                                                                                                                                                                                                                                                                                                                  KLKTQAPPETWQDLPVDFVNGKPSQEALLAGVAVHKTVADNLVN-PMRGY-----RQRYS 748
                                                                                                                                                                                                                                                                                                                                                     SKEHRHAIFPLKLNYNLLGHQTETFQAITANNPPLLLSLQSQFLAQMGYIYTFN----K 564
                                                                                                                                                                                                                                                                                                                                                                                                                         YNMNTAVNLSFPSIVFPGLLDKYYYYPTTTTFQASATALNRAHYFSMYSFGFSTTYEFQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DVYQSKK-----VPLYVFVASDKPRDGQIGLGW---GS---DTGTRLVTKFEHNLINRDG 612
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                                                                                                                                                                                                                                                                                                                                                                                      YQAGAELRLSEDKKGVKLYATKPLSHPLNDQLRAT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -LFTSKSNDFIGPGLNFALARRNVFGGGENLSWNIGGSYEWETGNR-PENSSNRLIDINS 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RVLAINHDDGVNRSILGRISDAVSAVARAILPDESENEVIDLPERTAL ---- ANRKTPA 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----DDETTRKSLARLG-AFSVIDLNFLQRDSISGLLDVRLLTTLDKPWDASLET--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GESPTDSLEVEDMKVLYYRKMPVRPKILAKRFRFFSGNLYRQK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YRFDEVVFFTIDPKTNQLTTDPDKLPVKRELLEQLLTVNMGEAYNL-----QAVRALS 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -EPVIETVELTD-GIL----MDISP-----IEFSASNLIQDKLNLVAAKARHLYDMPDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RD---NGYYYFRPQDIIYEADTLLVRGAVCLRAKLSEDTPPQAMRPWRIGKRTAVLLGMN
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                                                                                                                                                                                                                DRNQSLATRFGTGVIYSYG---
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                                 -NPIKLHFFIGTPF 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 224.5; DB : Pred. No. 7.8e-07
                                                                                                   ----DKGFTNDTKIGAGVGVRWASPVGQVRVDVATG
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<u>О</u>у Оу ОЪ

48 522 108

SI--LGRISDAVSA----

MLRSKGYFSSKVSLTEKDGAYTVHITÞGÞRTKIANVGVAILGDILSDGNLAEYYRNALEN

PDTESVKLKPKFPVRIDTQDSEIKDMVEEHLPLITQQQEEVLDKEQTGFLAEEAPDNVKT 107

----VARAILPDESENEVIDLPERTALAN 558

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RESULT 21
AAY74862
IDY 'A862
AAY74862
AXX AAY74
AXC AAY74
AXC Neiss
KW Neiss
KW antig
KW antig
KW antig
CC PR 01-M
PR 02-SI
PR 02
Qy
                                                              Matches
                                                                                                               Query Match
                                                                                                                                                                                                             AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54573 to AAZ54576 and AAZ54616 to AAZ54473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-OCT-1998;
09-OCT-1998;
09-OCT-1998;
                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel Neisserial polypeptides predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1998;
31-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia; antibacterial; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Petersen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neisseria meningitidis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-APR-1999;
                                                                                     Local Similarity
PVIETVELTDGILMDISPIEFSASNLIQDKLNLVAAKARHLYDMPDDRVLAINHDDGVNR 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000-062150/05
DB; AAZ53624.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J, Pizza M,
H, Venter JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 669; 1453pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and diagnostics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  meningitidis ORF 286 protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Galeotti C,
                                                                                                                                                                     615 AA;
                                                         Conservative
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98US-0103796.
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98US-0099062
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                                                                                  4.7%;
22.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Grandi G,
                                                         72;
                                                                                Score 220; DB 21;
Pred. No. 1.1e-06;
                                                         Mismatches
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Ratti G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ť
                                                                                                               DB 21;
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Scalato E,
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                                                                                                      Length
                                                         Indels 148;
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RESULT 2:
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The present sequence is a putative version of the Neisseria meningitidis strain ATCC13090 BASB040 protein sequence. This prosimilar to the D15 outer membrane protein of the bacterium. The
                                                                         Novel BASB040 polypeptides of Neisseria meningitidis useful for diagnostic, prophylactic and therapeutic purposes against microbial diseases comprise a specific amino acid sequence
                                                       Claim
                                                                                                                                  WPI; 2000-423426/36.
N-PSDB; AAA48507.
                                                                                                                                                                                                                            07-DEC-1998;
                                                                                                                                                                                                                                                      02-DEC-1999;
                                                                                                                                                                                                                                                                                                         WO200034480-A1
                                                                                                                                                                                                                                                                                                                                                                       BASB040; bacterial disease; respiratory
                                                                                                                                                                                                                                                                                                                                                                                               Neisseria meningitidis BASB040 putative
                                                                                                                                                                                                                                                                                                                                                                                                                             03-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY99623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY99623 standard;
                                                                                                                                                                                                  (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                                              15-JUN-2000
                                                                                                                                                                                                                                                                                                                                 Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                          meningitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          571 KRMKLKHGSGLGVRWFSPLAPFSFDIAYGHSDK--KIRWHISLGTRF 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  511
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                                                       4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FTNDTKIGAGVGVRWASPVGQVRVDVATGVKEEGNPIKLHFFIGTPF 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGGASSVRGYELDSIGLAGPNGSVLPERALLVGSLEYQLPFTRTLSGAVFHDMGDAAANF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MDKYETTLAAGISQPRNYRGNYWTSNVSYNRSTTQNLEKRAFSGGIWYVRDRAGIDARLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FDLSTRTLEHEISRSIIQNGGW---NRTYSLRYRLDKLKTQAPPETWQDLPVDFVNGKPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADFDRLQGDRVPVKVSVTEVKRHKLETGIRLDSEYGLGGKIAYDYYNLFNKGYIGSVVWD
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                                                   Page 59-60; 98pp; English.
                                                                                                                                                                                                                                                                                                                                                          cancer;
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                                                                                                                                                                                                                            98GB-0026886
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                                                                                                                                                                                                                                                                                                                                                          autoimmune
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                                                                                                                                                                                                                                                                                                                                                          disease.
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                                                                                                                                                                                                                                                                                                                                                                    tract infection; bacteraemia;
                                                                                                                                                                                                                                                                                                                                                                                               protein sequence
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130;
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                                                                                           RFFAGGDQSIRGYAHDSLSPISDKGYLTGGQVLAVGTAEYNYEFMKDLRLAVFGDIGNAY
                                 DKGFTNDTKIGAGVGVRWASPVGQVRVDVATGVKEEGNPIKLHFFIGTPF
                                                                  MFRSGGASSVRGYELDSIGLAGPNGSVLPERALLVGSLEYQLPFTRTLSGAVFHDMGDAA
                                                                                                                                     TALIRTS----ARAG-----YFFTPENKKLGTFIIRGQAGYTVARDNADVPSGL
                                                                                                                                                                    SGLVSDANMAIARAGISGVYSFGDNAYGSNRAHQMTGGI----QAGYIWSDNFNHVPYRL
                                                                                                                                                                                                      AEFLAEGRKIPGSDIDLGNSHATMLTASWKRQLLNNVLHPENGHYLDGKIGTTLGTFLSS
                                                                                                                                                                                                                                       QEALLAGVAV------HKT-----VADNLVNPMRGY-----RQRYSLEVGS
                                                                                                                                                                                                                                                                       MDKYETTLAAGISQPRNYRGNYWTSNVSYNRSTTQNLEKRAFSGGIWYVRDRAGIDARLG
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                                                                                                                                                                                                                                                                                                                                                                          ----RLSEDKKGVKLYATKPLSHPLNDQLRAT----LG-------YQQEVFGHSTNG 661
                                                                                                                                                                                                                                                                                                                                                                                                            ----IAFGDFEITGTQRYPEQIVSGLARFQPGTPYDLDLLLDFQQAL-EQNGHYSGASVQ 276
                                                                                                                                                                                                                                                                                                                                                                                                                                           RDGQIGLGWGSDTGTR------------LVTKFEHNLINRDGYQAGAEL- 619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             {\tt WQQPVGSDFDQDSWENSKTSVLGAVTRKGYPLAKLGNTRAAVNPDTATVDLNVVVDSGRP}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MLRSKGYFSSKVSLTEKDGAYTVHITPGPRTKIANVGVAILGDILSDGNLAEYYRNALEN 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SI--LGRISDAVSA---------VARAILPDESENEVIDLPERTALAN 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PDTESVKLKPKFPVRIDTQDSEIKDMVEEHLPLITQQQEEVLDKEQTGFLAEEAPDNVKT 101
                                                                                                                                                                                                                                                                                                          FDLSTRTLEHEISRSIIQNGGW---NRTYSLRYRLDKLKTQAPPETWQDLPVDFVNGKPS 718
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22.0%;
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Pred. No. 1.3e-06;
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RESULT 2:
AAY99624
BASB040; bacterial disease; res
meningitis; cancer; autoimmune
                                                                                           Neisseria meningitidis BASB040 putative protein sequence
                                                                                                             03-JAN-2001
                                                                                                                                            AAY99624 standard; Protein;
                      15-JUN-2000.
                                      WO200034480-A1
                                                     Neisseria meningitidis
                                                                                                            (first entry)
                                                                             respiratory
                                                                                                                                            609
                                                                     disease
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                                                                            tract
                                                                             infection;
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bacteraemia;

#2

02-DEC-1999;

99WO-EP09560

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RESULT 24
AAY99625
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AAY99625 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is a putative version of the Neisseria meningitidis strain ATCC13090 BASB040 protein sequence. This protein is similar to the D15 outer membrane protein of the bacterium. The protein, its gene, antibodies, antagonists and agonists can be used to diagnose and treat bacterial diseases such as those leading to upper respiratory tract infections, bacteraemia and meningitis. In addition, they can be used in vaccines for use against cancer and autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; Page 60-61; 98pp; English
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                                                                                                      ANFKRMKLKHGSGLGVRWFSPLAPFSFDTAYGHSDK--KIRWHISLGTRF
                                                                                                                                                                                         {\tt MFRSGGASSVRGYELDSIGLAGPNGSVLPERALLVGSLEYQLPFTRTLSGAVFHDMGDAA}
                                                                                                                                                                                                                                    RFFAGGDQSIRGYAHDSLSPISDKGYLTGGQVLAVGTAEYNYEFMKDLRLAVFGDIGNAY 869
                                                                                                                                                                                                                                                                                TALIRTS----ARAG------YFFTPENKKLGTFIIRGQAGYTVARDNADVPSGL
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                                                                                                                                                DKGFTNDTK1GAGVGVRWASPVGQVRVDVATGVKEEGNP1KLHFF1GTPF 919
                                                                                                                                                                                                                                                                                                                                                                                                                           QEALLAGVAV-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----IAFGDFEITGTQRYPEQIVSGLARFQPGTPYDLDLLLDFQQAL-EQNGHYSGASVQ
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Pred. No. 1.3e-06;
4; Mismatches 232;
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                        QEALLA-----
                                                                                                                                           ADFDRLQGDRVPVKVSVTEVKRHKLETGIRLDSEYGLGGKIAYDYYNLFNKGYIGSVVWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PVIETVELTDGILMDISPIEFSASNLIQDKLNLVAAKARHLYDMPDDRVLAINHDDGVNR 521
                                                           MDKYETTLAAGISQPRNYRGNYWTSNVSYNRSTTQNLEKRAFSGGVW-----YVRDRAG
                                                                                                   FDLSTRTLEHEISRSIIQNGGW---NRTYSLRYRLDKLKTQAPPETWQDLPVDFVNGKPS
                                                                                                                                                                                                                                                                              RDGQIGLGWGSDTGTR----
                                                                                                                                                                                                                                                                                                                    WQQPVGSDFDQDSWENSKTSVLGAVTRKAYPLAKLGNTQAAVNPDTATADLNVVVDSGRP
                                                                                                                                                                                                                                                                                                                                                                RKTPA-----DVYQSKK-----
                                                                                                                                                                                                                                                                                                                                                                                                      MLRSKGYFSSKVSLTEKDGAYTVHITPGPRTKIANVGVAILGDILSDGNLAEYYRNALEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SI--LGRISDAVSA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PDTESVKLKPKFPVLIDTQDSEIKDMVEEHLPLITQQQEEVLDKEQTGFLAEEAPDNVKT 79
                                                                                                                                                                                                                                  ----IAFGDFEITGTQRYPEQIVSGLARFQPGMPYDLDLLLDFQQAL-EQNGHYSGASVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     al Similarity
132; Conserv
                                                                                                                                                                                     RLSEDKKGVKLYATKPLSHPLNDQLRAT----LG------YQQEVFGHSTNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   meningitidis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.5%;
BASB040 putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 215; DB 21;
Pred. No. 2.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                -VARAILPDESENEVIDLPERTALAN 558
                                                                                                                                                                                                                                                                          ----LVTKFEHNLINRDGYQAGAEL-
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RESULT 25
AAY74861
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            AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54537 to AAZ54536 and AAZ54616 to AAZ54473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-OCT-1998;
09-OCT-1998;
09-OCT-1998;
25-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                         Novel Neisserial polypeptides predicted vaccines and diagnostics .
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31-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neisseria meningitidis; Neisseria gonorrheae; antigenic; diagnosis; immunogenic; infection; antibacterial; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fraser C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-SEP-1998;
02-SEP-1998;
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                                                                                                                                                                                                                                                                                                                         Page 667; 1453pp;
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, Pizza M, Rappuoli R,
     antibacterial agents.
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Venter J
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98US-0098994
98US-0099062
98US-0103774
98US-01103794
98US-01103796
98US-01121528
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Scalato E,
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may themselves of the invent
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RESULT 26
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31-MAY-1999;
17-JUN-1999;
21-JUL-1999;
                                                   31-MAY-2000;
                                                                                                                                                                 Microbial infection;
                                                                                                                                                                                                                  05-APR-2001
                                                                                                     WO200073502-A2
                                                                                                                           Helicobacter pylori
                                                                                                                                                    vaccine; screening
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nes 132; Conserv
                                                                                                                                                                                         pylori HPS120 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                 2000WO-EP05024
                                                                                                                                                                                                                 (first entry)
99DE-1024965.
99DE-1027740.
99DE-1034029.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene therapy protocols
                                                                                                                                                                 antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --GVAV-----HKT------VADNLVNPMRGY-----RQRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.5%;
                                                                                                                                                                                                                                                                    916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 215; DB 21;
Pred. No. 2.4e-06;
'3; Mismatches 225;
                                                                                                                                                                                                                                                                    A
                                                                                                                                                               Helicobacter pylori infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -VARAILPDESENEVIDLPERTALAN 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LVTKFEHNLINRDGYQAGAEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 615
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                                                                                                                                                                                                                                                                                                                                  615
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CC This invention describes a novel preparation of an agent (A) for CC detection, prevention and/or treatment of microbial infection by: CC (1) identifying essential genes (I) and corresponding polypeptides (CC (II); (ii) identifying compounds that are directed against (II) and CC inactivate the microbe; (iii) testing these for suitability for use; and CC (iv) formulating selected (A). Identifying essential genes (I) comprises (CI) formulating selected (A). Identifying essential genes (I) comprises (II) products of the invention for survival of the deficient organisms (CC inhibition (CAI) and/or subtractive recombination mutagenesis (SRM), CC then determining viability and/or survival of the deficient organisms. CC be a nucleic acid (Ia), vector or host cell containing (Ia), derived (CC polypeptide (IIa), or fragments, (IIa) reparticularly used for diagnosis, CC fragments or an inhibitor of (IIa)) are particularly used for diagnosis, CC (Ia) and (IIa) are used in DNA, subunit or live vaccines. The method CC generals, so identified (A) should have a broad spectrum of activity. Many generate field (A) should have a broad spectrum of activity. Many conditions are used for screened quickly, in an automated process, and the identified genes can be used for screening without purification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
      343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Preparing an agent for diagnosis or control of microbial infection, useful particularly against Helicobacter, based on identification of essential genes in defective mutants -
                               402 YNLQAVRALSNDL---IATRYFNMVNTETVFPEREQIQNDQVSFEQSSSSRTEPAQVDES 458
                                                                                                                                                                                                                           317
                                                                                                                                                                                                                                                                   192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 37; Page 236-239; 366pp; German
                                                                                                                                                                                                                                                                                                            260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 MTSQALAQQNNPANIINHVPAHDTAINQAKAGNPPVLLTPEQIQAR-LNAAGLNAKPQSQ 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
FNIEHLRADAQILKTEIADKGYAFA---VVKPDLDK--
                                                                                   FSTHDAKLHYKVKEGIQYRISDIL
                                                                                                                       -NTADVSLIYDT--GTQYRFDEVVFFTIDPKTNQLTTDPDKLPVKRELLEQLLTVNMGEA 401
                                                                                                                                                                  RMIESLSANKQRDFMGWMWGLNDGKLRLDQLEYDSMRIQDVYMRRGYLDAHISSPFLKTD
                                                                                                                                                                                                                                                                   GSV-
                                                                                                                                                                                                                                                                                              GEVDVIIHDLGEPVYIDYRAVEVRGEGADDKAFTTVAD---EVPLLIGDVFHHGKYETKK 316
                                                                                                                                                                                                                                                                                                                                            TEKEKDGLKSQMGIKKGDTFDEQKLE-----HAKTALKTALEGQGYY----
                                                                                                                                                                                                                                                                                                                                                                                  SSHOKTEPYANIKAALEDITQESAMDLNGSIPRLRQTAL-VAARAVGYYDIDLSIIRNSI 259
                                                                                                                                                                                                                    QGEQPNSEVVVPPTLEPEKPGLIKRLYARLFNDGVNKVPRLKAKFYQSSQSG--ETSAIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALDVVNFDDQSPISRIGEQSPPLGLDMSVIEETTPLSLEELFAQESTEMGINPNDYIPEY 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LTSPKEASQESQK---NEAPKNEVQRNEAQKETPQSNQTPKEMKVKSISYVGLSYMSDML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANEIVKI------RVGDIVDSKKIDTAVL------ALFNQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fuchs TM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           916
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                                                                                                                                                                                                                                                        ----VEVRTEKVSEGALLIVFDVNRGDSIYIKQSIYEGSAKLKR 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                               ----GYFKDVYA-TFEGGI-----LEFHFDEKARIAGVEIKGYG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 206.5; DB 44,
Pred. No. 1.6e-05;
""amatches 318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hueck CJ,
                                                                               IEIDNPVVPLK--TLEKALKVKRKDV 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22; Length 916;
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                                                                                                                                                                                                             -WLDRSVD--VILPD 344
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Вb Š В Š 밁 Ş В Ş 밁 δô рЬ Ş В ş В õ

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PF XX PR PR XX XX PA XX XX PI DR XX XX DR DR DR XX
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ID ABG2
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New isolated polynucleotide and encoded polypeptides, useful in
                                                                                                                          31-MAR-2000;
23-AUG-2000;
                                                                      Drmanac RT,
                                                                                             (HYSE-) HYSEQ INC
                                                                                                                                                               30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                      WO200175067-A2
                                                                                                                                                                                             11-OCT-2001.
                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                Novel human diagnostic protein #25549.
                                                                                                                                                                                                                                                                    Human; chromosome mapping; gene mapping; gene therapy; food supplement; medical imaging; diagnostic; genetic o
                                                                                                                                                                                                                                                                                                                                            18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                              ABG25558 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                845 VIGAGFERATWRASTGLQIEWISPMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              868
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             836 LTGGQVLAVGTAEYNYEFMK--DLRLAVFGDIG------
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                              2001-639362/73
DB; AAS89745.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AYDKGFTNDT-KIGAGVGVRWASPVG 892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WLGGDGIFTASTELSYGVLKAAKMRLAWFFDFGFLTFKTPTRGSFFYNAPVTTANFKDYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SYDNTDDYYFPRNGVIFS-----SYATMSGLPSSGTLNSWNGLGGNVRNTKVYGKFAAYH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HLQKYLLIDLIARFKTQGGYIFRYNTDDYLPLNSTFYMGGVTTVRGFRNGSVTPKDEFGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPRQCSTPASVIINRLSGGKTPLQPESCSSPGAITTSPEIRGIWDRDYHTPITSSFTLDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADYRISYQYIQQGGGFGVNVGRMLGNRTHVSLGYNLNVTKLLGFSSPLYNRYYSSVNEVV 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IATGGGRSYPGMPKGAGRMFAGNLSLTNP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --KKGVKLYATKP------LSHPLNDQLRATLGYQQEVFGHSTNGFDLSTRTL- 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T-LEPVIETVELTDGILMD----ISPIEFSASNLI------QDKLNLVAAKARHLYDMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -EHEISRSIIQNGG------WNRTY-SLRYRLDKLKTQAPPETWQDLPVDFVNG--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NGLVKVIYRIEVGDMVYINDVIISGNQRTSDRIIRRELLLGPKDKYNLTKLR------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --NSENSLRR--LGFFSKVKIEEKRV----NSSLMDL-
                                                                                                                        2000US-0540217
2000US-0649167
                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---IQAGYIWSDNF-NHVPYRLRFFAGGDQSIRGYAHDSLSPISDKGY
                                                                                                                                                                                                                                                                                                                                                                                                Protein;
                                                                      ΥŢ
                                                                                                                                                                                                                                                                                                                                                                                                 371
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                                                                                                                                                                                                                                                                                  forensic;
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RESULT 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC polynucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as CC a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. CC diagnostics, forensics, gene mapping, Identification of mutations in CC diagnostics for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences. ABG00010-ABG30377 represent novel human CC diagnostic amino acid sequences of the invention.

CC The polypeptide and sequences of the invention. On the printed CC specification, but was obtained in electronic format directly from WIPO at figure the printed control of the control of the control of the printed control of the control of the control of the printed control of the control of the printed control of the con
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                       Cytoplasmic; vaccine; prevention; identification; binding compound;
                                                                                                                                                                                                             H. pylori ORF
                                                                                                                                                                                                                                                                                                                                                              AAW55729 standard; Protein;
                                                                                                                                                                                                                                                                  13-JUL-1998
                                             Helicobacter
                                                                                                                inhibitor; duodenal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       631 YATKPLSHPLNDQLRATLGYQQEVFGHSTNGFDLSTRTLEHEISRSIIQNGGWNRTYSLR 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       691 YRLDKLKTQAPPETWQDLPVDFVNGKPSQEALL--AGVAVHKTVADNLVNPMRGYRQRYS 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YKMPLLKNPLEQYYLVQGGFKRT----DLNDTESDSTTL--VASRYWDLSSGWQRAINLR 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LRFFAGGDQSIRGYAHDSLSPISDKGYLTGGQVLAVGTAEYNYEFMKDLRLAVFGDIGNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LEVGSSGLVSDANMAIARAGISGVYSFGDNAYGSNRAHQMTGGIQAGYIWSDNFNHVPYR 808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WSLD-------HFTQGEITNTTMLFYPGVMISRTRSRGGLMPTWGDSQRYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YDKGFTNDTKIGAGVGVRWASPVGQVRV 896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LRFFAGGDRSIRGYQYKSIGPKLPNGDLKGASKLITGSLEYQYNVTGKCTKWQFGE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IDYSNTAWGSDVDFSVFQAQNVWIRTLYDR-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      371 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                               (first entry)
                                                                                          outer membrane protein;
                                                                                                                                                                                                                05ep10815_4719175_c1_115 cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       No 55917; 103pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.48;
                                                                                                                   ulcer disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to isolated polynucleotide (I) and
ences. (I) is useful as hybridisation probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -WLAP-GEVRL 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39;
                                                                                                                                                                                                                                                                                                                                                                 925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 206; DB 22;
Pred. No. 4.9e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English
                                                                                                                                         treatment; infection; envelope; bacteria; life cycle; activator;
                                                                                                                   chronic gastritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HRFVTRGTLGWIETGDFDKVPPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106;
                                                                                                                                                                                                                envelope
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                                                                                                                   diagnosis;
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CC membrane protein may be used in a vaccine to prevent or treat H. pylori CC infection or to identify H. pylori polypeptide binding compounds, CC useful as potential H. pylori life cycle activators or inhibitors. The CC useful as potential H. pylori life cycle activators or inhibitors. The CC PNA and probes derived from it may be used for the identification of CC H. pylori in a sample and the diagnosis of H. pylori infection. Nucleic CC acid sequences complementary to the DNA act as antisense sequences and CC against the protein can be used in immunoassays to evaluate the abundance CC and distribution of H. pylori-specific antigens. The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated CC by mechanically shearing the bacterial DNA. The sequences were analysed CC defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported conterest, particular regions can be isolated from H. pylori by PCR complification for recombinant solvepetide production. e.g. in E. coli
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Best Local Similarity
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29-MAR-1996;
02-APR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polypeptide(s) - useful in vaccines to treat or pr
infection and for diagnosis of H. pylori infection
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N-PSDB; AAV25138.
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28-OCT-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amplification for recombinant polypeptide production, e.g. in
                                                                                                                                                                                                                                                                                                                                                              116
                                                                                                                                                                                                                                                      116
                                                                                                                                                                                                                                                                                       154
 355
                                                                                                          204
                                                                                                                                                                                                                                                                                                                           56
T--GTQYRFDEVVFFTIDPKTNQLTTDPDKLPVKRELLEQLLTVNMGEAYNLQAVRALSN
                                                                                                                                                                                                                                                    TAVLALFNQGYFKDVYA-TFENGI-----LEFHFDEKARIAGVEIKGYGTEKEKDGLKSQ
                                                                                                                                                                                                                                                                                                                       TPKEAQKNEAQNETSQSNQTPKEMKVKSISYVGLSYMSDMLANETAKIRVGDMVDSKKID 115
                                                                                                                                                                                                                                                                                                                                                            TPLSLEELFAQEST-----EMGINPNDYIP-EYQ------GEQPNSEVVV 153
                                   RDFMGWMWGLNDGKLRLDQLEYDSLRIQDVYMRRGYLDAHISSPFLKTDFSTHDAKLHYK
                                                                                                          -----VEVRTEKVSEGALLIVFDVNRGDSIYIKQSIYEGSDKLKRRVIESLSANKQ
                                                                                                                                           EPVYIDYRAVEVRGEGADDKAFTTVAD---EVPLLIGDVFHHGKYETKKNLIENASAEH-
                                                                                                                                                                               MGIKKGDTFDEQKLE-----HAKTALKTALEGQGYY--
                                                                                                                                                                                                                IKAALEDITQESAMDLNGSIPRLRQTAL-VAARAVGYYDIDLSIIRNSIGEVDVIIHDLG
                                                                                                                                                                                                                                                                                     PPTLEPEKPGLIKRLYARLFNDGVNKVPRLKAKFYQSSQSG--ETSAIGSSHQKTEPYAN 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smith
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s) - useful in vaccines to treat or preven
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96US-0736905.
96US-0738859.
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96US-0625811.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA.
                                                                                                                                                                                                                                                                                                                                                                                                                    4.18;
19.98;
                                                                                                                                                                                                                                                                                                                                                                                                                    Score 194.5; DB 1
Pred. No. 0.00011;
                                                                        WLDRSVD--VILPD-NTADVSLIYD
                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 925;
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RESULT 29
AAY17183
ID AAY17
XX AAY17
AC AAY17
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XX OUTER
DT 03-AU
XX OUTER
XX OUTER
KW CELLU
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      (GENO-) GENOME THERAPEUTICS CORP
                                17-DEC-1997;
28-OCT-1997;
                                                                                            06-MAY-1999
                                                                                                                                                                       Outer membrane polypeptide; OMP; vaccine; H.
                                                                                                                                                                                             H. pylori outer membrane polypeptide
                                                                    28-OCT-1998;
                                                                                                                  W09921959-A2
                                                                                                                                      Helicobacter pylori
                                                                                                                                                               cellular immune
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                                                                                                                                                                                                                                                                                                                                   EWISPMG
                                                                                                                                                                                                                                                                                                                                                          RWASPVG 892
                                                                                                                                                                                                                                                                                                                                                                          KAAKMRLAWFEDEGFLTFKTPTRGSFFYNAPTTTANFKDYGVVGAGFERATWRASTGLQI
                                                                                                                                                                                                                                                                                                                                                                                                      K--DLRLAVFGDIG-----
                                                                                                                                                                                                                                                                                                                                                                                                                       YIFRYNTDDYLPLNSTFYMGGVTTVRGFRNGSITPKDEFGLWLGGDGIFTASTELSYGVL
                                                                                                                                                                                                                                                                                                                                                                                                                                           YIWSDNF-NHVPYRLREFAGGDQSIRGYAHDSLSPISDKGYLTGGQVLAVGTAEYNYEFM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----SYATMSGLPSSGTLNSWNGLGGNVRNTKVYGKFAAYHHLQKYLLIDLIAREKTQGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RTPLVPESCSSPGAITTSPEIKGIWDRDYHTPITSSFTLDVSYDNTDDYYFPRNGVIFS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---TVADNLVNP-----SGLVSDA
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                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                   879
                               97US-0993001.
97US-0959131.
                                                                98WO-US22883
                                                                                                                                                              response
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                                                                                                                                                                    pylori infection; humoral;
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Best Local S
Matches 192
           578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a vaccine for preventing or treating infections by Helicobacter pylori. The vaccine contains at least one isolated H. pylori polypeptide, or its fragments, in a carrier, where the carrier is a Salmonella, vibrio cholerae or Shigella vector containing a nucleic acid encoding the H. pylori polypeptide. The vaccines induce humoral and cellular immune responses. The vaccines are used to treat or prevent infections by H. pylori. Sequences AAX75779 to AAX75837 represent nucleic acid sequences encoding H. pylori outer membrane polypeptides (OMPs) AAX17160 to AAX17218.
                                                                                                                                           586 QI--GLGWGSDTGTRLVTKFEHNLINRDGYQAGAELRLSED--KKGVKLYATKP-----
                                                                    535 FAGNLSLTNP
                                                                                                                                                                                           450 FFSKVKIEEKRV----NSSLMDL----
                                                                                                                                                                                                                                                                                           469
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N-PSDB; AAX75802.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 TPLSLEELFAQEST-----EMGINPNDYIP-EYQ-------GEQPNSEVVV 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local L
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VGRMLGNRTHVSLGYNLNVTKLLGFSSPLYNRYYSSVNEVASPRQCSTPASVIINRLSGG
                             -----WNRTY-SLRYRLDKLKTQAPPETWQDLPVDFVN--GKPSQEALLAGVAVHK----
                                                                                       -----LSHPLNDQLRATLGYQQEVFGHSTNGFDLSTRTL--EHEISRSIIQNGG-----
                                                                                                                        QLQFGLGYGSYGGLML----NGSVSERNLFGTGQSMSLYANIATGGGRSYPGMPKGAGRM
                                                                                                                                                                                                                 RISDAVSAVARAILPDESENEVIDLPERTALANRKTPADVYQSKKVPLYVFVASDKPRDG
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                                                                                                                                                                                                                                                                               LTDGILMDISPIEFSASNLIQDKLNLVAAKARHLYDMPDDR---VLAINHDDGVNRSILG
                                                                                                                                                                                                                                                                                                                                           DL---IATRYFNMVNTEIVFPEREQIQNDQVSFEQSSSSRTEPAQVDEST-LEPVIETVE
                                                                                                                                                                                                                                                                                                                                                                          VKEGIQYRISDIL-----IEIDNPVVPLK--TLEKALKVKRKDVFNIEHLRADAQ
                                                                                                                                                                                                                                                                                                                   ILKTEIADKGYAFA---VVKPDLDK----
                                                                                                                                                                                                                                                                                                                                                                                                      T--GTQYRFDEVVFFTIDPKTNQLTTDPDKLPVKRELLEQLLTVNMGEAYNLQAVRALSN 412
                                                                                                                                                                                                                                                                                                                                                                                                                                      RDFMGWMWGLNDGKLRLDQLEYDSLRIQDVYMRRGYLDAHISSPFLKTDFSTHDAKLHYK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAVLALFNQGYFKDVYA-TFENGI-----LEFHFDEKARIAGVEIKGYGTEKEKDGLKSQ 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----GYFDGR----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ellis RW,
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Pred. No. 0.00011;
1; Mismatches 311;
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                                                          -DSWYSSTINLYADYRISYQYIQQGGGFGVN
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01-APR-1997;
01-APR-1997;
01-APR-1997;
01-APR-1997;
24-JUN-1997;
This claimed Helicobacter pylori polypeptide, designated GHPO 107, can be used in vaccination methods for preventing or treating Helicobacter infection. 85 Helicobacter polypeptides (see AAW71474-W71558) are claimed, as well as isolated polypucleotides (see AAV52009-93) that encode them. The invention also provides: methods for producing these Helicobacter polypeptides in recombinant host systems, and related expression cassettes, vector and transformed or transfected host cells; live vaccine vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                         Al-Garawi
Odenbreit
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(PLAC )
(INMR )
                                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                  Helicobacter polynucleotide and polypeptide treat or prevent gastrointestinal infection
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DB; AAV52012.
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MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN
MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
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PISDKGYLTGGQVLAVGTAEYNYEFMK--DLRLAVFGDIG----
                                              GKFAAYHHLQKYLLIDLIARFKTQGGYIFRYNTDDYLPLNSTFYMGGVTTVRGFRNGSVT
                                                                                                          SSFTLDVSYDNTDDYYFPRNGVIFS----SYATMSGLPSSGTLNSWNGLGGNVRNTKVY
                                                                                                                                                                                                         DFVNG--KPSQEALLAGVAVHKTVA-----DNLVNP-----MRGYRQR-----
                                                                                                                                                                                                                                                           LSTRTL--EHEISRSIIQNGG--------WNRTY-SLRYRLDKLKTQAPPETWQDLPV
                                                                                                                                           --YSLEVG-----SSGLVSDANMAIARAGISGVYSFGD----NAYGSNRAHQMTG
                                                                                                                                                                         SSVNEVVSPRQCSTPASVIINRLSGGKTPLQPESCSSPGAITTSPEIRGIWDRDYHTPIT
                                                                                                                                                                                                                                                                                                                                                                                       KTPADVYQSKKVPLYVEVASDKPRDGQI--GLGWGSDTGTRLVTKFEHNLINRDGYQAGA
                                                                                                                                                                                                                                        SSTINLYADYRISYQYIQQGGGFGVNVGRMLGNRTHVSLGYNLNVTKLLGFSSPLYNRYY
                                                                                                                                                                                                                                                                                                        SMSLYANIATGGGRSYPGMPKGAGRMFAGNLSLTNP----
                                                                                                                                                                                                                                                                                                                                      ELRLSED--KKGVKLYATKP------LSHPLNDQLRATLGYQQEVFGHSTNGFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----DEKNGLVKVIYRIEVGDMVYINDVIISGNQRTSDRIIRRELLLGPKDKYNLTKLR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSAKLKRRMIESLSANKORDFMGWMWGLNDGKLRLDQLEYDSMRIQDVYMRRGYLDAHIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NDYIPEYQGEQPNSEVVVPPTLEPEKPGLIKRLYARLFNDGVNKVPRLKAKFYQSSQSG- 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RHLYDMPDDRVLAINHDDGVNRSILGRISDAVSAVARAILPDESENEVIDLPERTALANR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAQVDEST-LEPVIETVELTDGILMD---ISPIEFSASNLI------QDKLNLVAAKA 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KVKRKDVFNIEHLRADAQILKTEIADKGYAFA---VVKPDLDK---------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TVNMGEAYNLQAVRALSNDL---IATRYFNMVNTEIVFPEREQIQNDQVSFEQSSSSRTE 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPFLKTDFSTHDAKLHYKVKEGIQYRISDIL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GKYETKKNLIENASAEH-----GYFDGR---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEIVKIRVGDIVDSKKIDTAVLALFNQGYFKDVYA-TFEGGI-----LEFHFDEKARIAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contain the polynucleotides of the invention and which can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --VILPD-NTADVSLIYDT--GTQYRFDEVVFFTIDPKTNQLTTDPDKLPVKRELLEQLL 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIIRNSIGEVDVIIHDLGEPVYIDYRAVEVRGEGADDKAFTTVAD---EVPLLIGDVFHH 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -ETSAIGSSHQKTEPYANIKAALEDITQESAMDLNGSIPRLRQTAL-VAARAVGYYDIDL 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    ----NSENSLRR--LGFFSKVKIEEKRV----NSSLMDL-----
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                                                                                                                                                                                                                                                                                                                                                                     -----LVSVEEGRTGQLQFGLGYGSYGGLML----NGSVSERNLFGTGQ
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19.7%;
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Pred. No. 0.00025;
"'amatches 294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -VEVRTEKVSEGALLIVFDVNRGDSIYIKQSIYE 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----IEIDNPVVPLK--TLEKAL
                                                                                                                                                                                                                                                                                                        ----RIF----DSWY
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                                                                                                                                                            Query Match
                                                                                                                                         Matches
                                                                                                                                                                                Sequence
                                                                                                                                                                                                  methods using the isolated genes
                                                                                                                                                                                                                   12085. Nucleotide sequences were determined for the D15 genes (AAQ66198-202) and the corresponding as sequences were derived (AAR53754-58). D15 OMP can be produced easily and on a large
                                                                                                                                                                                                                                                Outer membrane protein (OMP) D15 genes were isolated by screen chromosomal libraries of H. influenzae type b (Hib) strains Ca Eagan and Minn A, and the non-typeable (NTH) strains SB33 and
                                                                                                                                                                                                                                                                                        Disclosure; Fig. 1E; 161pp; English
                                                                                                                                                                                                                                                                                                                     Nucleic acid encoding D15 outer membrane protein - esp
Haemophilus influenzae, and related proteins, vectors,
etc. useful in vaccines, for diagnosis and for passive
                                                                                                                                                                                                                                                                                                                                                               N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                       WPI; 1994-200269/24.
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                                                                                                                                                                                                          free of other antigens and
                                                                                                                                                                                                                                                                                                              immunisation.
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  393
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                                                                                                                 227 LNGSIPRLRQTALVAARAVGYYDIDLSIIRNSI---GEV-DVIIHDLGEPVYIDYRA---
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  LLTVNMGEAY - - -
                  ATVEPIVNTLPNNRAEILIQINEDDKAKLASLTF----KGNE-SVSSSTLQEQMELQPD
                                                                            ---VEVRGEGA-DDKAFTTVADEVPLLIGDVFHHGKYETKKNLIENASAEHGYFDGRWLD 335
                                     RSVDVI----LPDNTADVSLIYDTGTQYRFDEVVFFTIDPKTNQLTTDPDKLPVKRELLEQ 392
                                                          ISDVKIKGNSVIPTEALKQNLDANGFKVGDVL----IREKLNEFAKSVKEHYASVGRY-N 146
                                                                                                VQGDLEQQIRASLPVRAGHGVTDNDVANIVRSLFVSGRFDDVKAHQEGDVLVVSVVAKSI 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           outer
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                                                                                                                                         al Similarity
167; Conserv
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·--NLQAVRALSNDLIATRYFNMVNTEIVFPEREQIQNDQVSFEQS 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein;
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                                                                                                                                       Score 184.5; DB 15;
Pred. No. 0.00043;
9; Mismatches 326;
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PDYGKSSRIRASTGVGFQWQSPIGPLVFSYAKPIKKYENDDVEQFQFSIGGSF 793
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                                                                                                                                              --GGQVLAVGTAE--YNYEFMKD-----LRLAVFGDIGNAY-
                                                                                                                                                                                                                                                                                                                                      DNLVNPMRGYRQRYSLEVGSSGLV----SDANMAIARAGISGVYSFGDNAYGSNRAHQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                     IIQNGGWNRT---YSLRYRLDKLKTQAPPETWQDLPVDFVNGKPSQEALLAGVAVHKTVA
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                                                                                              VIGGNAITTASAELIVPTPFVSDKSQNTVRTSLFVDAASVWNTKWKSDKNGLESKVLKDL
                                                                                                                                                                                           VSAKASAGYANGFGNKRLPFYQTYTAGGIGSLRGFAYGSIGPNAIYAEHGNGTFNKISSD
                                                                                                                                                                                                                                          MTGGIQAGYIWSDNFNHVPYRLRFFAGGDQSIRGYAHDSLSP---ISDKGYLT-----
                                                                                                                                                                                                                                                                                                                                                                                        ALE --- YNRNLY IQSMKFKGNGIKTN------DFDFSFGW----
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                                            -DKGFTNDTKIGAGVGVRWASPVGQVRVDVATGVK--EEGNPIKLHFFIGTPF 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LGERGYGNTTVNSVPDFDDANKTLAITFVVDAGRRLTVRQLRFEGNTVSADSTLRQEMRQ
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                                                                                                                                                                                                                                                                                       -NYNSLNRGYFPTKGVKASLGGRVTIPGSDNKYYKLSADVQGFYPL-----DRDHRWV
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H. influenzae SB33 D15 sequence 09-JUN-1994. W09412641-A 08-DEC-1994 AAR53757; AAR53757 standard; 23-NOV-1993; Haemophilus influenzae Vaccine; outer membrane protein. Nr (first entry) 93WO-CA00501 Protein; 792 NTH1. vector; A antiserum; diagnosis; D15;

WPI; 1994-200269/24

Yang Y; Chong P,

Klein M,

Loosmore

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Sia DYC,

Thomas Σ (CONN-) CONNAUGHT 23-NOV-1992;

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid encoding D15 outer membrane protein esp. Haemophilus influenzae, and related proteins, vectors, etc. useful in vaccines, for diagnosis and for passive
      868
                                       661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig. 1D; 161pp; English.
                                                                                                     809
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      ΑY
                              GPNAIYQGQNNKFNKISSD--VIGGNAIATASAELIVPTPFVSDKSQNTVRTSLFVDAAS
                                                                                                    QGFYPL---
                                                                                                                             SGVYSFGDNAYGSNRAH--QMTGGIQAGYIWSDNFNHVPYRLRFFAGGDQSIRGYAHDSL
                                                                       SP----
                                                                                                                                                                                            NGKPSQEALLAGVAVHKTVADNLVNPMRGYRQRYSLEVGSSGLV----SDANMAIARAGI
                                                                                                                                                                                                                            NENNSYYVGLGHTYNKISNFALE---YNRNLYIQSMKFKGNGIKTN-----DFDFS
                                                                                                                                                                                                                                                           STRT-----LEH---EISRSIIQNGGWNRT----YSLRYRLDKLKTQAPPETWQDLPVDFV 713
                                                                                                                                                                                                                                                                                           TKNDYGTSVNLGYTEPYFTKDGVSLGGNVFFENYDNSKSDTSSNYKRTTYGSNVTLGFPV
                                                                                                                                                                                                                                                                                                                          NRDGYQAGAELRLSE---DKKGVKLYATKPLSHPLNDQLRATLGYQQEVFGHS-TNGFDL
                                                                                                                                                                                                                                                                                                                                                          VDVVYKVK------ERNTGSINFGIGYGTESGISYQASVKQDNFLGTGAAVSIAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          I-LMDISPIEFSASNLIQDKLNLVAAKARHLYDMPD----DRVLAINHDDGVNRSIL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LNEFAQSVKEHYASVGRY-NATVEPIVNTLPNNRAEILIQINEDDKAKLASLTF----K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DVIIHDLGEPVYIDYRA-----VEVRGEG-ADDKAFTTVADEVPLLIGDVFHHGKYETK
                                                                                                                                                                                                                                                                                                                                                                                          ---VYQSKKVPLYVFVASDKPRDGQI--GLGWGSDTGTRLVTKF-EHNLI------
                                                                                                                                                                                                                                                                                                                                                                                                                           LRFEGNTVSADSTLRQEMRQQEGTWYNSQLVELGKIRLDRTGFFETVENRIDPINGSNDE 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRRSDIADVE----NAIKAKLGERGYGNTTVNSVPDFDDANKTLAITFVVDAGRRLTVHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KAQITKADVQLNDEKTKVNYTIDVNEGLQYDLRSARIIGNLGGMSAELEPLLSALHLNDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GNE-SVSSSTLQEQMELQPDSWWKLWGNKFEGAQFEKDLQAIR-----DYYLNNGYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EIVFPEREQIQNDQVSFEQSSSSRTEPAQVD------ESTLEPVIETVELTDG 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TNQLTTDPDKLPVKRELLEQLLTVNMGEAY-----NLQAVRALSNDLIATRYFNMVNT 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KNLIENASAEHGYFDGRWLDRSVDVI---LPDNTADVSLIYDTGTQYRFDEVVFFTIDPK 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DVKAHQEGDVLVVSVVAKSIISDVKIKGNSIIPPEALKQNLDANGFKVGDIL----IREK 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                160;
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                                                                                                DRDHLWVVSAKASAGYANGFGNKRLPFYQTYTAGGIGSLRGFAYGSI
                                                                                                                                                               -----NYNSLNRGYFPTKGVKASLGGRVTIPGSDNKYYKLSADV
                                                              ISDKGYLTGGQVLAVGTAE - - YNYEFMKD - - - - LRLAVFGDIGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.8%;
DKGFTNDTKIGAGVGVRWASPVGQVRVDVATGVK--EE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 178; DB 15; Pred. No. 0.0012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            306;
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Best Local
                                                                                                                                                                                                                                                used as probe for screening of genetic mutations, serotype, taxonomic classification or identification. BASB027 agonists, antagonists and antibodies may be used to prevent and/or treat bacterial infections.
                                                                                                                                                                                                                                                                                       The present sequence is BASB027 polypeptide, which shows significant homology to Neisseria meningitidis OMP85 outer membrane protein. It is encoded by DNA obtained from chromosomal DNA library of Moraxella catarrhalis strain Mc2931 (ATCC 43617). BASB027 polynucleotide and polypeptide can be used for diagnosis and staging of disease, determining susceptibility to a disease and to prepare medicaments for treating M. catarrhalis infections, especially office media. The BASB027 DNA can be
                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 3; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel BASB027 polynucleotide and polypeptides from Moraxella catarrhalis useful for treating M. catarrhalis infection such as otitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-JUN-1998;
08-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-105700/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vinals-Bassols C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M. catarrhalis BASB027 polypeptide
    185
                              280
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                                                                                   225
                                                                                                                                      165 IKRLYARLFNDGVNKVPRLKAKFYQSSQSGETSAIGSSHQKTEPYANIKAALEDITQESA 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SMIK)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASB027; OMP85;
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 VDINIIGNQHFSDADLIDVLAIKDNKINPLSKADRYTQEKLVTS---LENLRAKYLNAGF
                          VEVRGEGADDKAFTTVADEV------PLLIGDVFHHGKYETKKNLIENASAEH---GY
                                                     QPLKQATVQMIETELTNQYISQGYYNTEITVKQTMLDGNRVKLDMTFAE-GKPA----RV
                                                                               MDLNGSIPRLRQTALVAAR-AVGYYDIDLSIIRNSIG----EVDVIIHDLGEPVYIDYRA 279
                                                                                                           VKALYATGNFSDVQVYHQEGRIIYQVTERPLIAEINFEGNRLIPKEGLQEGLKNAGLAVG
                                                                                                                                                                   164;
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                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ29550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMITHKLINE
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                                                                                                                                                                                                                          813 AA;
                                                                                                                                                                     Conservative
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99GB-0005304
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18.7%;
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                                                                                                                                                                   119;
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                                                                                                                                                                               Score 176.5; DB Pred. No. 0.0016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein;
                                                                                                                                                                   Mismatches
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                                                                                                                                                                  338;
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                                                                                                                                                                   Indels
                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            treatment;
                                                                                                                                                                   257;
                                                                                                                                                                Gaps
                          328
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241
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AAY44391
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 03-JUN-1998;
08-MAR-1999;
                                          31-MAY-1999;
                                                                        09-DEC-1999.
                                                                                                  WO9963093-A2
                                                                                                                                                          diagnosis;
                                                                                                                                                                   BASB027; OMP85; outer membrane protein;
                                                                                                                                                                                                  M. catarrhalis
                                                                                                                              Moraxella catarrhalis
                                                                                                                                                                                                                               14-MAR-2000
                                                                                                                                                                                                                                                           AAY44391;
                                                                                                                                                                                                                                                                                   AAY44391 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242 VRFEIKDAKLNINEDKNRIFVEISLHEGEQYRFGQTQFL---
                                                                                                                                                                                                                                                                                                                                                     GATWYTPIGPLSISYAKPLNKKONDQTDTVQFQIGSVF 813
                                                                                                                                                                                                                                                                                                                                                                                    GVRWASPVGQVRVDVATGV--KEEGNPIKLHFFIGTPF
                                                                                                                                                                                                                                                                                                                                                                                                           QVRPVIFIEGGQVFDTTGMDKQTIDLTQFKDPQATAEQNAKAANRPLLTQDKQLRYSAGV
                                                                                                                                                                                                                                                                                                                                                                                                                                            DLRLAVFGDIGNAYD-KGFTNDT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GYGSVRGYDQSSLGPRS-QAYLTARRGQQTTLGEVVGGNALATFGSELILPLPFKGDWID 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GDQSIRGYAHDSLSPISDKGYLT-------GGQVLAVGTAE-----YNYEFMK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGISGYYSFGDNAYGSNRAHQ------MTGGIQAGYIWSDNFNHVPYRLRFFAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RLSEDKKGVKLYATKPLSHPLNDQLRATLGYQQEVFGHSTNGFDLSTRTLEHEISRSIIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DQVDVN-----FVVEEQPSGSSTIAAGYSQSGGVTFQFDVSQNNFMGTGKHVNASF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TPADVYQSKKVPLYVFVASDKPR-DGQIGLGWGSDTGTRLVTKFEHNLINRDGYQAGAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QL----EGALASNQKIQLSR------ARLMRTGFFKHVTVD---TRPVPNSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLEQLLTVNMGEAYNLQAVRALSNDLIATR-----YFNMVN--TEIVFPEREQIQNDQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NGGWNRTYSLRYRLD------KL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELEALLKFKAEEGFS-QAMLEQTTNNISTKFGDDGYYYAQIRPVTRI------NDE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FDGRWLDRSVDVILPDNTADVSLIYDTGTQYRFDEVVFFTIDPKTNQLTTDPDKLPVKRE 388
                                                                                                                                                        bacterial infection
                                                                                                                                                                                                                           (first entry)
98GB-0011945
99GB-0005304
                                         99WO-EP03822
                                                                                                                                                                                               (ATCC 43617) BASB027 polypeptide #2.
                                                                                                                                                                                                                                                                                    813
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                                                                                                                                                                    otitis media;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         ----KIGAGV
                                                                                                                                                                    treatment;
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                                                       514
                       707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel BASB027 polynucleotide and polypeptides from Moraxella catarrhalis useful for treating M. catarrhalis infection such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB;
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TPADVYQSKKVPLYVFVASDKPR-DGQIGLGWGSDTGTRLVTKFEHNLINRDGYQAGAEL
                                             SYGGSLSYG--YPIDENQRISFGLNADNTKLHGGRFMGISNVKQLMADGGKIQVDN---N
                                                                                                                                              RLSEDKKGVKLYATKPLSHPLNDQLRATLGYQQEVFGHSTNGFDLSTRTLEHEISRSIIQ
                                                                                    NGGWNRTYSLRYRLD----
                                                                                                               SRSETREVYSLGMTNPY------FTVNGVSQSLSGYYRKTKYDNKNISNYVLD
                                                                                                                                                                              DQVDVN-----FVVEEQPSGSSTIAAGYSQSGGVTFQFDVSQNNFMGTGKHVNASF
                                                                                                                                                                                                                                                                                                                                                                              QL----EGALASNQKIQLSR---
                                                                                                                                                                                                                                                                                                                                            SFEQSSSSRTEPAQVDESTLEPVIETVELTDGILMDISPIEFSASNLIQDKLNLVAAKAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VDINIIGNQHFSDADLIDVLAIKDNKINPLSKADRYTQEKLVTS---LENLRAKYLNAGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QPLKQATVQMIETELTNQYISQGYYNTEITVKQTMLDGNRVKLDMTFAE-GKPA----RV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MDLNGSIPRLRQTALVAAR-AVGYYDIDLSIIRNSIG----EVDVIIHDLGEPVYIDYRA 279
                                                                                                                                                                                                                                                                                                               -----SRTVDVEYYIDPVHPVY-------VRRINFTGNFKTQDE--VLRREMR
                                                                                                                                                                                                                                                                                                                                                                                                            LLEQLLTVNMGEAYNLQAVRALSNDLIATR-----YFNMVN--TEIVFPEREQIQNDQV 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FDGRWLDRSVDVILPDNTADVSLIYDTGTQYRFDEVVFFTIDPKTNQLTTDPDKLPVKRE 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VEVRGEGADDKAFTTVADEV------PLLIGDVFHHGKYETKKNLIENASAEH----GY 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164;
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18.7%;
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Pred. No. 0.0016;
Pred. No. 338;
                                                                                                                                                                                                                                               -ARLMRTGFFKHVTVD---TRPVPNSP
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RESULT 35
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ID ABB58
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  Query Match
Best Local Similarity
Matches 177; Conserv
                                                                                                                            The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                       Sequence
                                                                                           The sequence data for this patent did not form specification, but was obtained in electronic f
                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 3321; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                               New isolated nucleic a
genes from Drosophila
interactions -
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11-JUL-2000; 2000US-0614150
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                                                                ecification, but was obtained in electronic format directly from ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                      2001-656860/75.
DB; ABL02946.
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                                                      2748 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     developmental biology; cell signalling; insecticide;
  Conservative
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  131;
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Score 173.5; DB 22;
Pred. No. 0.014;
1; Mismatches 312;
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RESULT 36
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                                                                                                                                                                                                                                                                                                    SELEKELLVVST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TESTAVEVIASESINTVVEPVSVAQSPT-----IEDSTPEEVTQCSAVNSTDTEVASA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IP-----TSTTAVTTSDGASTEMPEPPKIYCETAPPAAEEIEQNETVETLSVSADTT 1418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KPEPMENATEIEIEEMVSPTSVEIVPTTTEDLHQAESVVETARP----VSAVEEVKPI--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----TEIVFPEREQIQNDQVSFEQSSSSRTEPAQVDESTLEPVIE--TVELTDGILMDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --ESAMDLNGSIPRLRQTALVAARAVGYYDIDLSIIRN-----SIGEVDVII------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VPRLKAKFYQSSQSGETSAIGSSHQKTEP----YANIKAALEDITQ-----
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                                                                                                                                                                                                                                                                                                                                                                                                      ---LYVFVASDKPRDGQIGLGWGSDTGTRLVTKFEHNLINRDGYQAGAELRL
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08-DEC-1994 AAR53755;

(first entry)

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Yang Y;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid encoding D15 outer membrane protein - esp. Haemophilus influenzae, and related proteins, vectors, etc. useful in vaccines, for diagnosis and for passive
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   409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             methods using the isolated genes
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   VDVVYKVK-----
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DB; AAQ66199.
                           ---VYQSKKVPLYVFVASDKPRDGQI--GLGWGSDTGTRLVTKF-EHNLI------
                                                         LRFEGNTVSADSTLRQEMRQQEGTWYNSQLVELGKIRLDRTGFFETVENRIDPINGSNDE
                                                                                                                 FRRSDIADVE - - - - NAIKAKLGERGYGSATVNSVPDFDDANKTLAITLVVDAGRRLTVRQ
                                                                                                                                             I-LMDISPIEFSASNLIQDKLNLVAAKARHLYDMPD----DRVLAINHDDGVNRSIL---
                                                                                                                                                                          KAQITKTDVQLNDEKTKVNVTIDVNEGLQYDLRSARIIGNLGGMSAELEPLLSALHLNDT
                                                                                                                                                                                                      EIVFPEREQIQNDQVSFEQSSSSRTEPAQVD------ESTLEPVIETVELTDG 472
                                                                                                                                                                                                                                GNE-SVSSSTLQEQMELQPDSWWKLWGNKFEGAQFEKDLQSIR------DYYLNNGYA 232
                                                                                                                                                                                                                                                           TNQLTTDPDKLPVKRELLEQLLTVNMGEAY-----NLQAVRALSNDLIATRYFNMVNT 425
                                                                                                                                                                                                                                                                                        LNEFAKSVKEHYASVGRY-NATVEPIVNTLPNNRAEILIQINEDDKAKLASLTF----K 181
                                                                                                                                                                                                                                                                                                                     KNLIENASAEHGYFDGRWLDRSVDVI---LPDNTADVSLIYDTGTQYRFDEVVFFTIDPK 372
                                                                                                                                                                                                                                                                                                                                                 DVKAHQEGDVLVVSVVAKSIISDVKIKGNSVIPTEALKQNLDANGFKVGDVL----IREK 127
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                                                                                                                                                                                                                                                                                                                                                                                                            158;
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                                                                                    -GRISDAVSAVARAILPDES---ENEVIDLP----ERT----ALANRKTPAD-----
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· ERNTGSINFGIGYGTESGISYQASVKQDNFLGTGAAVSIAG
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                                                                                                                                                                                                                                                                                                                                                                                                         Score 171.5; DB Pred. No. 0.0034; 1; Mismatches 30
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Outer membrane protein (OMP) D15 genes were isolated by screening chromosomal libraries of H. influenzae type b (Hib) strains Ca, Eagan and Minn A, and the non-typeable (NTHi) strains SB33 and PAI 12085. Nucleotide sequences were determined for the D15 genes (AAQ66198-202) and the corresponding aa sequences were derived
                                                                          Disclosure; Fig.
                                                                                                              Haemophilus influenzae, and related proteins, etc. useful in vaccines, for diagnosis and fo
                                                                                                                                       Nucleic acid encoding D15 outer membrane protein - esp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       K--EEGNPIKLHFFIGTPF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGVYSFGDNAYGSNRAH--QMTGGIQAGYIWSDNFNHVPYRLRFFAGGDQSIRGYAHDSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NGKPSQEALLAGVAVHKTVADNLVNPMRGYRQRYSLEVGSSGLV----SDANMAIARAGI 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NENNSYYVGLGHTYNKISNFALE---YNRNLYIQSMKFKGNGIKTN-----DFDFS
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                                                                                                                                                                                                                                                                                                                                                                                                    passive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard;
                                                                                                                                                                                                               Klein M,
                                                                                                                                                                                                                                                                                                                                                                                     membrane protein;
                                                                                                                                                                                                                                                                                                                                                              influenzae type b Minn A strain
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                                                                            1C; 161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                    immunization; vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein;
                                                                                                                                                                                                                Loosmore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -ISDKGYLTGGQVLAVGTAE--YNYEFMKD----LRLAVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -NYNSLNRGYFPTKGVKASLGGRVTIPGSDNKYYKLSADV
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                                                                                                                                                                                                               Sia
                                                                                                                                                                                                               DYC,
                                                                                                                                                                                                                                                                                                                                                                                                    antiserum; diagnosis; D15;
                                                                                                              for passive
                                                                                                                                                                                                                Thomas
                                                                                                                             vectors,
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RESULT 38
AAR53754
ID AAR53
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AC AAR53
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Best Local Sim
Matches 158;
           AAR53754;
                                   AAR53754 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AAR53754–58). D15 OMP can be produced easily and on a large scale, free of other antigens and lipooligosaccharides, by recombinant DNA methods using the isolated genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   263 DVIIHDLGEPVYIDYRA-----VEVRGEGA-DDKAFTTVADEVPLLIGDVFHHGKYETK 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72
                                                                                                                                                                                               GPNAIYAEYGNGSGTGTFKKISSD--VIGGNAIATASAELIVPTPFVSDKSQNTVRTSLF
                                                                                                                                                                                                                                                QGFYPL-----DRDHLWVVSAKASAGYANGFGNKRLPFYQTYTAGGIGSLRGFAYGSI
                                                                                                 KKYENDDVEQFQFSIGGSF
                                                                                                                          K--EEGNPIKLHFFIGTPF
                                                                                                                                                                                                                    SP-----YNYEFMKD-----LRLAVF
                                                                                                                                                                                                                                                                       SGVYSFGDNAYGSNRAH--QMTGGTQAGYIWSDNFNHVPYRLRFFAGGDQSIRGYAHDSL
                                                                                                                                                                                                                                                                                                                      NGKPSQEALLAGVAVHKTVADNLVNPMRGYRQRYSLEVGSSGLV----SDANMAIARAGI 769
                                                                                                                                                                                                                                                                                                                                                   NENNSYYVGLGHTYNKISNFALE---YNRNLYIQSMKFKGNGIKTN-----DFDFS
                                                                                                                                                                                                                                                                                                                                                                           STRT----LEH---EISRSIIQNGGWNRT---YSLRYRLDKLKTQAPPETWQDLPVDFV
                                                                                                                                                                                                                                                                                                                                                                                                    TKNDYGTSVNLGYTEPYFTKDGVSLGGNVFFENYDNSKSDTSSNYKRTTYGSNVTLGFPV
                                                                                                                                                                                                                                                                                                                                                                                                                          NRDGYQAGAELRLSE---DKKGVKLYATKPLSHPLNDQLRATLGYQQEVFGHS-TNGFDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             I-LMDISPIEFSASNLIQDKLNLVAAKARHLYDMPD----DRVLAINHDDGVNRSIL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TNQLTTDPDKLPVKRELLEQLLTVNMGEAY-----NLQAVRALSNDLIATRYFNMVNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LNEFAKSVKEHYASVGRY-NATVEPIVNTLPNNRAEILIQINEDDKAKLASLTF-----K
                                                                                                                                               VDAASVWNTKWKSDKNGLESDVLKRLPDYGKSSRIRASTGVGFQWQSPIGPLVFSYAKPI
                                                                                                                                                                                                                                                                                                        FGW----
                                                                                                                                                                                                                                                                                                                                                                                                                                                      VDVVYKVK------ERNTGSINFGIGYGTESGISYQASVKQDNFLGTGAAVSIAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---VYQSKKVPLYVFVASDKPRDGQI--GLGWGSDTGTRLVTKF-EHNLI------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     {\tt LRFEGNTVSADSTLRQEMRQQEGTWYNSQLVELGKIRLDRTGFFETVENRIDPINGSNDE}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRRSDIADVE----NAIKAKLGERGYGSATVNSVPDFDDVKKTLAITLVVDAGRRLTVRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KAQITKTDVQLNDEKTKVNVTIDVNEGLQYDLRSARIIGNLGGMSAELEPLLSALHLNDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EIVFPEREQIQNDQVSFEQSSSSRTEPAQVD------ESTLEPVIETVELTDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GNE-SVSSSTLQEQMELQPDSWWKLWGNKFEGAQFEKDLQSIR------DYYLNNGYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KNLIENASAEHGYFDGRWLDRSVDVI---LPDNTADVSLIYDTGTQYRFDEVVFFTIDPK 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DVKAHQEGDVLVVSVVAKSIISDVKIKGNSVIPTEALKQNLDANGFKVGDVL----IREK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative 120; Mismatches 306;
                                                                                                                                                                                                                                                                                                 ------NYNSLNRGYFPTKGVKASLGGRVTIPGSDNKYYKLSADV
                                   Protein;
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                                                                                                                                                                      DKGFTNDTKIGAGVGVRWASPVGQVRVDVATGV
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Best Local Sim
Matches 156;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chong P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-NOV-1992;
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Outer membrane protein (OMP) D15 genes were isolated by screening chromosomal libraries of H. Influenzae type b (HLD) strains Ca, Eagan and Minn A, and the non-typeable (NTH1) strains SB33 and PAN 12085. Nucleotide sequences were determined for the D15 genes (AAQ66198-202) and the corresponding as sequences were derived (AAR53754-58). D15 OMP can be produced easily and on a large sce free of other antigens and lipooligosaccharides, by recombinant DN methods using the isolated genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid encoding D15 outer membrane protein - esp
Haemophilus influenzae, and related proteins, vectors,
etc. useful in vaccines, for diagnosis and for passive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1994-200269/24.
                                                                                                                                                                                                                                                                                                                                                                                                       373 TNQLTTDPDKLPVKRELLEQLLTVNMGEAY-----NLQAVRALSNDLIATRYFNMVNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              263 DVIIHDLGEPVYIDYRA-----VEVRGEGA-DDKAFTTVADEVPLLIGDVFHHGKYETK 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               influenzae b Ca D15 sequence
                                               LRFEGNTVSADSTLRQEMRQQEGTWYNSQLVELGKIRLDRTGFFETVENRIDPINGSNDE
---VYQSKKVPLYVFVASDKPRDGQI--GLGWGSDTGTRLVTKF-EHNLI----
                                                                                                                                                 FRRSDIADVE----NAIKAKLGERGYGSATVNSVPDFDDANKTLAITLVVDAGRRLTVRQ
                                                                                                                                                                                                 I-LMDISPIEFSASNLIQDKLNLVAAKARHLYDMPD----DRVLAINHDDGVNRSIL---
                                                                                                                                                                                                                                                      KAQITKTDVQLNDEKTKVNVTIDVNEGLQYDLRSARIIGNLGGMSAELEPLLSALHLNDT
                                                                                                                                                                                                                                                                                                     EIVFPEREQIQNDQVSFEQSSSSRTEPAQVD------ESTLEPVIETVELTDG
                                                                                                                                                                                                                                                                                                                                                       GNE-SVSSSTLQEQMELQPDSWWKLWGNKFEGAQFEKDLQSIR------DYYLNNGYA 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                            LNEFAKSVKEHYASVGRY-NATVEPIVNTLPNNRAEILIQINEDDKAKLASLTF----K 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KNLIENASAEHGYFDGRWLDRSVDVI---LPDNTADVSLIYDTGTQYRFDEVVFFTIDPK 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DVKAHQEGDVLVVSVVAKSIISDVKIKGNSVIPTEALKQNLDANGFKVGDVL----IREK 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          797 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   influenzae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1A; 161pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.4%; Score 161.5; DB 15; 19.5%; Pred. No. 0.017; tive 121; Mismatches 307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                type b
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                                                                                                    -ERT----ALANRKTPAD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                307; Indels
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RESULT 39
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11-APR-1990;
09-APR-1990;
12-APR-1990;
04-APR-1990;
                                              Claim 52; Fig 1 and
                                                                                                 synthase
                                                                                                                    Contiguous nucleic acid
                                                                                                                                                                  WPI; 1993-404004/50.
N-PSDB; AAQ53522.
                                                                                                                                                                                                                                    Ben-Bassat A,
Meade JH, Tal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US5268274-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Acetobacter xylinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cellulose synthase operon, gene C product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-JUN-1994
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                                                                                                                                                                                                                                                                                                          (CETU ) CETUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-APR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacterial; cellulose synthase;
gene D; transcription vector; ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cellulose synthesis.
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90IE-0001317.
90IL-0094053.
90NZ-0233312.
90WO-US01811.
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R, Wong
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recombinant microorganism;
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represent the proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPHSLAVEYYQTMAGVPAQWDQARAGLAGVVASNPQDYRAQLAFAQALTYNTSTRMEGLT
                                               LQQVEGTRAASGAGAAQEDAL---APPSTNPFRPRGYGHQTELGAPVTGGSYSAEAASPD
                                                                                                                AMDGVQESPMDARAWLAMAVADQADGH-----
                                                                                                                                             YATKPLSHPLNDQLRATLGYQQEVFGHSTNGFDLSTRTLEHEISRSIIQNGGWNRTYSLR
                                                                                                                                                                             PKLALARLYNGHGKPGKALEID-----LAVLRHNPQDLDARQAAVQAAVNSDHNSLATRL
                                                                                                                                                                                                              PR-----DGQIGLGWGSDTGTRLVTKFEHNLINRDGYQAGAELRLSEDKKGV--KL
                                                                                                                                                                                                                                            GDGTGSATGSALLPEQVQTLQQLRMGISVAQSDLLNQRGDQAQAYDHLAPALQADPEATS
                                                                                                                                                                                                                                                                             SDAY-SAVARAILPDESE-----NEVIDLPERTALANRKTPADVYQSKKVPLYVFVASDK
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                                                                                                                                                                                                                                                                                                                                                                                                                                           REAMAQAPRDPWVRINLANALQQQGDVAEAGRVMQPILANPVTAQDRQAGILYTYGSGND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----AAHQYTEAKQQLATLARQPGQYTGATLMLADLQRSTGQIAAAEQEYRGILSREPNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201;
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               -LLAGVAVH-KTVADNL---VNPMRGYRQRYSLEVGSSGLVSDANMAIA---
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-GORTIE----
                                                                              -WQDLPVDFVNGKPSQEA----
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RESULT 40
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a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                     polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical
                                                                                                                                                                                                                                                                                        The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The
                                                                                                                                                                                                                                                                                                                                                                                           Claim 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
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23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                            TKIGAGVGVRWASPVGQVRVDVATGVKE 904
                                                                                                                 MPFYENFYAGGSSTVRGFQSNTIGPKAVYFPHQASNYDPDYDYECATQDGAKDLCKSDDA 537
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IRMSAGIALQWMSPLGPLVFSYAQPFKK 625
                                                        VGGNALAVASLEFITPTPFISDKYANSVRTSFFWDMGTVWDTNWDSSQYSGYPDYSDPSN
                                                                                      TGGQVLAVGTAEY-----NYEFMKDLRLAVFGDIGNAYDKGF----
                                                                                                                                                  VPYRLRFFAGGDQSIRGYAHDSLSPIS---
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Gapop 10.0 , Gapext 0.5
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                                                                   /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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US-08-433-522A-8
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US-08-433-522A-6
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US-09-135-166-6
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US-09-135-166-6
US-09-135-166-6
US-08-942-046-4
US-08-942-046-6
US-08-942-046-6
US-08-942-046-6
US-08-942-046-8
US-08-942-046-9
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US-08-945-567D-3
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US-08-945-567D-3
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US-08-945-567D-3
US-08-945-567D-3
US-08-945-567D-3
US-08-945-567D-3
US-09-134-001C-3159
US-09-134-001C-5080
US-09-134-001C-5080
US-09-134-001C-5080
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                 Sequence 10, Appl
Sequence 10, Appl
Sequence 8, Appli
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Sequence 8, Appli
Sequence 4, Appli
Sequence 6, Appli
Sequence 7, Appli
Sequence 4, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 3, Appli
Sequence 118, Appli
Sequence 118, Appli
Sequence 118, Appli
Sequence 5080, Appsequence 5080, Appli
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Sequence 5080, Appli
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122.5	123.5	123.5	123.5	123.5	123.5	124	124	124	124	124	124	125	125	125	125	127.5	128.5
2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.7	2.7
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US-09-134-001C-4588	US-08-441-139-9	PCT-US95-04080-34	US-08-394-232A-34	US-09-135-642-34	US-08-436-664-34	US-08-994-570-5	US-08-769-309A-5	US-09-092-458-2	US-08-719-822B-2	US-08-072-610-2	US-09-134-001C-3172	US-09-024-429-3	US-08-863-010-3	US-08-537-002A-3	US-09-134-001C-5584	US-08-962-859A-2	US-09-134-001C-4547
Sequence 4588, Ap	Sequence 9, Appli	Sequence 34, Appl	Sequence 34, Appl	Sequence 34, Appl	Sequence 34, Appl	Sequence 5, Appli	Sequence 5, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 3172, Ap	Sequence 3, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 5584, Ap	Sequence 2, Appli	Sequence 4547, Ap

## ALIGNMENTS

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SEQUENCE CHARACTERISTICS:
LENGTH: 793 amino acids
TYPE: maino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-433-522A-10
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US-08-433-522A-10
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                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: CHONG,
APPLICANT: THOMAS,
                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/433,522A
FILING DATE: 12-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-434 MISTELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, VC
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                 TELEPHONE: (416) 595-11:
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: 1
APPLICANT: 1
TITLE OF INV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN NUMBER OF SEQUENCES: 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Toronto
STATE: Ontario
COUNTRY: Canada
263 DVIIHDLGEPVYIDYRA-----VEVRGEGA-DDKAFTTVADEVPLLIGDVFHHGKYETK 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
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YANG, Yan Ping
LOOSMORE, Sheena
SIA, Dwo Yuan Charles
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                                                         Conservative 121; Mismatches 306;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sim & McBurney
                                                                         3.8%; Score 180.5; DB 3
20.1%; Pred. No. 1.7e-06;
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                                                                                                 DB 3;
                                                                                           Length
                                                           Indels 207;
                                                           Gaps
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GENERAL INFORMATION:
APPLICANT: CHONG, Pele
APPLICANT: THOMAS, Wayne
APPLICANT: YANG, Yan Ping
APPLICANT: LOOSMORE, Sheena
APPLICANT: SIA, Dwo Yuan Charles
APPLICANT: KLEIN, Michel
                                                                                                                                                                                                                                                                                                                                            Sequence 10, Application US/09135166
Patent No. 6083743
               ADDAM
STREET: 01...
CITY: Toronto
CTTS: Ontario
                                                                                                        TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      907 NPIKLHEFICTPF 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                781 DVEQFQFSIGGSF 793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          661 GPNAIYAEHGNGTFNKISSDVIGGNAITTASAELIVPTPFVSDKSQNTVRTSLFVDAASV 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        828 SP---ISDKGYLT-----GGQVLAVGTAE--YNYEFMKD-----LRLAVFGDIGNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      409 VDVVYKVK-----ERNTGSINFGIGYGTESGISYQTSIKQDNFLGTGAAVSIAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          473 I-LMDISPIEFSASNLIQDKLNLVAAKARHLYDMPD----DRVLAINHDDGVNRSIL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182 GNE-SVSSSTLQEQMELQPDSWWKLWGNKFEGAQFEKDLQAIR------DYYLNNGYA 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  373 TNOLTTDPDKLPVKRELLEOLLTVNMGEAY-----NLQAVRALSNDLIATRYFNMVNT 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128 LNEFAKSVKEHYASVGRY-NATVEPIVNTLPNNRAEILIQINEDDKAKLASLTF----K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        316 KNLIENASAEHGYFDGRWLDRSVDVI---LPDNTADVSLIYDTGTQYRFDEVVFFTIDPK 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WNTKWKSDKNGLESKVLKDLPDYGKSSRIRASTGVGFQWQSPIGPLVFSYAKPIKKYEND 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QGFYPL-----DRDHRWYVSAKASAGYANGFGNKRLPFYQTYTAGGIGSLRGFAYGSI 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGVYSFGDNAYGSNRAHQ--MTGGTQAGYIWSDNFNHVPYRLRFFAGGDQSIRGYAHDSL 827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NGKPSQEALLAGVAVHKTVADNLVNPMRGYRQRYSLEVGSSGLV----SDANMAIARAGI 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NENNSYYVGLGHTYNKISNFALE---YNRNLYIQSNKFKGNGIKTN-----DFDFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NRDGYQAGAELRLSE---DKKGVKLYATKPLSHPLNDQLRATLGYQQEVFGHS-TNGFDL 664
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                                                                    6TH Floor, 330 University Avenue
                                                                                               Sim & McBurney
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INFORMATION FOR SEO ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 amino acids
TYPE: amino acid
TYPE: mino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-135-166-10
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                  566
                                                                                                                                                                                                                   609 NRDGYQAGAELRLSE---DKKGVKLYATKPLSHPLNDQLRATLGYQQEVFGHS-TNGFDL
                                                                                                                                                                                                                                                                                                                                                     349 LRFEGNTVSADSTLRQEMRQQEGTWYNSQLVELGKIRLDRTGFFETVENRIDPINGSNDE 408
                                                                                                                                                                                                                                                                              409 VDVVYKVK-----
                                                                                                                                                                                                                                                                                                          565 ---VYQSKKVPLYVFVASDKPRDGQI--GLGWGSDTGTRLVTKF-EHNLI-------
                                                                                                                                                                                                                                                                                                                                                                                                                                           293 FRRSDIADVE----NAIKAKLGERGYGNTTVNSVPDFDDANKTLAITFVVDAGRRLTVRQ 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               373 TNQLTTDPDKLPVKRELLEQLLTVNMGEAY-----NLQAVRALSNDLIATRYFNMVNT 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     316 KNLIENASAEHGYFDGRWLDRSVDVI---LPDNTADVSLIYDTGTQYRFDEVVFFTIDPK 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         263 DVIIHDLGEPVYIDYRA-----VEVRGEGA-DDKAFTTVADEVPLLIGDVFHHGKYETK 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/4 FILING DATE: 12-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/135,166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                        NGKPSQEALLAGVAVHKTVADNLVNPMRGYRQRYSLEVGSSGLV----SDANMAIARAGI 769
                                                                                    NENNSYYVGLGHTYNKISNFALE---YNRNLYIQSMKFKGNGIKTN-----DFDFS
                                                                                                                               STRT----LEH---EISRSIIQNGGWNRT---YSLRYRLDKLKTQAPPETWQDLPVDFV
                                                                                                                                                                          TKNDYGTSVNLGYTEPYFTKDGVSLGGNIFFENYDNSKSDTSSNYKRTTYGSNVTLGFPV
                                                                                                                                                                                                                                                                                                                                                                                                ----GRISDAVSAVARAILPDES---ENEVIDLP----ERT----ALANRKTPAD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    I-LMDISPIEFSASNLIQDKLNLVAAKARHLYDMPD----DRVLAINHDDGVNRSIL--- 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KAQITKTDVQLNDEKTKVNVTIDVNEGLQYDLRSARIIGNLGGMSAELEPLLSALHLNDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EIVFPEREQIONDOVSFEQSSSSRTEPAOVD------ESTLEPVIETVELTDG 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GNE-SVSSSTLQEQMELQPDSWWKLWGNKFEGAQFEKDLQAIR------DYYLNNGYA 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LNEFAKSVKEHYASVGRY-NATVEPIVNTLPNNRAEILIQINEDDKAKLASLTF----K
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y: Canada
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative 121;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.8%; Score 180.5; DB 3;
20.1%; Pred. No. 1.7e-06;
ative 121; Mismatches 306;
                                                                                                                                                                                                                                                                 ---ERNTGSINFGIGYGTESGISYQTSIKQDNFLGTGAAVSIAG
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-NYNSLNRGYFPTKGVKASLGGRVTIPGSDNKYYKLSADV
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Gaps

39;

181

US-09-135-166-10

ADDRESSEE:

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                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid;
TOPOLOGY: linear;
MOLECULE TYPE: protein
US-08-942-046-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/433,522
FILING DATE: 12-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
REGISTRATION NUMBER: 24 973
REFERENCE/DOCKET NUMBER: 1038-732 MIS:jb
TELECHONE: (416) 595-1155
TELECHONE: (416) 595-1163
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 3
US-08-942-046-10
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                                                                                                                                                                  Ouery Match 3.8%; Score 180.5; DB 4; Best Local Similarity 20.1%; Pred. No. 1.7e-06; Matches 159; Conservative 121; Mismatches 306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 6264954
GENFERY THE CONTROL OF THE CONTR
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 793 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6TH Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: THOMAS, Wayne
APPLICANT: YANG, Yan Ping
APPLICANT: LOOSMORE, Sheena
APPLICANT: SIA, DWO Yuan Charles
APPLICANT: KLEIN, Michel
TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 55
                                                                               263 DVIIHDLGEPVYIDYRA-----VEVRGEGA-DDKAFTTVADEVPLLIGDVFHHGKYETK 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         661 GPNAIYAEHGNGTFNKISSDVIGGNAITTASAELIVPTPFVSDKSQNTVRTSLFVDAASV 720
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72 DVKAHQEGDVLVVSVVAKSIISDVKIKGNSVIPTEALKQNLDANGFKVGDVL----IREK 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 6TH F
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                                                                                                                                                                                                                                             Length 793;
                                                                                                                                                                  Indels 207;
                                                                                                                                                              Gaps
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STATE: Ontario COUNTRY: Canada	٠. ٠.
pronto	٠.,
ADDRESSEE: Sim & McBurney STREET: 6TH Floor, 330 University Avenue	٠. ٠.
ICE ADDRI	٠. ٠
OF SECURION	
APPLICANT: KLEIN, Michel	٠. ٠
: LOOSMORE, Sheena	
: YANG, Ya	·. ·
APPLICANT: THOMAS Wayne	
ENERAL INFORMATION:	
.08-433-522A-8 equence 8, Application US/08433522A atent No. 6013514	. S. d
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781 DVEQFQFSIGGSF 793	DЬ
907 NPIKLHEFIGTPF 919	Qy
721 WNTKWKSDKNGLESKVLKDLPDYGKSSRIRASTGVGFQWQSPIGPLVFSYAKPIKKYEND 780	рь
869 YDKGFTNDTKIGAGVGVRWASPVGQVRVDVATGVKEEG 906	Qу
661 GPNAIYAEHGNGTFNKISSDVIGGNAITTASAELIVPTPFVSDKSQNTVRTSLFVDAASV 720	ф
AEYNYEFMKDLRLA	Qy
608 QGFYPLDRDHRWVVSAKASAGYANGFGNKRLPFYQTYTAGGIGSLRGFAYGSI 660	DЬ
DQSIR	Qy
566 FGWNYNSLNRGYEPTKGYKASLGGRVTIPGSDNKYYKLSADV 607	Db
714 NGKPSQEALLAGVAVHKTVADNLVNPMRGYRQRYSLEVGSSGLVSDANMAIARAGI 769	Qy
518 NENNSYYVGLGHTYNKISNFALEYNRNLYIQSMKFKGNGIKTNDFDFS 565	Db
665 STRTLEHEISRSIIQNGGWNRTYSLRYRLDKLKTQAPPETWQDLPVDFV 713	Qy
458 TKNDYGTSVNLGYTEPYFTKDGVSLGGNIFFENYDNSKSDTSSNYKRTTYGSNYTLGFPV 517	DЬ
609 NRDGYQAGAELRLSEDKKGVKLYATKPLSHPLNDQLRATLGYQQEVFGHS-TNGFDL 664	Qy
409 VDVVYKVKERNTGSINFGIGYGTESGISYQTSIKQDNFLGTGAAVSIAG 457	рь
Ö	Qy
349 LRFEGNTVSADSTLRQEMRQQEGTWYNSQLVELGKIRLDRTGFFETVENRIDPINGSNDE 408	Db
WIDLP	Qy
293 FRRSDIADVENAIKAKLGERGYGNTTVNSVPDFDDANKTLAITFVVDAGRRLTVRQ 348	Db
	Qy
233 KAQITKTDVQLNDEKTKVNVTIDVNEGLQYDLRSARIIGNLGGMSAELEPLLSALHLNDT 292	рь
γ	Qу
182 GNE-SVSSSTLQEQMELQPDSWWKLWGNKFEGAQFEKDLQAIRDYYLNNGYA 232	Db
373 TNQLTTDPDKLPVKRELLEQLLTVNMGEAYNLQAVRALSNDLIATRYFNMVNT 425	Qy
128 LNEFAKSVKEHYASVGRY-NATVEPIVNTLPNNRAEILIQINEDDKAKLASLTFK 181	Дb
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMERR: US/08/433,522A
FILING DATE: 12-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 792 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                       458
                                                                                                                                                                                                                                                                                                                                    409
                                                                                                                                                                                                                                                                                                                                                                             565
                                  770 SGVYSFGDNAYGSNRAH--QMTGGIQAGYIWSDNFNHVPYRLRFFAGGDQSIRGYAHDSL
                                                                                                                                                                   518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128 LNEFAQSVKEHYASVGRY-NATVEPIVNTLPNNRAEILIQINEDDKAKLASLTF-----K 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  316 KNLIENASAEHGYFDGRWLDRSVDVI---LPDNTADVSLIYDTGTQYRFDEVVFFTIDPK 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   263 DVIIHDLGEPVYIDYRA-----VEVRGEG-ADDKAFTTVADEVPLLIGDVFHHGKYETK 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 DVKAHQEGDVLVVSVVAKSIISDVKIKGNSIIPPEALKQNLDANGFKVGDIL----IREK 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
                                                                                                                        NGKPSQEALLAGVAVHKTVADNLVNPMRGYRQRYSLEVGSSGLV----SDANMAIARAGI 769
                                                                                                                                                                                                                                                TKNDYGTSVNLGYTEPYFTKDGVSLGGNVFFENYDNSKSDTSSNYKRTTYGSNVTLGFPV
                                                                                                                                                                                                                                                                                                                                                                      ---VYQSKKVPLYVFVASDKPRDGQI--GLGWGSDTGTRLVTKF-EHNLI-------
                                                                                                                                                                 NENNSYYVGLGHTYNKISNFALE...YNRNLYIQSMKFKGNGIKTN......DFDFS
                                                                                                                                                                                                       STRT-----LEH---EISRSIIQNGGWNRT---YSLRYRLDKLKTQAPPETWQDLPVDFV 713
                                                                                                                                                                                                                                                                                       NRDGYQAGAELRLSE---DKKGYKLYATKPLSHPLNDQLRATLGYQQEVFGHS-TNGFDL 664
                                                                                                                                                                                                                                                                                                                                VDVVYKVK-----ERNTGSINFGIGYGTESGISYQASVKQDNFLGTGAAVSIAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRRSDIADVE----NAIKAKLGERGYGNTTVNSVPDFDDANKTLAITFVVDAGRRLTVHQ 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KAQITKADVQLNDEKTKVNVTIDVNEGLQYDLRSARIIGNLGGMSAELEPLLSALHLNDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GNE-SVSSSTLQEQMELQPDSWWKLWGNKFEGAQFEKDLQAIR------DYYLNNGYA 232
                                                                                                                                                                                                                                                                                                                                                                                                               LRFEGNTVSADSTLRQEMRQQEGTWYNSQLVELGKIRLDRTGFFETVENRIDPINGSNDE 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----GRISDAVSAVARAILPDES---ENEVIDLP----ERT----ALANRKTPAD-----
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-- DRDHLWVVSAKASAGYANGFGNKRLPFYQTYTAGGIGSLRGFAYGSI 660
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                                                                                 -NYNSLNRGYFPTKGVKASLGGRVTIPGSDNKYYKLSADV
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Pred. No. 2.8e-06;
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                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 160; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/09135166 Patent No. 6083743 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (410/ TELEFAX: (410/ TELEFAX: 10 NO: 8 SEQUENCE CHARACTERISTICS: TENCTH: 792 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCE.
CORRESPONDENCE ADDRESS:
CORRESPONDENCE Sim & McBurney
CORRESSEE: Sim & McBur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                 316 KNLIENASAEHGYFDGRWLDRSVDVI---LPDNTADVSLIYDTGTQYRFDEVVFFTIDPK 372
128 LNEFAQSVKEHYASVGRY-NATVEPIVNTLPNNRAEILIQINEDDKAKLASLTF-----K
                                                                                                                                                                                                                   263 DVIIHDLGEPVYIDYRA-----VEVRGEG-ADDKAFTTVADEVPLLIGDVFHHGKYETK 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    779 DDVEQFQFSIGGSF 792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   868 AY-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: STEWART, Michael REGISTRATION NUMBER: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
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                                                                                                                                              DVKAHQEGDVLVVSVVAKSIISDVKIKGNSIIPPEALKQNLDANGFKVGDIL----IREK 127
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(416) TD NO: 8:
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LOOSMORE, Sheena
SIA, Dwo Yuan Charles
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THOMAS, Wayne
                                                                                                                                                                                                                                                                                                    Conservative 118;
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PRR: 08/433,522
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                                                                                                                                                                                                                                                                                            3.8%; Score 178; DB 3;
20.2%; Pred. No. 2.8e-06;
ative 118; Mismatches 306
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                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION: APPLICANT: CHONG,
                                                                                                                                                                                                                                           APPLICANT: THOMAS, Wayne
APPLICANT: YANG, Yan Ping
APPLICANT: LOOSMORE, Sheena
APPLICANT: SIA, DWO YUAN Charles
APPLICANT: KLEIN, Michel
                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                    TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
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                                                                         COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                    STREET:
                                                                                                                                                                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EIVFPEREQIQNDQVSFEQSSSSRTEPAQVD------ESTLEPVIETVELTDG 472
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                                                                                                                                Toronto
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6TH Floor, 330 University
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PC-DOS/MS-DOS
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-942-046-8
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I
REGISTRATION NUMBER: 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/4
FILING DATE: 12-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KNLIENASAEHGYFDGRWLDRSVDVI----LPDNTADVSLIYDTGTQYRFDEVVFFTIDPK 372
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                                    QGFYPL-----DRDHLWVVSAKASAGYANGFGNKRLPFYQTYTAGGIGSLRGFAYGSI
                                                                      SGYYSFGDNAYGSNRAH--QMTGGIQAGYIWSDNFNHVPYRLRFFAGGDQSIRGYAHDSL
                                                                                                                                                                                        NENNSYYVGLGHTYNKISNFALE---YNRNLYIQSMKFKGNGIKTN-----DFDFS
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SP---
                                                                                                                  FGW----
                                                                                                                                                  NGKPSQEALLAGVAVHKTVADNLVNPMRGYRQRYSLEVGSSGLV----SDANMAIARAGI 769
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-ISDKGYLTGGQVLAVGTAE--YNYEFMKD-----LRLAVFGDIGN
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MAICHES 158; CONSERVATIVE 121; Mismatches 305; Indels 215; Gaps 39;  Qy 263 DVIIHDLGEPVYIDYRAVEVRGEGA-DDKAFTTVADEVPLLIGDVFHHGKYETK 315	TELEFAX: (416) 595-1163  INFORMATION FOR SEQ ID NO: 2:  SEQUENCE CHARACTERISTICS: LENGTH: 797 amino acids TYPE: amino acids TOPOLOGY: linear MOLECULE TYPE: protein US-08-433-522a-2  Query Match Query Match Could this the county of the count	CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: STEWART, Michael I REGISTRATION NUMBER: 24,973 REFERENCE/DOCKET NUMBER: 1038-434 MIS:jb TELECOMMUNICATION INFORMATION: TELEPHONE: (416) 595-1155	BH BH ST	Or 6 SEV	2 1 1 2 2 X X X	661 GPNAIYQGQNNKFNKISSDVIGGNAIATASAELIVPTPFYSDKSQNTVRTSLFVDAAS 718  868 AYDKGFTNDTKIGAGVGVRWASPVGQVRVDVATGVKEE 905  1719 VWNTKWKSDKNGLESNVLKDLPDYGKSSRTRASTGVGFQWQSPSGPVVFSYAKPIKKYEN 778  906 GNPIKLHFFIGTPF 919  1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
ADDRESSEE: Sim & McBurney STREET: 6TH Floor, 330 Universit CITY: Toronto STATE: Ontario COUNTRY: Canada ZIP: M5G 1R7 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible COMPUTER: Floppy disk COMPUTER: Patentin Release #1.0, OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION NUMBER: US/08/433,5; FILING DATE: 12-SEP-1995 CLASSIFICATION: 435	INI CANI CANI CANI CANI CANI CANI	αω ω	828 661 863 719	Qy         714 NGKPSQEALLAGVAVHKTVADNLVNPMRG           I         I           I         I           I         I           I         I           I         I           I         I           I         I           I         I           I         I           I         I           I         I           I         I           I         I           I         I           I         I           I         I           I         I           I         I           I         I           I         I           I         I           I         I           I         I           I         I           I         I           I         I           I         I           I         I           I         I           I         I           I         I           I         I           I         I      I         I           I	409 VD 609 NR 658 TK 665 ST 518 NE	Db 233 KAQITKTDVQLNDEKTKVNVTIDVNEGLQ Qy 473 I-LMDISPIEFSASNLIQDKLNLVAAKAR   ::    : :  Db 293 FRRSDIADVENAIKAKLGERGYGSA Qy 525GRISDAVSAVARAILPDESENE         :::  Db 349 LRFEGNTVSADSTLRQEMRQQEGTWYNSQ OV 565VYOGKKVPLYVFVASDKPRDGOIG

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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 797 amino acids
TYPE: amino acid
TOPOLOGY: linear
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Best Local Similarity
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REFERENCE/DOCKET NUMBER: 1038-434 MIS:jb
TELECOMMUNICATION INFORMATION:
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NAME: STEWART, Michael I
                   903
                                                                                                                      661 GPNAIYAEYGNGSGTGTFKKISSD--VIGGNAIATASAELIVPTPFVSDKSQNTVRTSLF
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K--EEGNPIKLHFFIGTPF 919
                                                 VDAASVWNTKWKSDKNGLESDVLKRLPDYGKSSRIRASTGVGFQWQSPIGPLVFSYAKPI
                                                                                                                                                                                            QGFYPL-----DRDHLWVVSAKASAGYANGFGNKRLPFYQTYTAGGIGSLRGFAYGSI 660
                                                                                                                                                                                                                               SGVYSFGDNAYGSNRAH--QMTGGIQAGYIWSDNFNHVPYRLRFFAGGDQSIRGYAHDSL 827
                                                                                                                                                                                                                                                                                                         NGKPSQEALLAGVAVHKTVADNLVNPMRGYRQRYSLEVGSSGLV----SDANMAIARAGI 769
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                                                                                         GDIGNAY---
                                                                                                                                                                                                                                                                                                                                                                                                                      TKNDYGTSVNLGYTEPYFTKDGVSLGGNVFFENYDNSKSDTSSNYKRTTYGSNVTLGFPV 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---VYQSKKVPLYVFVASDKPRDGQI--GLGWGSDTGTRLVTKF-EHNLI------
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                                                                                                                                                                                                                                                                                                                                               NENNSYYVGLGHTYNKISNFALE---YNRNLYIQSMKFKGNGIKTN-----DFDFS 565
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                                                                                                                                                            ------ISDKGYLTGGQVLAVGTAE--YNYEFMKD-----LRLAVF 862
                                                                                                                                                                                                                                                                       -----NYNSLNRGYFPTKGVKASLGGRVTIPGSDNKYYKLSADV 607
                                                                                     -DKGFTNDTKIGAGVGVRWASPVGQVRVDVATGV 902
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US-08-433-522A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 3.8; Score 171.5; DB Best Local Similarity 19.8%; Pred. No. 1e-05; Matches 158; Conservative 121; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (416) 595-1163 INFORMATION FOR SEQ ID NO:
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LENGTH: 797 amino acids
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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APPLICANT: SIA, Dwo Yuan Charles
APPLICANT: KLEIN, Michel
                       525
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                                                                                                                                                                                                                                                                                                                                                                     72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
TOPOLOGY: linear
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                  KAQITKTDVQLNDEKTKVNVTIDVNEGLQYDLRSARIIGNLGGMSAELEPLLSALHLNDT
----GRISDAVSAVARAILPDES---ENEVIDLP----ERT----ALANRKTPAD-----
                                                                                          I-LMDISPIEFSASNLIQDKLNLVAAKARHLYDMPD----DRVLAINHDDGVNRSIL---
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THOMAS, Wayne
YANG, Yan Ping
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RESULT 10
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Patent No. 6083743
GENERAL INFORMATION:
APPLICANT: CHONG, Pele
APPLICANT: THOMAS, Wayne
                                                                                                                                                                  CIP: MSU IN.

COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

""" TCATION NUMBER: US/09/135,166
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10:
TELECOMMUNICATION INFORMATION:
                                                                                  FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/433,522
FILING DATE: 12-SEP-1995
CLASSIFICATION:
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APPLICANT: SIA, Dwo Yuan Charles
APPLICANT: KLEIN, Michel
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CITY: Toronto
STATE: Ontario
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ZIP: M5G 1R7
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6TH Floor, 330 University Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 3.6%; Score 171.5; Best Local Similarity 19.8%; Pred. No. 1e-0 Matches 158; Conservative 121; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 797 amino acids
   779
                                   903 K--EEGNPIKLHFFIGTPF 919
                                                                  719 VDAASVWNTKWKSDKNGLESDVLKRLPDYGKSSRIRASTGVGFQWQSPIGPLVFSYAKPI
                                                                                                                                           661 GPNAIYAEYGNGSGTGTFKKISSD--VIGGNAIATASAELIVPTPFVSDKSQNTVRTSLF
                                                                                                                 863 GDIGNAY--
                                                                                                                                                                                                                                                                                                                                                                                  518
                                                                                                                                                                                                                                                                                                                                           714
                                                                                                                                                                                                                                                                                                                                                                                                                                            458 TKNDYGTSVNLGYTEPYFTKDGVSLGGNVFFENYDNSKSDTSSNYKRTTYGSNVTLGFPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       409 VDVVYKVK-----ERNTGSINFGIGYGTESGISYQASVKQDNFLGTGAAVSIAG
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KKYENDDVEQFQFSIGGSF 797
                                                                                                                                                                                                                   QGFYPL-----DRDHLWVVSAKASAGYANGFGNKRLPFYQTYTAGGIGSLRGFAYGSI 660
                                                                                                                                                                                                                                                                                                                               NGKPSQEALLAGVAVHKTVADNLVNPMRGYRQRYSLEVGSSGLV----SDANMAIARAGI 769
                                                                                                                                                                                                                                                                                                                                                                    NENNSYYVGLGHTYNKISNFALE---YNRNLYIQSMKFKGNGIKTN-----DFDFS
                                                                                                                                                                                            SP-----
                                                                                                                                                                                                                                                      SGVYSFGDNAYGSNRAH--QMTGGIQAGYIWSDNFNHVPYRLRFFAGGDQSIRGYAHDSL 827
                                                                                                                                                                                                                                                                                                                                                                                                       STRT-----LEH----EISRSIIQNGGWNRT---YSLRYRLDKLKTQAPPETWQDLPVDFV 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---VYQSKKVPLYVFVASDKPRDGQI--GLGWGSDTGTRLVTKF-EHNLI------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LRFEGNTVSADSTLRQEMRQQEGTWYNSQLVELGKIRLDRTGFFETVENRIDPINGSNDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KAQITKTDVQLNDEKTKVNVTIDVNEGLQYDLRSARIIGNLGGMSAELEPLLSALHLNDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GNE-SVSSSTLQEQMELQPDSWWKLWGNKFEGAQFEKDLQSIR-----DYYLNNGYA 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----GRISDAVSAVARAILPDES---ENEVIDLP----ERT----ALANRKTPAD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EIVFPEREQIQNDQVSFEQSSSSRTEPAQVD------ESTLEPVIETVELTDG 472
                                                                                                                                                                                                                                                                                             ------NYNSLNRGYFPTKGVKASLGGRVTIPGSDNKYYKLSADV
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                                                                                                                                                                              -----ISDKGYLTGGQVLAVGTAE--YNYEFMKD-----LRLAVF
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19.8%; Pred. No. 1e-05;
                                                                                                       -----DKGFTNDTKIGAGVGVRWASPVGQVRVDVATGV 902
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RESULT 11 US-09-135-166-4

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ZIP: M5G 1R7
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/135,166
FILING DATE:
CLASSIFICATION DATA:
APPLICATION UMBER: 08/433,522
FILING DATE: 12-SEP-1995
CLASSIFICATION UMBER: 08/433,522
FILING DATE: 12-SEP-1995
CLASSIFICATION UMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-829 MIS:jb
TELEPHONE: (416) 595-1163
INFORMATION FOR SEQ ID NO: 4:
SECHENCE CLASSIFICATION
TELEPHONE: (416) 595-1163
INFORMATION FOR SEQ ID NO: 4:
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 797 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: YANG, Yan Ping
APPLICANT: LOOSMORE, Sheena
APPLICANT: SIA, Dwo Yuan Charles
APPLICANT: KLEIN, Michel
TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: CHONG, Pele APPLICANT: THOMAS, Wayne
349 LRFEGNTVSADSTLRQEMRQQEGTWYNSQLVELGKIRLDRTGFFETVENRIDPINGSNDE 408
                                                       525
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                                                                                                                                                                                                                   426 EIVFPEREQIQNDQVSFEQSSSSRTEPAQVD------ESTLEPVIETVELTDG 472
                                                                                                                                                                                                                                                                    182 GNE-SVSSSTLQEQMELQPDSWWKLWGNKFEGAQFEKDLQSIR------DYYLNNGYA 232
                                                                                                                                                                                                                                                                                                             373 TNQLTTDPDKLPVKRELLEQLLTVNMGEAY-----NLQAVRALSNDLIATRYFNMVNT 425
                                                                                                                                                                                                                                                                                                                                                         128 LNEFAKSVKEHYASVGRY-NATVEPIVNTLPNNRAEILIQINEDDKAKLASLTF-----K 181
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                                                                                                                                                                                                                                                                                                                                                                                  316 KNLIENASAEHGYFDGRWLDRSVDVI---LPDNTADVSLIYDTGTQYRFDEVVFFTIDPK 372
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CITY: Toronto
STATE: Ontario
COUNTRY: Canada
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                                              ----GRISDAVSAVARAILPDES---ENEVIDLP----ERT----ALANRKTPAD-----
                                                                                       FRRSDIADVE----NAIKAKLGERGYGSATVNSVPDFDDANKTLAITLVVDAGRRLTVRQ 348
                                                                                                                                     I-LMDISPIEFSASNLIQDKLNLVAAKARHLYDMPD----DRVLAINHDDGVNRSIL---
                                                                                                                                                                          KAQITKTDVQLNDEKTKVNVTIDVNEGLQYDLRSARIIGNLGGMSAELEPLLSALHLNDT 292
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NAME: STEWART, Michael I  REGISTRATION NUMBER: 24,973  REFERENCE/DOCKET NUMBER: 1038-829 MIS:jb  TELECOMMUNICATION INFORMATION: TELEPHONE: (416) 595-1155	
EY/	
( G C)	
TYPE: Floppy disk ER: IBM PC compatible	
; COMPUTER READABLE FORM:	
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TH Floor, 330 U	
McBurn	
TION:	
CANT:	
LOOSMORE, Shee	
; APPLICANT: THOMAS, Wayne ; APPLICANT: YANG, Yan Ping	
ENERAL INFORM APPLICANT:	
RESULT 12 US-09-135-166-6 ; Sequence 6, Application US/09135166 ; Patent No. 6083743	
Db 779 KKYENDDVEQFQFSIGGSF 797	
QY 903 KEEGNPIKLHFFIGTPF 919	
Db 719 VDAASVWNTKWKSDKNGLESDVLKRLPDYGKSSRIRASTGVGFQWQSPIGPLVFSYAKPI 778	
WASP	
Db 661 GPNAIYAEYGNGSGTGTFKKISSDVIGGNAIATASAELIVPTPFVSDKSQNTVRTSLF 718	
Qy 828 SPISDKGYLTGGQVLAVGTAEYNYEFMKDLRLAVF 862	
Db 608: QGFYPLDRDHLWVVSAKASAGYANGFGNKRLPFYQTYTAGGIGSLRGFAYGSI 660	
Oy 770 SGVYSFGDNAYGSNRAHQMTGGIQAGYIMSDNFNHVPYRLRFFAGGDQSIRGYAHDSL 827	
Db 566 FGWNYNSLNRGYFPTKGVKASLGGRVTIPGSDNKYYKLSADV 607	
Qy 714 NGKPSQEALLAGVAVHKTVADNLVNPMRGYRQRYSLEVGSSGLVSDANMAIARAGI 769	
Db 518 NENNSYYVGLGHTYNKISNFALEYNRNLYIQSMKFKGNGIKTNDFDFS 565	
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Db 458 TKNDYGTSVNLGYTEPYFTKDGVSLGGNVFFENYDNSKSDTSSNYKRTTYGSNYTLGFPV 517	
QY 609 NRDGYQAGAELRLSEDKKGVKLYATKPLSHPLNDQLRATLGYQQEVFGHS-TNGFDL 664	
Db 409 VDVVYKVKERNTGSINFGIGYGTESGISYQASVKQDNFLGTGAAVSIAG 457	
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RESULT 13
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Best Local Similarity
Matches 158; Conserv
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INFORMATION FOR SEQ ID NO:
                                                                                                                                        903
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LENGTH: 797 amino acids
TYPE: amino acid
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                                                                                                                                  K--EEGNPIKLHFFIGTPF 919
                                                                                                                                                              VDAASVWNTKWKSDKNGLESDVLKRLPDYGKSSRIRASTGVGFQWQSPIGPLVFSYAKPI 778
                                                                                                   KKYENDDVEQFQFSIGGSF 797
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                                                                                                                                                                                                                                                                                                                                         SGVYSFGDNAYGSNRAH--QMTGGIQAGYIWSDNFNHVPYRLRFFAGGDQSIRGYAHDSL 827
                                                                                                                                                                                                                                                                                                                                                                                                             NGKPSQEALLAGVAVHKTVADNLVNPMRGYRQRYSLEVGSSGLV----SDANMAIARAGI 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRT----LEH---EISRSIIQNGGWNRT---YSLRYRLDKLKTQAPPETWQDLPVDFV 713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TKNDYGTSVNLGYTEPYFTKDGVSLGGNVFFENYDNSKSDTSSNYKRTTYGSNVTLGFPV 517
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                                                                                                                                                                                                 -ISDKGYLTGGQVLAVGTAE--YNYEFMKD-----LRLAVF 862
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; MOLECULE TYPE: protein
US-08-942-046-2
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 158;
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 797 amino acids
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-113
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APPLICANT: THOMAS, Wayne
APPLICANT: YANG, Yan Ping
APPLICANT: LOGSMORE, Sheena
APPLICANT: SIA, Dwo Yuan Charles
APPLICANT: KLEIN, Michel
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/4
FILING DATE: 12-58P-1995
CLASSIFICATION: 435
349 LRFEGNTVSADSTLRQEMRQQEGTWYNSQLVELGKIRLDRTGFFETVENRIDPINGSNDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                        263 DVIIHDLGEPVYIDYRA-----VEVRGEGA-DDKAFTTVADEVPLLIGDVFHHGKYETK 315
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ZIP: M5G 1R7
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                                                                          FRRSDIADVE----NAIKAKLGERGYGSATVNSVPDFDDANKTLAITLVVDAGRRLTVRQ 348
                                                                                                                  I-LMDISPIEFSASNLIQDKLNLVAAKARHLYDMPD----DRVLAINHDDGVNRSIL---
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                                                                                                                                                                                                 EIVFPEREQIQNDQVSFEQSSSSRTEPAQVD------ESTLEPVIETVELTDG 472
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RESULT 14
US-08-942-046-4
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APPLICANT:
      NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-732
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                            APPLICATION NUMBER: 08/4:
FILING DATE: 12-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: LOOSMORE, Sheena
APPLICANT: SIA, DWO YUAN CHARLES
APPLICANT: KLEIN, Michel
TITLE OF INVENTION: HAEMOPHILUS
                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                            APPLICATION NUMBER:
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M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                             Toronto
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(416)
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                                                                                                                                             08/433,522
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RESULT 15
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                                                                   KKYENDDVEQFQFSIGGSF 797
                                                                                                                                                                 GDIGNAY-----
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                                                                                                                                                                                                                                                                                                                           FGW-----PNYNSLNRGYFPTKGVKASLGGRYTIPGSDNKYYKLSADV
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19.8%; Pred. No. 1e-
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Sequence 6, Application US/08942046 Patent No. 6264954

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Best Local Similarity
Matches 158; Conserv
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ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
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APPLICATION NUMBER: 08/4
FILING DATE: 12-SEP-1995
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CURRENT APPLICATION DATA
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ADDRESSEE: Sim & McBurney
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NAME: STEWART, Michael I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN NUMBER OF SEQUENCES: 55
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STREET: ...
Toronto
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                                                                                                       FRRSDIADVE----NAIKAKLGERGYGSATVNSVPDFDDANKTLAITLVVDAGRRLTVRQ
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                                 LRFEGNTVSADSTLRQEMRQQEGTWYNSQLVELGKIRLDRTGFFETVENRIDPINGSNDE 408
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                                                                                                                                                                                                                                               GNE-SYSSSTLQEQMELQPDSWWKLWGNKFEGAQFEKDLQSIR------DYYLNNGYA 232
                                                                                                                                                                                                                                                                                                                                                    KNLIENASAEHGYFDGRWLDRSVDVI---LPDNTADVSLIYDTGTQYRFDEVVFFTIDPK 372
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-VYQSKKVPLYVFVASDKPRDGQI--GLGWGSDTGTRLVTKF-EHNLI-----
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LOOSMORE, Sheena
SIA, Dwo Yuan Charles
KLEIN, Michel
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19.8%; Pred. No. 1e-
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RESULT 16
US-07-689-008-2
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                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                   APPLICATION NUMBER: US 49
FILING DATE: 23-MAR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Murphy, Lisabeth Re
                                                                                    APPLICATION NUMBER: US 337,194
FILING DATE: 12-APR-1989
PRIOR APPLICATION DATA:
                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                     SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES:
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                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 19910 CLASSIFICATION: 43
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NAME: Murphy, Lisab REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                      CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                       STATE:
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Calhoon, Roger D
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19910422
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dero Center
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TELEPHONE: (415) 393-2000
TELEPAX: (415) 393-2286
TELEX: 340817 MACPAG SFO
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3031 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 3.4%; Score 159.5; DB 1; Length 3031; Best Local Similarity 19.2%; Pred. No. 0.001; Matches 201; Conservative 131; Mismatches 360; Indels 357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                      2390 LQQVEGTRAASGAGAAQEDAL---APPSTNPFRPRGYGHQTELGAPVTGGSYSAEAASPD 2446
                                                                                                                      2348 AMDGVQESPMDARAWLAMAVADQADGH-------GQRTIE-------DLRRAYDLR 2389
                                                                                                                                                                                                     2293 PKLALARLYNGHGKPGKALEID-----LAVLRHNPQDLDARQAAVQAAVNSDHNSLATRL 2347
                                                                                                                                                                                                                                                                                       2233 GDGTGSATGSALLPEQVQTLQQLRMGISVAQSDLLNQRGDQAQAYDHLAPALQADPEATS 2292
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----LLAGVAVH-KTVADNL---VNPMRGYRQRYSLEVGSSGLVSDANMAIA-----RAG 768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGMGLVSMRQGDTA--EARRYFEEAMAADPK----TADRWRPALAGMAVSGEYASVRQLI 1938
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511 859	403 VIELYELIUGILMULSPLEKSASNILQUKLNIVAAKARHLYDMPDDRVL;	D 4	
462	411 SNDLLATRENMVNTEIVFPEREQIQNDQVSFEQSSSSRTEPAQVDESTLEP .	Db Qy	
759		Db	
410	AL	Qy	
699	40 KGQEFTISNLYSNGNTPNTFETITFAGENGISISNDIAKGKVKVGIDPINGLTTPKLTVG	Db	
639	46 TADVSLIVDTG-TOVREDEVVF	0 5	
4	LLIGDVFHHGKYETKKNLIENASAEHGYFDGRWLDRSVDVILPDN	y Qy	
595	50 KFGTTRITEEEIGFADADGKVDKKSPYLDKKQLQVGGVKITKDSGI	Db	
) 28.5	TDYRAVEVRGE	Qy	
549	NET	D 5	
501	SNKAGATOGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	Ov Db	
178	EMGINPNDYIPEYQGEQPNSEVVVPPTLEPEKPGLIKRLYARLFNDGVN	Qy	
479	435 AELQSGGLTFTPTTNASTDKTVYGTDGLKFTDNSNTALEDTTRIT	DЪ	
119		Qy	
ıps 53;	ry Match 2.9%; Score 138; DB 4; Length 2314; t Local Similarity 19.3%; Pred. No. 0.042; ches 189; Conservative 132; Mismatches 315; Indels 342; Ga	Que Bes Mat	
	LEVID NO 49 LEVID TYPE: PRT TYPE: PRT ORGANISM: Haemophilus influenzae )9-268-347-49	S - 0	
	RRENT APPLICA RRENT FILING MBER OF SEQ I TTWARE: Paten	2	
SNIE	TINVENTATION: Sheena M. TINVENTION: RECOMBINANT H TERENCE: 1038-860	G	
	ESULT 17 S-09-268-347-49 Sequence 49, Application US/09268347 Patent TNO. 6335182 GENERAL TROCKSTON.	RESULT US-09-: ; Sequent ; Patent	
	74 GNS	Db	
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879	LSPISDKGYLTGG	Qy	
2543	GSVY	Db	
822	769 ISGVYSFGDNAYGSNRAHQMTGGIQAGYIWSDNFNHVPYRLRFFAGGDQSIRGY-	Qy	
2504	: : :  :  :  :    :    :    :    :	Db	

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RESULT 18
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                                                                                                                                                                                                             COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALENTIN Release #1.0, Ver.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/621,944A
FILING DATE: 26-MAR-1996
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: SASAKI
APPLICANT: HARKNE
                                 REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-587
TELECOMMUNICATION INFORMATION:
                                                                                       CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
                                                                                                                                                                                                                                                                                                                                                   ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/478,370
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OF TITLE OF INVENTION: MEMBRANE PROTEIN OF MORAXELLA
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                    TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENGITTKVNKGVVRVGI------DQTKGLTTPKLTVGNNNGKGIVIDS------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YQQEVFGHSTNGFDLSTRTLEHEISRSIIQN-----GGWNRTYSLRYRLD-KLKTQAPP 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QVGADGVKFAKVDKGNSSTGIDGTSRITKDQIGFTGANGSLDTTKP--HLTKDKLKVG-- 1027
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M5G 1R7
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Suite 701, 330 University Avenue
(416) 595-1163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HARRNESS, Robin E.
LOOSMORE, Sheena M.
KLEIN, MIGHEL H.
KVEIN HIGH MOLECULAR WEIGHT MAJOR OUTER
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                  (416) 595-1155
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SEQUENCE CHARACTERISTICS:
LENGTH: 1833 amino acids
823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  621 LKNNNNPIDFVS------TYDIVDFANGNATTATVTHDTAN--KTSKVVYDVN 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    561 NVKITNTGINAGGKAITGLSPTLPSIADQSSRNIELGNTIQDKDKSNAASINDILNTGFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       294 PYLDKKQLKVGSVAITIDNGIDAGNKKISNLAKGSSANDAVTIEQLKAAKPTLNAGAGIS 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               226 DLNGSIP--RLRQTALVAARAVGYYDIDLSIIRNSIGEVDVIIHDLGEPVYIDYRAVEV- 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
es 191; Conserv
AHDSLSPISDKGYLTGGQVLAVGTAEYNYEFMKD----LRLAVFGDI---
                                         AIARAGISGVYSFGDNAYGSNRAHQMTGGIQAGYIWSDNFNHVPYRLRFFAGGDQSIRGY
                                                                                                                                                                      NGKPSQEALLAGVAVHK-TVAD-----NLVNPMRGYRQRYSLEV----GSSGLVSDANM
                                                                                                                                                                                                                                                                                                        TRDEIGFTGTNG-----SLDK-----SKP-----HLSK
                                                                                                                                                                                                                                                                                                                                   TKFEHNLINRDGYQAGAELRLSEDKKGVKLYATKPLSHPLNDQLRATLGYQQEVFGH-ST
|: |
                                                                                                                                                                                                                                                          NGFDLSTRTLEHEISRSIIQN-----GGWNRTYSLRYRLDKLKTQAPPETWQDLPVDFV
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                                                                                                                                                                                                                      DGINAGGKKITNIQSGEIAQNSHDAVTGG--KIYDLKTELE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NN----QVNTLTLKGENGLNIKTDKNGTVTFGINTTSGLK------AGKSTLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YETKKNLIENASAEHGYFDGRWLDRSVDVI--LPDNTADVSLIYDTGTQYRFDEVVF-FT 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NVNGSNPGTGIANTARITRDKIGFAGSDGAV------DTNKP-YLDQDKLQVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GKNGLTVATKKDGTVTFGLSQDSGLT--IGKSTLNNDG-LTVKDTNEQI-QVGANGIKFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VTPTEISVDAKSGNVTAPTYNIGVKTTELNSDGTSDKFSVKGSGTNNSLVTAEHLASYLN 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AKPQSQALDVVNFDDQSPISRIGEQSPPLGLD-----MSVIEETTPLSL--EELFAQEST 129
                                                                                                                               -NKISSTAKTAQNSLHEFSVADEQGNNFTVSNPYSSYDTSKTSDVITFAGENGITTKVNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----RGEGADDKAFTTVADEVPLL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.9%; Score 136; DB 4; lilarity 19.7%; Pred. No. 0.042; Conservative 128; Mismatches 351;
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-GNAY 869
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Query Match Best Local Similarity 19.7%; Pred. No. 0.042; Matches 191; Conservative 128; Mismatches 351; Indels 298; Gaps 49;  Qy 22 PLMTSQALAQQNNPANIINHVPAHDTAI-NQAKAGNPPVLITPEGIGARLNA-AGLN 76	Db 1017 SWTLANVTNDKGSVRTTEQG-NIIKDEDKERAASIVDVLSAGENLQGNGEAV 1067  Oy 870 DKGFTMDT 877  Db 1068 DFVSTYDT 1075  RESULT 19 US-08-945-567D-4  Sequence 4, Application US/08945567D  Sequence 4, Application US/08945567D  APPLICANT: HARKNESS, Robin E. APPLICANT: HARKNESS, Robin E. APPLICANT: HARKNESS, Robin E. APPLICANT: CHONG, Pele APPLICANT: LOSMONER, Sheena M. APPLICANT: LOSMONER, Pele APPLICANT: LOSMON
US-08-621-944A-3  US-08-621-944A-3  Sequence 3, Application US/08621944A  Patent No. 6440425  GENERAL INFORMATION:  APPLICANT: SASAKI, Ken APPLICANT: HARKNESS, Robin E. APPLICANT: LOSNORE, Sheena M. APPLICANTON. HIGH MOLECULAR WEIGHT MAJOR OUTER TITLE OF INVENTION: HEGH MOLECULAR WEIGHT MAJOR OUTER TITLE OF INVENTION: CORRESSEE: Sin & MCBURNOY STREET: Suite 701, 330 University Avenue STATE: Ontario COUNTRY: Canada ILP: MSG 187 COMPUTER READABLE FORM: COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: Floppy disk COMPUTER: John PC compatible OPERATING SYSTEM: PC DOS/MS-DOS SOFTWARE: PC-DOS/MS-DOS COMPUTER: John PC compatible COMPUTER: John PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PC-DOS/MS-DO	Db 666 VDDTTIHLTGTDDNKKLGVKTTKLN

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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1992 amino acids
TYPE: amino acid
STRANDEDNESS: single
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1075
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REFERENCE/DOCKET NUMBER: 10:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                    1036
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                                                                                                                                                                                                                                                                                                                                                                                                                                            869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                426 EIVFPEREQIQN-DQVSFEQSSSSRTEPAQVDESTLEPVIETVELTDGILMDISPIEFSA 484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   226 DLNGSIP--RLRQTALVAARAVGYYDIDLSIIRNSIGEVDVIIHDLGEPVYIDYRAVEV- 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AK------FYQSSQSGETSAIGSSHQKTEPYANIKAALEDITQESA-----M 225
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                                      NGKPSQEALLAGVAVHK-TVAD-----NLVNPMRGYRQRYSLEV----GSSGLVSDANM 762
                                                                                  DGINAGGKKITNIQSGEIAQNSHDAVTGG--KIYDLKTELE-
                                                                                                                         NGFDLSTRTLEHEISRSIIQN-----GGWNRTYSLRYRLDKLKTQAPPETWQDLPVDFV 713
                                                                                                                                                                         TRDEIGFTGTNG-----SLDK-----SKP-----SKP-----HLSK 1039
                                                                                                                                                                                                                                                                                                                                                                                            SNLIQDKLNLVAAKARHLYDMPDDR----VLAINHDDGVNRSILGRISDAVSAVARAILP 540
                                                                                                                                                                                                                                                                                                       DESENEVIDLPERTALANRKTPADVYQSKKVPLYVFVASDKPRDGQIGLGWGSDTGTRLV 600
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-NKISSTAKTAQNSLHEFSVADEQGNNFTVSNPYSSYDTSKTSDVITFAGENGITTKVNK 113:
                                                                                                                                                                                                                TKFEHNLINRDGYQAGAELRLSEDKKGVKLYATKPLSHPLNDQLRATLGYQQEVFGH-ST 659
                                                                                                                                                                                                                                                              DGG----LSTKNPTGSEQTQVGADGVKFAKV-----NNNGVVGAG---IDGTTRI
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TYPE: PRT
ORGANISM: Moraxella catarrhalis
US-08-945-567D-3
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Best Local Similarity
Matches 191; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Applic Patent No. 6448386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE PROTEIN OF TITLE OF INVENTION: MORAXELLA FILE REFERENCE: 1038-745 MIS CURRENT APPLICATION NUMBER: US/08/945,567D CURRENT FILING DATE: 1996-04-29 PRIOR APPLICATION NUMBER: 08/431,718 PRIOR APPLICATION NUMBER: 08/478,370 PRIOR FILING DATE: 1995-05-07 PRIOR FILING DATE: 1995-06-07 PRIOR FILING DATE: 1995-06-07 PRIOR FILING DATE: 1995-06-07 PRIOR FILING DATE: 1996-03-26 PRIOR APPLICATION NUMBER: 08/621,944 PRIOR APPLICATION NUMBER: 08/621,944 PRIOR APPLICATION NUMBER: PCT/CA96/00264 PRIOR APPLICATION NUMBER: PCT/CA96/00264 PRIOR FILING DATE: 1996-04-29 PRIOR FILING DATE: 1996-04-29 PRIOR FILING DATE: 1996-04-29 PRIOR FILING DATE: 1996-04-29
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APPLICANT: KLEIN, Michel H.
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                                                  720 NVKITNTGINAGGKAITGLSPTLPSIADQSSRNIELGNTIQDKDKSNAASINDILNTGFN 779
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                                                                                                                                                                                                      DLNGSIP--RLRQTALVAARAVGYYDIDLSIIRNSIGEVDVIIHDLGEPVYIDYRAVEV- 282
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YETKKNLIENASAEHGYFDGRWLDRSVDVI--LPDNTADVSLIYDTGTQYRFDEVVF-FT
                                                                                                       -----RGEGADDKAFTTVADEVPLL------
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                                                                                                    -----IGDVFHHG-K 311
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Query Match Query Query Query Query Query Query Match Query Match Query Match Query	FVS	
RESULT 23 US-09-134-001C-3159 US-09-134-001C-3159 Sequence 3159, Application US/09134001C Fatent No. 3880370 GENERAL INFORMATION: APPLICANT: Lynn Doucette-Stamm et al FITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC FITTLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007 CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13	09 10 DECINNO	_

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TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3159
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PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3159
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                                                                                                                              622 SEDKKGVKLYATKPLS------HPLNDQLRATLGYQQEVFGHSTNGFDLSTRTL
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                                        EHEISRSIIQNGGWNRTYSLRYRLDKLKTQAPPETWQDLPVDFVNGKPSQE 720
ESKINET-VOTDGMTQQSVENYKQAKIKAQNESSIAQTL---INNGDASDQ 3396
                                                                                   TENRANTII--NKPIRSVEEVNNALHEVNQLNQRLTDTINLLQPL--ANKESLKEARNRL
                                                                                                                                                                                                                 PADVYQSKKVPLYVFVASDKPRDGQIGLGWGSDTGTRLVTKFEHNLINRDGYQAGAELRL 621
                                                                                                                                                                                                                                                                                                     VLAINHDDGVNRSILG---RISDAVSAVARA---ILPDES--ENEVIDLPERTALANRKT 561
                                                                                                                                                                                                                                                                                                                                              EVTKAINILQDKEDNSELVRAKEKLDQAINSQPSLNGMTQESINNYTTKRREAQNIASSA 3214
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                                                                                                                                                                                                                                                                                                                                                                                        IEFSASNLIQDK------ 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VFPE-----REQIONDQVSFEQSSSSRTEPAQVDESTLEPVIETVELTDGILMDISP 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEQLLTVNMGEA-----YNLQAVRALSNDL----IATRYFNM---VNTEI 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PKLTEAINMLQNKENNTELVNAKNRLENAVNDT-DP-THGMTQETINNYNAKKREAQNEI 3041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PDNTADVSLIYD-----TGTQYRFDEVVFFTIDPKTNQLTTD-----PDKLPVKREL 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INNYNDKQREAERALTSAQRVID---NGDATTQEITSEKS-----KVEQAMQALTNA 2905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -KFYQSSQSGETSAIGSSHQKTEPYANIKAALEDITQESAMDLNGSIPRLRQT--ALVAA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VQPKVNQAIALLQPKENNSELVQAK------KRL----QDAVNDIPQTQGMTQQT 2856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INP--NDYIPEYQGEQPNSEVVVPPTLEPEKPGLIKRLYARLENDGVNKVPRLKA----- 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IENVSTNGKKPASIRQYETAKARIQNQINDAKNEAERILGNDNPQVSQVTQALNKIKAIQ 2983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IGDVFHHGK------YETKKNLIENASAEHGYFDGRWLD------RSVDVIL 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RAVGYYDIDLSIIRNSIGEVDVIIHDLGEPVYIDYRAVEVRGEGADDKAFTTVADEVPLL 302
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Pred. No. 0.93;
06; Mismatches 293; Indels 266
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                                                                                                                                                                         -SAYNNTIHSLOSEITO 3293
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RESULT 24

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-961-083-118
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION NUMBER: US/08/961,083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: PETELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION: NAME: Brookes, A. Anders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 2.8%; Score 134; DB 4 Local Similarity 19.4%; Pred. No. 0.024;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Rockville
STATE: Maryland
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-ALEVTTRNRTEIQNI-----PYTTEEIQDPTLLKNRKIERQ------GQA-----
                                                                                                                                                                                                             YYDIDLSIIRNSIGEVDVIIHDLGEPVYIDYRAVEVRG-EGADDKAFTTVADEVPLLIGD 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLNAKPQSQALDVVNFDD-----QSPISRIGEQSPPLGLDMSVIEETTPLSLEELFAQE 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LTSQILSAYNSQLSIGVGEHLPEPLKIEGYQYIGYIKTKKQDNTELSRT---VDGKYSAQ 108
                                         VSLIYDTGTQYRFDEVVFFTIDPKTNQLTTDPDKLPVKRELLEQLLTVNMGEAYNLQAVR 408
                                                                                   LATKGTQEPGHEGKATVREETLEYTEPVATKGTQEPEH---EG---ERXVEEELP-----
                                                                                                                          VF------HHGKYETKKNLIE------NASAEHGYFDGRWLDRSVDVILPDNTAD 348
                                                                                                                                                                      -----GEA-AVREDL--PVYT--KPLETKGTQGPGHEGEAAVREEEPAYTEP 271
                                                                                                                                                                                                                                                                                              YQSSQSGETSAIGSSHQKTEPYANIKAALEDI-TQESAMDLNGSIPRLRQTALVAARAVG 246
                                                                                                                                                                                                                                                                                                                                        SFASQVEQN---PDHKGES-----VVRPTV-PEQGNPVSA--
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                                                                                                                                                                                                                                                       -TTVQSAEEEVLATTNDRPE----YKLPLETKGTQEPGHE-----
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9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative 124; Mismatches 318;
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                                                                                                                                                                                                                                                         ----- 229
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                                                                                                                                                                            ; LENGTH: 3696
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5080
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US-09-134-001C-5080
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                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: LYNN DOUGETTE-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING:
TITLE OF INVENTION: EPIDERWIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EPIDERWIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT ELLING CATE: 1998-08-13
PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 5880
                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5080, Application US/09134001C Patent No. 6380370
                                                                                                                     Matches
                                                 2064
               101
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     QSPPLGLDMSVIEETTPL-SLEELFAQESTEM-GINPNDYIPE--YQGEQPNSEVVVP-- 154
                                       HESTQDNQVDNVKA------QAITAIKLINANAHKRQDAINILTNLAESKKSDIRA 2113
                                                                       HVPAHDTAINQAKAGNPPVLLTPEQIQARLNAAGLNAKPQSQALDVVNFDDQSPISRIGE 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LTGGQVL-----AVGTAEYNYEFMKDLRLAVFGDIGNAYDKGFTNDTKIGAGVG--VRW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KSKAEQPGVYTSFKQLVTAMQSNLSGVYTLASDMTADEVSLGDKQTSYLTGAFTGSLIGS
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                                                                                                        2.8%; Score 131; DB 4; Length 3696; ilarity 16.9%; Pred. No. 0.37; Conservative 136; Mismatches 318; Indels 25
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                                                                                                          36;
                                                                                 GENERAL INFORMATION:
APPLICANT: TONOUCHI, Naoto
APPLICANT: TOCHIDA, Takayasu
APPLICANT: YOSHINAGA, Fumihiro
APPLICANT: TAHARA, Naoki
APPLICANT: HAYASHI, Takahisa
TITLE OF INVENTION: NOVEL GENE, GROUP OF
FILE REFERENCE: 6537-011-0PCT
                                                                                                                                                                                                                          RESULT 26
US-09-147-236-5
; Sequence 5, Application US/09147236A
; Patent No. 6316251
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CURRENT APPLICATION NUMBER: US/09/147,236A CURRENT FILING DATE: 1999-04-08 EARLIER APPLICATION NUMBER: PCT/JP97/03633 EARLIER FILING DATE: 1997-10-09 NUMBER OF SEQ ID NOS: 12
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SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 5

LENGTH: 1326

TYPE: PRT

ORGANISM: Acetobacter xylinum

FEATURE:
OTHER INFORMATION: n at positions 15741 and 15767 may be a,
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                                       757 VSDANMAIA-----RAGISGVYSFGDNAYGSNRAHQMTGGIQAGYIWSDNFN-----HVP 806
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  LTEANIPIVGRLPLQAGASA-----
                                                                              APVTGGSYSAEAASPDTSDQMLSSIAGQIH-TLRENLAPSIDGGLGFRSR-SGEHG-MGR 931
                                                                                                                    VDFVNGKPSQEA-----LLAGVA--VHKTVADNL---VNPMRGYRQRYSLEVGSSGL 756
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-LTFSITPTMIWSGQLNTGSVYDVP 975
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		EPY	Ωy
		TPLSLEELFAQESTEMGINPNDYIPEYQGE	Дb
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45;		Ouery Match 2.7%; Score 129; DB 3; Length 1115; Best Local Similarity 19.9%; pred. No. 0.072; Matches 205; Conservative 102; Mismatches 335; Indels 388;	M Be
		TELERAX: 212-649-2054 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1115 amino acids TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: protein 08-323-477-2	JS-
		REGISTRATION NUMBER: 28,601 REFERENCE,/DOCKET NUMBER: SPA-2-2P TELECOMMUNICATION INFORMATION: TELEPHONE: 212-645-1405	
		CLASSIFICATION: 424 CLASSIFICATION DATA: PRIOR APPLICATION DATA: APPLICATION NUMBER: US/07/920,963 FILING DATE: 28-JUL-1992 ATTORNEY/AGENT INFORMATION: NAME: Poit Trying N	
		COMPOTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION UMBER: US/08/323,477 FILING DATE.	
		ADDRESSEE: ImClone Systems Incorporated STREET: 180 Varick Street CITY: New York STATE: New York COUNTRY: United States of America ZIP: 10014	
OF TOXINS	FAMILY C	SSULT 27 :-08-323-477-2 :-08-323-477-2 Sequence 2, Application US/08323477 Sequence 2, Application US/08323477 Sequence 2, Application US/08323477 Patent No. 6086896 GENERAL INFORMATION: APPLICANT: Sparling, P. Frederick APPLICANT: Thompson, Stuart TITLE OF INVENTION: ANTIGENIC IRON REPRESSIBLE PROTEINS FROM TITLE OF INVENTION: N. MENINGITIDIS RELATED TO THE HEMOLYSIN NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS:	RESULT US-08 Sequ Pate GENN A N N CO
		865 IGNAYDKGFTNDTKIGAGVGVRWASPVGQVRVDVATGVK 903	Qy Db
	FGD 864	807 YRLREFAGGDQSIRGYAHDSLSPISDKGYLTGGQVLAVGTAEYNYEFMKDLRLAVFGD	Qy

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US-09-134-001C-4547
Sequence 4547, Application US/09134001C; Patent NO. 6380370; GENERAL INFORMATION:
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APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLETC ACID AND AMINO ACID SEQUENCES RELATING TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR APPLICATION NUMBER: US 60/055,779
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; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (18)
; OTHER INFORMATION: I
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; SEQ ID NO 4547
; LENGTH: 675
; TYPE: PRT
; ORGANISM: Staphylococcus e
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VQDKGMASYNAKIS---
                                  ----GTAEYNYEFMKDLRLAVFGDIGNAYDKGFTNDTK
                                                                    QQVVNKTHKEDIYRSYANLIGKSGTAELKMKQGETGRQIGWFISYDKDNPNMMMAINVKD
                                                                                                        QSI-----RGYAH----DSLSPISDKGYLTGGQV-----
                                                                                                                                             DSGYGQGEILINPVQILSIYSALENNGNINAPHLLKDTKNKVWKKNIISKENINLLTDGM
                                                                                                                                                                             DNAYGSNR-----PYRLRFFAGGD 816
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION UNMBER: US/08/962,859A
FILING DATE: 03-NOV-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/035,072
APPLICATION NUMBER: 60/035,072
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Jackson, Arthur E
REGISTRATION NUMBER: 34,354
REFERENCE/DOCKET NUMBER: 34,354
REFERENCE/DOCKET NUMBER: GM50001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609/520-3254
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TITLE OF INVENTION: Dehydrgenase Gene
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSE: Dechert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 19103-2793
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 495 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                    497
                                                                                                 440
                                                                                                                                        170
                                                                                                                                                                                                                       136
                                                            211
                                                                                                                                                                                382
                                                                                                                                                                                                                                                           322
                                                                                                                                                                                                                                                                                                                                                                                                    207 EPYANIKAALEDITQESAMDLNGSIPRLRQTALVAARAVGYYDIDLSIIRNSIGEVDVII 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 148 NSEVVVPPTLEPEKPGLIKR-LYARLFNDGVNKVPRLKAKFYQSSQSGETSAIGSSHQKT 206
                                                                                                                                                                                                                                                                                                                                          267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Philadelphia
STATE: PA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                    83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 609/520-3259
AKARHLYDMPDDRVLAINHDDGVNRSILGRISDAVSAVARAILPDESENEVIDLPERTAL 556
                                                                                               VSFEQSSSSRTEPAQVDES-TLEPVIE--TVELTDGILMDISPIEFSASNLIQDKLNLVA 496
                                                                                                                                                             KLPVKRELLEQLLTVN--MGEAYNLQAVRALSNDLIATRYFNMVNTEIVFPEREQIQNDQ 439
                                                                                                                                                                                                                                                                                                                                       HDLGE-PVYIDYRAVEV----RGEGADDKAFTTVADEVPLLIGDVFHHGKYETKKNLIEN 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSKVIV--TIFGASGDLAKRKLY------PSLLDLYKSGNLSKHFAVIGTARR--
                                                            ITFAERLGVKERGGYYDQSGALRDMVQNHTLQLLSLLAMD~KPASFTKDEIRAEKIKVF~
                                                                                                                                                                                                                     -----DGKGFERLI-VEKPFGT------DYATASKLNDELLATFDE-----
                                                                                                                                                                                                                                                         ASAEHGYFDGRWLDRSVDVILPDNTADVSLIYDTGTQYRFDEVVFFTIDPKTNQLTTDPD 381
                                                                                                                                                                                                                                                                                                    HDVNDLEHYIALRQLQAELNEKYQAEHNKLF--FLSMAPQFFGTIAKHLKSE---NIV-- 135
                                                                                                                                                                                                                                                                                                                                                                               -PWS--KEYFESVVVESILDLADSTEQAQEFA----SHFYYQ----
                                                                                                                                    -----EQIFRIDHYLG-----KEMIQSIFAVRFANLIFENVW--NKDFIDNDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 495;
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02	469 LTDGIL	Qy Db
9 8	448 SRTEPAQVDESTLEPVIETV	Qy Db
: 7 )9	389 LLEQL-LTVNMGEAYNLQAVRALSNDLIATRYFNMVNTEIVFPEREQIQNDQVSFEQSSS 447	Qy Db
2 8	329 FDGRWLDRSVDVILPDNTADVSLIYDTGTQYRFDEVVFFTIDPKTNQLTTDPDKLPVKRE 38	Qy Db
.2 8	283 RGEGADDKAFTTVADEVPLLIGDVFHHGKYETKKNLIENASAEHGY 328 	Qy Db
ม ม	226 DLNGSIPRLRQTALVAARAVGYYDIDLSIIRNSIGEVDVIIHDLGEPVYIDYRAV-EV 282	Qy Db
ລ ທ	169 YARLENDGVNKVPRLKAKEYOSSQSGETSAIGSSHQKTEPYANIKAALEDITQESAM 225	Оу Дъ
. E	119 SLEELFAQESTEMGINPNDYIPEYQGEQPNSEVVVPPTLEPEKPGLIKRL 16   :   :   :   :   :   :   :   :   :	Qy Db
29;	Query Match 2.6%; Score 125; DB 4; Length 801; Best Local Similarity 18.1%; Pred. No. 0.09; Matches 127; Conservative 115; Mismatches 239; Indels 222; Gaps	Z H O
STAPHYLOCOCC	US-09-134-001C-5584  RESULT 30  US-09-134-001C-5584, Application US/09134001C  PATENT NO. 6380370  GENERAL INFORMATION: APPLICANT: LYNN DOUGETTE-Stamm et al APPLICANT: LYNN DOUGETTE-Stamm et al APPLICANT: LYNN DOUGETTE-STAMM ET AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: REPLIENTINS FOR DIAGNOSTICS AND THERAPEUTICS  FILE REFERENCE: GTC-007  CURRENT APPLICATION NUMBER: US 60/054,964  PRIOR APPLICATION NUMBER: US 60/064,964  PRIOR FILING DATE: 1997-11-08  PRIOR FILING DATE: 1997-18-14  NUMBER OF SEQ ID NOS: 5674  SEQ ID NO 5584  LENGTH: 801  TYPE: PAT  ORGANISM: Staphylococcus epidermidis	US S
	676 SIIQNGGWNRTYSLRYRLDKIKTQAPÞETWQDLÞVDFVN 714 ::                     ::     :  392 NLAÞNSLDYRTDATATGASÞEÞYEKLIYDVLN 423	Qy Db
1		Db
ហ	616 GAELRISEDKKGVKLYATKPISHPINDQIRATIGYQQEVFGHSTNGFDISTRTIEHEISR 675	Qy
<b>→</b> 5	557 ANRKTPADVYQSKKVPLYVFVASDKPRDGQIGLGWGSDTGTRLVTKFEH-NLINRDGYQA 615   :: :	Оу
o	269KNLYH-PTDEELKEHFIRGQYRSGKI-DGMKYISYRSEPN 306	Db

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                                                                                                                                                  TOPOLOGY: linear;
MOLECULE TYPE: peptide
US-08-537-002A-3
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US-08-537-002A-3
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                                                           Query Match 2.6%; Score 125; DB 1; Length 963; Best Local Similarity 24.3%; Pred. No. 0.12; Matches 98; Conservative 46; Mismatches 130; Indels 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08537002A Patent No. 5773282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:

APPLICANT: TSUSAKI, Keiji

APPLICANT: KUBOTA, Michio

APPLICANT: SUGIMOTO, Toshiyuki

TITLE OF INVENTION: RECOMBINANT THERMOSTABLE ENZYME FOR

TITLE OF INVENTION: CONVERTING MALTOSE INTO TREHALOSE

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/537,002A FILING DATE: 29-SEP-1995 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: JP 260984/1994 FILING DATE: 01-OCT-1994 PRIOR APPLICATION NUMBER: JP NO. 5773282 YELING DATE: 08-SEP-1995 ATTORNEY/AGENY INFORMATION: NAME: BROWDY, ROGET L. REGISTRATION NUMBER: 25,618 REFERENCE/DOCKET NUMBER: TSIIGAKI-1 REGISTRATION NUMBER: TSIIGAKI-1
                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: TSUSAKI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 24863
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 963 amino acids
TYPE: amino acid
CTBANDEDUECC.
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        580 VHRL---IRKYLIENS------MDKKEIRHWEETLPEL 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             666 TRTLEHEISRSIIQNGGWNRTYSLRYRLDKLKTQAPPETWQDL 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      610
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                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
ZIP: 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 419 Seven CITY: Washington STATE: D.C.
ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AEHFNKLEVP-FIYRVHEQPKSDRLRQFFDFITNFGIMIKGTGEDIHPTTLQSIQEEVEG 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RDGYQAGAELRLSEDKKGVKLYATKPLSHPLNDQLRATLGYQQEVFGHSTNGF----DLS 665
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419 Seventh Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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                                                             Gaps
                         52
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	LENGTH: 963 amino acids	E	٠. ،
	ATION FOR SEQ ID NO: 3:	INFORMATION	
	TELEFAX: 202-737-3528 TELEX: 248633	23	٠. ٠.
	LEPHONE: 202-628-5197		٠.
	FERENCE/DOCKET NUMBER: TSUSAKI-1 COMMUNICATION INFORMATION:	TEL	٠. ٠.
	REGISTRATION NUMBER: 25,618	<b>Z</b> :	٠
		ATT	
	FILING DATE: 08-SEP-1995	ל פי	
	APPLICATION DATA:	PRIOR	
	: 29-SEP-1995	Þ ŦJ	
	CICATION NUMBER: US	APPI	٠
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	CATION NUMBER G DATE:	™ Þ	·. ·.
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	S/MS-DOS	s o	,
	IBM PC compati	a :	٠
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	ZIP: 20004	20	٠
	ğ	S O	
	Washington	G (	
	Seventh Street N W	o >	٠. ٠.
	PONDENCE ADDRES	COR	•••
	OF INVENTION: CONVERTING MALTOSE INTO TREHALOS R OF SECULENCES: 17	TITLE .	
	OF IN	TITLE	٠. ٠
	ICANT: KUBOTA,	APPL	
	CANT: TSUSAKI	APPL	
	TNFORMATION:	Patent N	
	3,	Sequence	·
		E TIIIZA	zo
	8 GAFLELEGE-VYLVALGAEKRGTVEEDLARLAYDV 881	Db 84	D
	)GEPVYIDYRAVEVRGEGADDKAFTTVADEVPLLIGDV 306	Qy 270	n
847	RLRGHAPGTPGLLPGALHE	Db 793	
269	DLNGSIPRLRQT-ALVAARAVGYYDIDLSIIRNSIGEVDVI	Оу 226	n
792	4 RTERVLPRLDLPWVLRPEGGLFWERGASRRVLALTGSLPPGRP-QDLFAALEVRLLESLP	Db 734	ь
1 225	1	Qy 177	0
733	7 LLLARLKEGFEGRSLRAYYRGRHPGPVPEAVDLLRPGLAAGEGVWVQLGLVQDGGLD	Db 677	_
176	IPEYQGEQPNSEV	Qy 139	0
676	8 -QKDPPLYLTLLQLENHRTLQVSLPLLWSPQRREGPGLFARTHGQPGYFYELSLDPGFYR	Db 618	-
138	GEQSPPLGLDMSVIEETTPLSLEELFAQEST	Qу 99	2
617	7 MPGGPEVLLVDTLVHERGREELLNALAQTLKEKSWLALKPQKVALLDALRF	Db 567	_
98	NAAGLNA	Qy	_
1 566	7 PVELFSQQPFPPVEGRYRLTLGPHGFALFALKPVEAVLHLPSPDWAEEPAPEEADLPRVH	Db 507	_

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TYPE: amino acid
STRANDEDNESS: sinc
TOPOLOGY: linear
MOLECULE TYPE: peptl
US-08-863-010-3
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US-09-024-429-3
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                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/024,429
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/537,002
FILING DATE: US 08/537,002
FILING DATE: 29-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/537,002
FILING DATE: 01-0CT-1994
FILING DATE: 01-0CT-1994
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/09024429 Patent No. 6165768
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
   PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     848 GAFLELEGE-VYLVALGAEKRG-----TVEEDLARLAYDV 881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        793 RLRGHAPGTPGLLPGALHETEALV--RLLG---VRLALLHRALGEVEGVVGGHPLLGRGL
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                                                                                                                                                                                                                                                                                                                                                CITY: Washington
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                                                                                                                                                                                                                                                                                                ZIP: 20004
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                                                                                                                                                                                                                                                                                                                                       STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DLNGSIP------RLRQT-ALVAARAVGYYDIDLSIIRNSIGEVDVII--HDL----- 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --VNKVPRLK------AKFYQSSQSGETSAIGSSHQKTEPYANIKAALEDITQESAM 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GEQSPPLGLDMSVIE--ETTPLSLEELFAQEST------EMGINPNDY- 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MPGGPEVLLVDTLVHERGREELLNALAQTLKEKSWLALKPQKVALLDALRF----- 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PV-LFANRSFMPVALAAYLPLMTSQALAQQNNPANIINHVPAHDTAINQA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLLARLKEGFEGRSLRAYYRGRHPGP---VPEAVDLLRPGLAAGEGVWVQLGLVQDGGLD 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----IPE-----YQGEQPNSEVVVPPTLEPEKPGLIKR----LYARLFNDG--- 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -QKDPPLYLTLLQLENHRTLQVSLPLLWSPQRREGPGLFARTHGQPGYFYELSLDPGFYR 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 2.6%; Score 125; DB 1.1 Similarity 24.3%; Pred. No. 0.12; 98; Conservative 46; Mismatches
                                                                                                                                                                                                                                                                                                                                     D.C.
                                                                                                                                                                                                                                                                                                                                                                  E: BROWDY AND NEIMARK
419 Seventh Street, N.W.,
                                                                                                                                                                                                                                                                                                                    USA
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JP 255829/1995
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GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
ITILE OF INVENTION: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO S
ITILE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

LENGTH: 563

TYPE: DET
; ORGANISM: Staphylococcus epidermidis US-09-134-001C-3172
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US-09-134-001C-3172
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                                                                                                                                                                                                                                                                                                                                                       Sequence 3172, Application US/09134001C Patent No. 6380370
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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SEQUENCE CHARACTERISTICS:
                                             TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION: NAME: YUN, Allen C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   848 GAFLELEGE-VYLVALGAEKRG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              793 RLRGHAPGTPGLLPGALHETEALV--RLLG---VRLALLHRALGEVEGVVGGHPLLGRGL
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REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: TS
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TOPOLOGY: 11
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linear
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RESULT 35
US-08-072-610-2
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Barnwe
                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 19930602
                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Plasmodium vivax Blood Stage Antigens, TITLE OF INVENTION: Monoclonal Antibodies, and Diagnostic Assays NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    434
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                                                                                                                                                                         COUNTRY:
ZIP: 100
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                                                                                                                                                                                                                 STREET: 805 Th
CITY: New York
STATE: New Yor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DPKTNQLTTDPDKLPVKRELLEQLLTVN------MGEAYNLQAVRALSNDLIATRYFN 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NKIASGGELSRIMLALKSIFVKSRGQTAILFDEVDSGVSGQAAQKMAEKMRDIAQYIQVI 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LRYRLDKLKTQAPPETWQDLPVDFVNGKPSQEALLAGVAVHKTVADNLVNPMRGYRQRYS
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                                                                                                                                                                       RY: USA
10022-7513
                                                                                                                                                                                                                   New York
                                                                                                                                                                                                                                                             805 Third
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                                                                                                                                                                                                                                                                                                                                                                                        Barnwell,
                                                                                                                                                                                                                                                                               Darby and Darby
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                                                                                                                                                                                                                                                             Ave.
                                                                                                                                                                                                                                                                                                                                                                                        John
                      US/08/072,610
                                                                  #1.25
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 59
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gogoris, Adda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1018 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRAGMENT TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: pr
HYPOTHETICAL: YES
ANTI-SENSE: NO
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TELEFAX: 236687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Plasmodium vivax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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DGQIGLG
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                                        EEVEEVEVPAVVEVEVPAVVEEEVPEEVEEEEEEEEPVEEEDVLQLVIPSEEDIQLDKPK 779
                                                                                  ---EVIDLP----ERTALANRKTPADVYQSKK-----
                                                                                                                              PEEVEEVPAEVEEVEEVPEE----
                                                                                                                                                                  QDKLNLVAAKARHLYDMPDDRVLAINHDDGVNRSILGRISDAVSAVARAI--LPDESEN-
                                                                                                                                                                                                               EEELEATPEDDFELEEPTGEEVEETVEGEETAEGEEVEEVPAEVEEVEEVPAEVEEVEEV 674
                                                                                                                                                                                                                                                       FEQSSSSRTEPAQVDESTLEPVIETV-----ELTDGILMDIS-----PIEFSASNLI
                                                                                                                                                                                                                                                                                                   AQEVPTEELMQLQED-----DFELEGTAEAPEEGELVLEGEGEPTEEEPREGEPTEGEVP 614
                                                                                                                                                                                                                                                                                                                                           GEAYNLQAVRALSNDLIATRYFNMVNT-----EIVF-----
                                                                                                                                                                                                                                                                                                                                                                                      PTADETLFVDILDNDLTYADITSF--EPLFKQILKDPDAGEAVTVPSKEAPVQVPVAVGP 559
                                                                                                                                                                                                                                                                                                                                                                                                                                -TADVSLIYD-TGTQYRFDEVVFFTIDPKTNQLTTDPD-----KLPVKRELLEQLLTVNM 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTVADEVPLLIGDVFHHGKYETKKNLIENASAEHGYFDGRWLDRSVDVILPDN------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VAARAVGYYDIDLSIIRNSIGEVDVIIHDLGE-----PVYIDYRAVEVRGEGADDKAF 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRRRNRRNVEGEETEEAAEGEVSEETPEGEEELEATPED --- DFALD-GTTLEETEETAE 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRLKAKFYQSSQSGETSAIGSSHQKT-EPYANIKAALEDITQESAMDLNGSIPRLRQTAL 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AEEPAQVPAEELDATPEDDFALDVT------ESP-----EEVELVLDEE 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EQIQARLNAAGLNAKPQSQ-ALDVVNFDDQSPISRIGEQSPPLGLDMSVIEETTPLSLEE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124;
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  590
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                                                                                                                              -----VEEVPEEVEEVPEEVEEVPEEVEEV 719
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                                                                                  -VPLYVFVASDKPR 583
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US-08-719-822B-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (212)753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
CLONE: PVMB3.3.1
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ORIGINAL SOURCE:
240 VAARAVGYYDIDLSIIRNSIGEVDVIIHDLGE------PVYIDYRAVEVRGEGADDKAF 292
                                          361 CRRNRRNVEGEETEEAAEGEVSEETPEGEEELEATPED---DFALD-GTTLEETEETAE 416
                                                            181 PRLKAKFYQSSQSGETSAIGSSHQKT-EPYANIKAALEDITQESAMDLNGSIPRLRQTAL 239
                                                                                                           328
                                                                                                                             123 LFAQESTEMGINPNDYIPEYQGEQPNSEVVVPPTLEPEKPGLIKRLYARLFNDG--VNKV 180
                                                                                                                                                                   290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (212)527-7700
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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nes 124; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Gogoris, Adda
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US
FILING DATE: 09/30/96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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Pred. No. 0.16;
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RESULT 37
US-09-092-458-2
; Sequence 2, Application US/09092458
; Patent No. 6231861
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                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1018 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Barnwe
                                                                                                            REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 598
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)527-7700
TELEFAX: (212)753-6237
                                                                                                                                                                                                     APPLICATION NUMBER: 08/7
FILING DATE: 09/30/96
ATTORNEY/AGENT INFORMATION:
NAME: Gogoris, Adda
                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
TOPOLOGY: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Barnwell, TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                     TELLEFAX: (2-
TELEFAX: 236687
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                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE:
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ADDRESSEE: Bos Third Ave.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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                              amino acid
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                                             1018 amino acids
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RESULT 38
US-08-769-309A-5
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                                                                                                     Sequence 5, Application US/08769309A Patent No. 5741890 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local :
APPLICANT: Scott, John D.,
APPLICANT: Nauert, Brian J.,
APPLICANT: Klauck, Theresa M.
TITLE OF INVENTION: Protein Binding Domains of Gravin
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: NO
FRAGMENT TYPE: C-terminal
ORIGINAL SOURCE:
ORGANISM: Plasmodium vivax
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                                                                                                                                                                                                                                                                                                                            ---EVIDLP----ERTALANRKTPADVYQSKK------VPLYVFVASDKPR 583
                                                                                                                                                                                                                                                                                            EEVEEVEVPAVVEVEVPAVVEEEVPEEVEEEEEEEPVEEEDVLQLVIPSEEDIQLDKPK
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                                                                                                                                                                                                                                                                                                                                                                                                                                EEELEATPEDDFELEEPTGEEVEETVEGEETAEGEEVEEVPAEVEEVEEVPAEVEEVEEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEQSSSSRTEPAQVDESTLEPVIETV-----ELTDGILMDIS-----PIEFSASNLI 488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -TADVSLIYD-TGTQYRFDEVVFFTIDPKTNQLTTDPD-----KLPVKRELLEQLLTVNM 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GEETVEGEETVE-----GEETVEGEEAAEGEEELEATPEDDFQLEEPSGEGE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VAARAVGYYDIDLSIIRNSIGEVDVIIHDLGE------PVYIDYRAVEVRGEGADDKAF 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EQIQARLNAAGLNAKPQSQ-ALDVVNFDDQSPISRIGEQSPPLGLDMSVIEETTPLSLEE 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                           1338 QVEREKTEAEPTHVNEEKLEHETAVTV--SEEVSKQLLQTVNVPIIDGAKEVSSLEGSPP
                                                                                                                                          1281 GLEGSID---TGITVSREKVTEVALKGEGTEEAECKKDDALELQSHAKSPPSPVEREMVV 1337
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TOPOLOGY: linear
MOLECULE TYPE: protein
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LENGTH: 1780 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: NO. 5741890and, Greta
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & STREET: 6300 Sears Tower/233 South Wacker Drive CITY: Chicago STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                           TLAGVKS--QEMVMEQAIPPDSVETPTDSETDGSTP-----VADFDAPGTTQK 1187
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                                                                                                                                                                                                                           QSKMEDTLEH-----TDKEVSV-----ETVSILSKTEGTQEADQYADEKTKDVPFFE 1280
                                                                                                                                                                                                                                                                                                            DEIVE----IHEENE-----VHLVPVRGTEAE--AVPAQKERPPAPSSFVFQE---ETKE 1233
                                                                                                                                                                                                                                                                                                                                                                                                                                    PYANIKAALEDITQESAM------DLNGSIPRLRQTALVAARAVGYYDIDLSIIR 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E-----TDVVLKVDAQEAKTEPFTQGKVVGQTTPESFEKAPQVTESIESSELVTTCQAE 1141
                                                                                                                                                                                                                                                                    NLIENASAEHGYFDGRWLDRSVDVILPDNTADVSLIYDT-GTQ-----YRFDEVVFF- 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RLYARLFNDGVNKVPRLKAK---FYQSSQSGETS-----AIGSSHQKT----E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------SLEELFAQESTEMGI-NPNDYIPEYQ----GEQPNSEVVVPPTLEPEKPGLIK 166
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                                                                                                    LTVNMGEAYNLQAVRALSNDLIATRYFNMVNTEIVFPERE------
-QIQNDQVSFEQSSSSRTEPAQVDESTLEPVIETVELTDGILMDISPI 480
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TELLI...
TELEFAX: 31.4
TELEX: 25-3856
TELEX: 25-8856
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 1780 amino acid;
TYPE: amino acid;
TYPE: amino acid;
                                                                                                                                                                                        ; MOLECULE TYPE:
US-08-994-570-5
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Patent No. 6090929
GENERAL INFORMATION:
APPLICANT: Scott, John D.,
APPLICANT: Nauert, Brian J.,
APPLICANT: Klauck, Theresa M.
TITLE OF INVENTION: Protein Binding Domains of NUMBER OF SEQUENCES: 24
                                                                                                                                           Query Match
                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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ADDRESSEE: Marshall, O'Toole, Gerstein, Mu
STREET: 6300 Sears Tower/233 South Wacker
                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: NO. 6090929and, Greta
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  541 DESENEVIDLPERTALANRKTPADVYQS-KKVPLYVFVASDKPRDGQIGLGWGS-----
                                             23 LMTSQALAQ----QNNPANIINHVPAH-----DTAINQAKAGNPPVLLTPEQIQARLNAA 73
                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER:
    LLTEEVLEREVIAEEEPPTVTEPLPENREARGDTVVSEAE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAKEESESTAVGQ-----AHSDISKDMSEASEKTMTVEVEGSTVNDQQLEEVVLPSEEEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GWNRTYS------LRYRLDKLKTQAPPETWQDLPVDFVNGKPSQEALLA 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HPLNDQLRATLGYQQEVFGHSTNGFDL---STRTLEHEISRSII------QNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EFSASNLIQDKLNLVAAKARHLYDMPDDRVLAINHDDGVNRSILGRISDAVSAVARAILP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EEKSSEKNED-----FAAH----PGEDAVPTGPDCQAKSTPV----IVSATTKKGLS 1495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------DTGTRLVT---KFEHNLINRDGYQAGAELRLSEDKKGVKLYATKPLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RY: United States of America 60606-6402
                                                                                                                                                                                                                                                                              1780 amino acids
                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                        2.6%; Score 124; DB 3; Length 1780;
19.2%; Pred. No. 0.42;
vative 129; Mismatches 294; Indels 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murray & Borun
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    ---LTPEAVTAAETAG 982
                                                                                             298;
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US-08-436-664-34
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                                                                                                                                                                                                                          Sequence 34, Application US/08436664
Patent No. 5874282
GENERAL INFORMATION:
                                                                                                       APPLICANT: RIGGS, MICHAEL G.
APPLICANT: SIVARAM, MATHOOR
APPLICANT: TUDOR, STARLA D.
TITLE OF INVENTION: PURIFED DNA POLYMERASE FROM BACILLUS
TITLE OF INVENTION: STAROTHERMOPHILUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1396
                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                          1666 GGAGTKSVPEDDGHALLAERIEK----SLVEPKEDEKGDDVDDPENQNSALA 1713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1496
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                                                                                           NUMBER OF SEQUENCES:
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  CITY:
                     STREET:
                                           ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   SAKEESESTAVGQ-----AHSDISKDMSEASEKTMTVEVEGSTVNDQQLEEVVLPSEEEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IIQTAVDQFVRTEETATEMLTSELQTQAHVIKADSQDAGQETEKEGEEPQASAQDETPIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QVEREKTEAEPTHVNEEKLEHETAVTV--SEEVSKQLLQTVNVPIIDGAKEVSSLEGSPP 1395
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San Diego
                   E: Gen-Probe Incorporated 9880 Campus Point Drive
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; MOLECULE TYPE: pi
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: ir
; ORIGINAL SOURCE:
US-08-436-664-34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/394,232
FILING DATE:
APPLICATION NUMBER: 08/307,410
FILING DATE: 16-SEP-1994
APPLICATION NUMBER: 08/222,612
FILING DATE: 16-SEP-1994
APPLICATION NUMBER: 08/222,612
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Fisher, Carlos A
REGISTRATION NUMBER: 36,510
REFERENCE/DOCKET NUMBER: GP94003
TELEPHONE: 619-535-2807
TELEPHONE: 619-546-7929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 876 amino acids
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MEDIUM TYPE: DISKETTE
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,6
FILING DATE: 08-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                      103 PPLGLDMSVI---EETTPLSLEELFAQESTEMGINP-NDYIPEYQGEQPNSEVVVPPTLE 158
              375 QLTTDPDKLPVKRELLEQLLTVNMGEAYNLQAVRALSNDLIATRYFNMVNTEIVFPEREQ 434
                                                                                                                                                                                 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 QAKAG---NPPVL----LTPEQIQARLNAAGLNAKPQSQALDVVNFDDQSPISRIGEQS 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 ANRSEMPVAL------AAY-LPLMTSQALAQQNNPANIINHVPA-----HDTAIN 50
                                                      IVGIALANERGRF-----FLRPETALADPKFLAWLG-----DETKKKTMFDSKRA 376
                                                                                                                                                                                                                                                                                                                                                                               EREGFAVKVISGDRDLTQLASPQV-TVEITKKGITDIESYTPE-----TVVEKYGLT 172
                                                                                           LIENASA-EHGYFDGRWLDRSVDVILPDNT-ADVSLIYDTGTQYRFDEVVFFTI-DPKTN 374
                                                                                                                                                                             EPVYIDYRAVEV-RGE----GADDKAFTTVADE-----VPLLIGDVFHHGKYETKKN 317
                                                                                                                                                                                                                                             ITQESAMDLNGSIPRLRQTALVAAR-AVGYYDIDLSIIRNSI---GE----VDVIIHDLG 270
                                                                                                                                                                                                                                                                                               PEQIVDLKGLMGDK-SDNIPGVPGI-----GEKTAV----KLLKQFGTVENVLAS 217
                                                                                                                                                                                                                                                                                                                               PEKPGLIKRLYARLENDGVNKVPRLKAKFYQSSQSGETSATGSSHQKTEPYANIKAALED 218
                                                                                                                                     FQSFLDKMAVQTDEGEKPLAGMDFAIADSVTDEMLADKAALVVEVVGDNYHHAP-----
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Search completed: April 28, 2003, 16:24:54 Job time: 65 secs

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Title:
Perfect score:
Sequence:
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No.
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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Sequence 5635, Ap
Sequence 12389, A
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Sequence 1267, Ap
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Sequence 13, Application US/10080505

Publication No. US20030073166A1

GENERAL INFORMATION:
APPLICANT: St. Geme. Joseph W.

TITLE OF INVENTION: HARMOPHILUS ADHERENCE AND PENETRATION PROTIENS
FILE REFERENCE: A 59941-1/RFT/DCF/DHR

CURRENT FILING DATE: US/10/080,505

CURRENT FILING DATE: 2002-02-22

PRIOR APPLICATION NUMBER: US 08/296,791

PRIOR APPLICATION NUMBER: US 09/839,996

PRIOR APPLICATION NUMBER: US 09/839,996

PRIOR APPLICATION NUMBER: US 09/839,996

NUMBER OF SEG ID NOS: 58

SOFTWARE: Patentin version 3.1

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TYPE: PRT
ORGANISM: Haemophilus
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                                                                                                                                                                                                                                                                FAQYQWGDLQFGVNVGTGISASKMAEEQSRKIHRKAINYGVNASYQFRLGQLGIQPYFGV 1317
                                           RAHQMTGGIQAGYIW 798
                                                                                       VQTTVNSTV----LQQPFGRYWQK----EVGLKAEILHFQLS
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                                                                                                                             ----VHKTVADNLVNPMRGYRQRYSLEVGSSGLVSDANMAIARAGISGVYSFGDNAYGSN 783
                                                                                                                                                                                                                  -------YRLDKLKTQAPPETWQD------LPVDFVNGKPSQEALLAGVA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NFDDQSPISRIGEQSPPLGLDMSVIEETTPLSLEELFAQESTEMGINPNDYIPEYQGEQP 147
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                                                                                                                                                                                                                                                                                                                                                     -----QIGVQKALANGRIGA-VFSHSRSDNTFDEQVKNHATLTMMSG
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                                                                                       -AFISKSQGSQ 1421
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US-09-815-242-5635; Sequence 5635; Application; Patent No. US20020061569Al

US/09815242

GENERAL INFORMATION:

APPLICANT:

Haselbeck, Robert

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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 5635
LENGTH: 2368
TYPE: PRT
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Best Local Similarity
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PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
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TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA,011A
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NASTTEEKQAAYTELDTKKQEARTNLDAANTNSDVTTAKDNGIAAINQVQAATTKKSDAK
                                 SAE------HGYFDGRWLDRSVDVILPDNTADVSLIYDTG-----TQYRFD--
                                                                                                          EPVYIDYRAVEVRGEGADDKAFTTVADEVPLL-----IGDVFHHGKYETKKNLIENA 322
                                                                                                                                                                                                                                                                                                                                                                            INNDKNNAIAEINKQTTAQGVTTEKDNGIAVLDQDVITPTVKPQAKQDIIQAVTTRKQQI 698
                                                                       KQGLHDIQVVKSKQEVADTK--SKVLDKINAIQTQAKVKPAADTEVENAYNTRKQEIQNS 932
                                                                                                                                                 RVKNEEISKIENITDSTQTKMDAYNEVKQAATARKTQNATVSNATNEEVAEADAAVEAAQ
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                                                                                                                                                                                                                                                                                                   KKSNASLQDEKDVANDKIGKIETKAIKDIDAATTNAQVEAIKTKAINDINQ-TAPATTAK
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Zyskind, Judith W.
Wall, Daniel
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                                      DVATGVKE----EGNPIK 910
                                                                                                             TGGQVLAVGTAEYNYEFMKDLRLAVFGDIGNAYDKGFTNDTKIGAGVGVRWASPVGQVRV 896
                                                                                                                                                                                            DNAYGSNRAHQMTGGIQAGYIWSDNFNHVPYRLRFFAGGDQSIRGYAHDSLSPISDKGYL 836
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                                                                                                                                                                                                                                                                                -SQEALLAGVAVHKTVADNLVNPMRGYRQRYSLEVGSSGLVSDANMAIARAGISGVYSFG
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RESULT 4

US-09-815-242-12389

Sequence 12389, Application US/09815242

Patent No. US2002061569A1

GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Kari L.

APPLICANT: Ohlsen, Kari L.

APPLICANT: Trawick, John D.

APPLICANT: Yamamoto, Robert T.

APPLICANT: Yamamoto, Yamamoto, Yamamoto, Robert T.

APPLICANT: Yamamoto, Yohn D.

APPLICANT: Yamamoto, Yohn D.

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APPLICANT: Yamamoto, Yohn D.

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PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASTSEQ FOR Windows Version 4.0
SEQ ID NO 12389
LENGTH: 2368
TYPE: PRT
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NKKATAVTDAKNNI---TAATDDNGVDTAKDAGKNSIQSTQPATAVKSNAKN-DVDQAVT 1272
                                   NRKTPADVYQSKKVPLYVFVASDKPRDGQIGLGWGSDTGTRLVTKFEHNLINRDGYQA-- 615
                                                                                                                     PDDRVLAINHDDGVNRSILGRISDAVSAVARAILPDESENEV-----IDLPERTALA 557
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                                                                                 -- ANVDNAVTQANNNIEAANSQNDVDQAKTTGEASIDQVTPTV 1216
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TITLE OF INVENTION: IGNATION OF ESSENT
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
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LENGTH: 2076
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APPLICANT: Haselbeck,
APPLICANT: Ohlsen, Ka
APPLICANT: Zyskind,
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PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
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PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
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APPLICANT: Yamamoto, Rob
APPLICANT: Xu, H. Howard
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GILMDISPIEFSASNLIQDKLNLVAAKARHLYDMPDDRVLAINHDDGVNRSILGRISDAV 531
                                            TNAEVDRTETDGNDNIKVILPKVQVKPAARQSVGVKAEAQNALIDQSDLSTEEE-----
                                                                                                                                                                                                                                    LKQAQQE-----IENTNQDAAVTDVRNQTIKAIEQIKPKVRRKRAALDSIEENNKN----
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                                                                                         VNTEIVFPEREQIQNDQV-----
                                                                                                                                        ----QLDAIRNTLDTTQDERDVAIDTLNKI------VNTIKNDIAQ----NK 1710
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                                                                                                                                                                                     EVVFFTIDPKTNQLTTDPDKLPVKRELLEQLLTVNMGEAYNLQAVRALSNDLIATRYFNM 422
                                                                                                                                                                                                                                                                                    FHHGKYETKKNLIENASAEHGYFDGR-WLDRSVDVILPD---NTADVSLIYDTGTQYRFD
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                                                                                                                                                                                                                                                                                                                                                                                DIDLSIIRNSIGEVDVIIHDLGEPVYIDYRAVEVRGEGADDKAFTTV--ADEVPLLIGDV 306
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Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.9%; Score 135; DB 10; milarity 19.0%; Pred. No. 1.1; Conservative 110; Mismatches 301;
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                                                                                         -SFEQSSSSRTEP--AQVDESTLEPVIETVELTD
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US-09-815-242-12913
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                                                                                                                                                                                      SOFTWARE: FastSEQ
SEQ ID NO 12913
LENGTH: 2186
                                                                                       Matches
                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12913,
                                                                                                                                                                                                                                              PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                           PRIOR
PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
                                                                                                                                                                            LENGTH: 21
TYPE: PRT
                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/206,848 PRIOR FILING DATE: 2000-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                           1382 VASQALAKEKEKAL------AAIDQA------QTNSQVNQAATNGVSAIKI 1420
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                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/
FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/242,578 FILING DATE: 2000-10-23
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                                                       MTSQALAQQNNPANIINHVPAHDTAINQAKAGNPPVLLTPEQIQARLNAAGLN-----
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-AKPQSQALDVVNFDDQSPISRIGEQSPPLGLDMSVIEETTPLSLE---ELFAQEST 129
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Zyskind, Judith W.
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                                                                                    Conservative 110;
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                                                                                    2.9%; Score 135; DE 19.0%; Pred. No. 1.2; tive 110; Mismatches
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RESULT 8
US-09-765-272-118
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Patent No. US20020061545A1

GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1811 TVKATALQQIQNIATNKINLIKANNEATDEEQNIAIAQVEKELIKAKQQIASAVTNADV- 1869
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          687 YSLRYRLDKLKTQAPPETWQDLPVDFVNGKPSQEALLAGVAVHKTVADNLVNP---MRGY 743
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ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                     CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Human Genome ScientsTREET: 9410 Key West Avenue
                                                                                                                                                                                                                                         COUNTRY:
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; STRANDENNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 118: US-09-765-272-118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 2.8%; Score 134; DB 10; Length 1040; Best Local Similarity 19.4%; Pred. No. 0.44; Matches 190; Conservative 124; Mismatches 318; Indels 348;
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TELEPHONE: (301) 309-8504
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 118:
SEQUENCE CHARACTERISTICS:
LENGTH: 1040 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 306
633 TKPLSHPLNDQLRATLGYQQEVFGHSTNGFDLSTRTLEHEISRSIIQNGGWNRTYSLRYR 692 : | | : : : | | :: :
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FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                  VKVKPTVEIT-----NLTKVENKKSITVSYNLIDTTSAYVSAKTQ------VFH 442
                                                                                                                                                                                                                                          EPVIETVELTDGILMDISPIEFSAS-----NLIQDKLNLVAAKARHLYDMPDDRVLAINH 515
                                                                                                                                                                                                                                                                                                                                                                                                 VSLIYDTGTQYRFDEVVFFTIDPKTNQLTTDPDKLPVKRELLEQLLTVNNGEAYNLQAVR 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YYDIDLSIIRNSIGEVDVIIHDLGEPVYIDYRAVEVRG-EGADDKAFTTVADEVPLLIGD 305
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                                                           -----TYNLGENNEENTETSTQDFQLEYKKIE-----IKDIDSVELYG
                                                                                               FVASDKPRDGQIGLGWGSDTGTRLVT---KFEHNLINRDGYQAGAELRLSEDKKGVKLYA 632
                                                                                                                                                                           DDGVNRSILGRISDAVSAVARAILPDESENEVIDLPERTALANRKTPADVYQSKKVPLYV 575
                                                                                                                                                                                                                                                                                                                        ALSNDLIATRYFN----WVNTEIVFPEREQIQNDQVSFEQSSSSRTEPAQVDE----STL 460
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                                                                                                                                                                                                                                                                                             -----GTRTIQYEDYIVNGNVV------ETKEVSRTEVAPVNEVVKVGTL 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
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	LNGSIPRLRQTALVAARAVGYYDIDLSIIRNSIGEVDVIIHDLGEPVYIDYRAVEVRGE- 285 :  :         :   :   :   :   :   :   :	NKVPRLKAKFYQ-SSQSGETSAIGSSHQKTEPYANIKAALEDITQESAMD 226	NSEVVVPPTLEPEKPGLIKRLYARLFNDGV 177	MSVIEETTPLSLEELFAQESTEMGINPNDYIPEYQGEQP 147 :::	AKAGNPPYLLTPEQIQARLNAAGLNAKPOSQALDVVNFDDQSPISRIGEQSPP-LGLD 108	h 2.8%; Score 133.5; DB 9; Length 4349; Similarity 17.4%; Pred. No. 4.4; 99; Conservative 162; Mismatches 388; Indels 395; Gaps 5	H: 4349 PRT ISM: Homo sapiens -758-15	OF SEQ ID NOS: 16  RE: PatentIn version 3.1  NO 15	APPLICATION NUMBER: US 60/328,605 FILING DATE: 2001-10-10 APPLICATION NUMBER: US 60/357,253 FILING DATE: 2002-02-15	PPLICATION NUMBER: US 60/296, ILING DATE: 2001-06-05	FERENCE: EX02-089C APPLICATION NUMBER: US/10/160,758	GENERAL INFORMATION: APPLICANT: EXELIXIS, INC. TIPLE OF INVENTION: CADS AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF US	-10-160-758-15 Sequence 15, Application US/10160758 Publication No. US20030036076A1		SSRVNKVRVDALISTNARNN 779	ASPVGQVRVDVATGVKEEGN 907	ISGAKSVAGLVASATNTVIENSSFTGKLIANHQDSN-KNDTGGIVGNITGN 759	LTGGQVLAVGTAEYNYEFMKDLRLAVFGDIGNAYDKGFTNDTKIGAGVGVRW 887	DGTKSYAIYDLKKPLEDTLNGATVRDLDIKTVSADSKENVAALAKAANSANINNVAVEGK 709	DNF-NHVPYRLRFFAGGDQSIRGYAHDSLSPISDKGY 835	KSKAEQPGVYTSFKQLVTAMQSNLSGVYTLASDMTADEVSLGDKQTSYLTGAFTGSLIGS 649	SSGLVSDANMAIARAGISGVYSFGDNAYGSNRAHQMTGGIQAGYIWS 799	SDRFKEMY	LDKLKTQAPPETWQDLPVDFVNGKPSQEALLAGVAVHKTVADNLVNPMRGYRQRYSLEVG 752	KENDRYRRYLSLSEAPTDTAKYFVKVK 541
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RESULT 10
US-09-815-242-12610
Sequence 12610, Application US/09815242
Patent No. US20020061569A1
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                               Trawick, John D. Carr, Grant J. Yamamoto, Robert T. Xu, H. Howard
                                                                                                                                         Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
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        Identification of Essential Genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILLING DATE: 2000-10-23
PRIOR PELLORTION NUMBER: 60/253,625
PRIOR FILLING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
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SEQ ID NO 12610
LENGTH: 5795
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/2191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
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1273 FLRWVNFPQDYTVTWTNVKIANRPTDG--GLSWSDD------HKSLIYRYDATLGTQ 1321
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                                                                                                         ISKVKQAFI -- NANRDVITLAEGDISVTNTPNGANVSTITVNINKGRLTKSFASNLANMN 1272
                                                                                                                                                                VSAVARAILPDESENEVIDLPE-RTALANRKTPADVY------
                                                                                                                                                                                                                 --EVSQMNAGTQLYHIVASNAYH-KDTEDFYISLKIVDVKQPEGDQRVYRTSTYDLTTDE
                                                                                                                                                                                                                                                                       PIEFSASNLIQDKLNLVAAKARHLYDMPDD----RVLAINHDDGVNR----SILGRISDA 530
                                                                                                                                                                                                                                                                                                                             FTLSNGQAI------PSGTFTNITSDRTIPTAQ-
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                                                   -----QSKKVPLYVFVASDKPRDGQIGLGWGSDTGTRLVTKFEHNLINRDGYQAGAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EVDVIIHDLGEPVYIDYRAVEVRGEGADDKAFTTVADEVPLLIGDVFHHGKYETKKNLIE 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEVVFFTIDP---KTNQLTTDPDKLPVKRELLEQLLTVNMGEAYNLQAVRALSNDLIATRY
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GENERAL INFORMATION:

APPLICANT: APPLICANT:

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INVENTION:

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TYPE: PT
; ORGANIEM: Streptococcus
US-09-815-242-13264
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                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                             SEQ ID NO 13264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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SOFTWARE: FastSEQ for Windows Version
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
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PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Identification of Essential Genes TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2001-02-16
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                               148 NSEVVVPPTLEPEKPGLIKR-LYARLFNDGVNKVPRLKAKFYQSSQ-SGETSAIGSSHQK 205
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FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
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   SSKVIV--TIFGASGDLAKRKLYPSLF----
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Zyskind, Judith W.
Wall, Daniel
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                                                                     Conservative
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                                                                                    2.8%;
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                                                                  Score 132.5; I
Pred. No. 0.18
79; Mismatches
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-RLYKSGNLSKHFAVIGTARR-
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382 LNGKQVGEEFNLAPN-----SLDYRTDATATGASPEPYEKLIYDVLN
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                                 666 TRTLEHEISRSIIQNGGWNRTYSLRYRLDKLKTQAPPETWQDLPVDFVN 714
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                                                                                                            NLINRDGYQAGAELRLSEDKKGVKLYATKPLSHPLNDQLRATLGYQQEVFGHSTNGFDLS
                                                                                                                                                                              VIDLPERTALANRKTPADVYQSKKVPLYVFVASDKPRDGQIGLGWGSDTGTRLVTKFEH-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NASAEHGYFDGRWLDRSVDVILPDNTADVSLIYDT--GTQY------RFDEVVF 366
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                                                                                                                                                                                                                                                                                                                                    IVFPEREQIQNDQVSFEQSSSSRTEPAQVDESTLEPVIETVELTDGILMDISPIEFSASN 486
                                                                                                                                                                                                                                                                                                                                                                             FRIDHY ------LGKEMIQSIFAVRFA---NLIFENVWNKDFID-----NVQ
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                                                                                                                                                 -----GVPFFFRTGKRLTEKGTHV
                                                                                                                                                                                                                           IRAEKIKVF----KNLYH-PTDEELKEHFIRGQYRS--GKI-DGMKYISYRSEPN-----
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                                                                      --FKQMDSIFGEPLAPNI---LTIYIQPTEGFSLS
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RESULT 12 US-09-815-242-11134 CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/2191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26 GENERAL INFORMATION Sequence 11134, Application US/09815242 Patent No. US20020061569A1 PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16 PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22 APPLICANT:
APPLICANT: NUMBER OF SEQ ID NOS: 14110 SOFTWARE: FastSEQ for Windows Version PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23 TITLE OF INVENTION: Identification TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A APPLICANT: APPLICANT: Haselbeck, PRIOR APPLICATION NUMBER: 60/253,625 APPLICANT: APPLICANT: APPLICANT: ID NO 11134 Xu, H. Howard Wall, Daniel Trawick, John D. Ohlsen, Kari L. Zyskind, Judith W. Carr, Grant J.
Yamamoto, Robert T. Robert of Essential Genes

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RESULT 13
US-10-108-605-237
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                      TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF FILE REFERENCE: 31133B
CURRENT APPLICATION NUMBER: US/10/108,605
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US 09/761,142
PRIOR APPLICATION NUMBER: US 09/761,142
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-14
NUMBER OF SEQ ID NOS: 361
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 237
LENGTH: 3503
                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Broadus, Julie
APPLICANT: Stam, Lynn
APPLICANT: Bachmann, Jane
APPLICANT: Kamdar, Kim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NSEVVVPPTLEP--EKPGLIKRLYARLENDGVNKVPR-LKAKFYQSSQSGETSAIGSSHQ 204
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                      APPLICANT:
                                                                              APPLICANT: APPLICANT:
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Best Local Similarity
Matches 129; Conserv
                                                                                                                     APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                       870
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Carr, Grant J.
Yamamoto, Robert
Xu, H. Howard
                                                                          Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
                                                         Trawick, John D.
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US-09-815-242-5816
Sequence 5816, Application US/09815242
Patent No. US/0020061569A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                              RDGYQAGAELRLSEDKKGVKLYATKPLSHPLNDQ----LRATLGYQQEVFGHSTNGF---
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TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5816
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PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
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Best Local Similarity
Matches 218; Conserv
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LENGTH: 2478
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
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    RYFNMVNTEIVFPE--
                                        ETAQKASERKTAIEAMNDSTTEEQQ--AAKDKVDQAVVTANADIDN----AAANNDVDNA 105
                                                                                                                  ASTTEEKQAAYTELDTKKQEARTNLDAANTNSDVTTAKDNSIAAINQVQAATTKKSDAKA
                                                                                                                                                         AE-----HGYFDGRWLDRSVDVILPDNTADVSLIYD-----TGTQYRFD---
                                                                                                                                                                                             QGLHDIQVVKSKQEVADTK--SKVLDKINAIQTQAKVKPAADTEVENAYNTRKQEIQNSN
                                                                                                                                                                                                                                 PVYIDYRAVEVRGEGADDKAFTTVADEVPLL-----IGDVFHHGKYETKKNLIENAS 323
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                                                                              EVVFFTIDPKT-----NQLTTDPDKLPVKRELLEQLLTVNMGEAYNLQAVRALSNDLIAT 417
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RESULT 15
US-09-815-242-12967
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                                                                                                                          PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR PRIOR PRIOR NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                       FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,
CURRENT FILING DATE: 2001-03-21
                                      PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                       APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification
TITLE OF INVENTION: Prokaryotes
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                      PRIOR
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                    APPLICATION NUMBER: 60/257,931
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Yamamoto, Robert T.
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Trawick, John D.
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Zyskind, Judith W.
DATE:
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PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 12967
LENGTH: 2478
TYPE: PRT
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                                                                                 1222 KKATARNEITAILNNKLQEIQATPDATDEEKQAA----DAEANTENGKANQAISAATTNA
                                                                                                                                                                                                                                                                        1112
                                                                                                                                                                                                                                                                                                                                                         1052 KTTNEATIAAITPDANVKPAAKQAIADKVQAQETAIDGNNGSTTEEKAAAKQQVQTEKTT
                                     599 LYTKFEHNLINRDGYQAGAELRLSE-DKKGYKLYATKPLSHPLNDQLRATLGYQQEVFGH
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QV--
                                                                                                                                                                                                                                                                 ADAAIDAAHTNAEVEAAKKAAIAKIEAIQPATTTKDNAKEAIATKANERKTAIAQTQDIT 1171
                                                                                                                                                                                                                                                                                                                                                                                                 RYFNMVNTEIVFPE-----REQIQNDQVSFEQSSSRTE-----PAQVDEST 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AE-----HGYFDGRWLDRSVDVILPDNTADVSLIYD-----TGTQYRFD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QGLHDIQVVKSKQEVADTK--SKVLDKINAIQTQAKVKPAADTEVENAYNTRKQEIQNSN 937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PVYIDYRAVEVRGEGADDKAFTTVADEVPLL-----IGDVFHHGKYETKKNLIENAS 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TKEVLFPDKS------LKLSYKVNVANIDTPKNIDFNEKLTYRTASDVVINNAQ----
                                                                                                                                                                          AEEIAAANAD------VDNAVTQANSNIEAANSQNDVDQAKTTGENSIDQVTPTVN 122
                                                                                                                                                                                                                    DDRVLAINHDDGVNRSILGRISDAVSAVARAILPDESENEV-----ID-----
                                                                                                                                                                                                                                                                                                             LEPVIE----TVELTDGILMDISPIEF-----SASNLIQDKLNLVAAKARHLYDMP 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VKNEETSKTENTTDSTQTKMDAYNEVKQAATARKAQNATVSNATNEEVAEADAAVDAAQK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AALE---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGINPNDYIPEY-----QG---EQPN----SEVVVPPTLEPE-KPGLIKRLYAR----
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                                                                                                                              -----LPERTALANRK-----TPADVYQSKKVPLYVFVASDKPRDGQIGLGWGSDTGTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                EIAQKASERKTAIEAMNDSTTEEQQ--AAKDKVDQAVVTANADIDN----AAANNDVDNA 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EVVFFTIDPKT-----NQLTTDPDKLPVKRELLEQLLTVNMGEAYNLQAVRALSNDLIAT 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASTTEEKQAAYTELDTKKQEARTNLDAANTNSDYTTAKDNSIAAINQVQAATTKKSDAKA 997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------LFNDGVNKVPRLKAKFYQSSQSG-----ETSAIGSSHQKTEPYANIK 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----SIGEVDVIIHDLGE 271
·DEAKANAEAAINAVTPKVVKKQAAKDEI-----DQLQAT----QTNVINN
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APPLICANT: XU, H. HOWARD

TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: prokaryotes

FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PRILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-23
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/269,308
                                                                                                                      NAME/KEY: VARIANT
LOCATION: (1)...(2025)
OTHER INFORMATION: Xaa
US-09-815-242-5703
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US-09-815-242-5703
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                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 5703
LENGTH: 2025
Query Match 2.8%; Score 131.5; Best Local Similarity 19.6%; Pred. No. 1.9; Matches 187; Conservative 130; Mismatches
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                                                                                                                                                                                                                                                   ORGANISM: Staphylococcus aureus FEATURE:
                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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Zyskind, Judith W.
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                                                            DB 10;
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                                                            Length 2025;
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Indels 301;

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RESULT 17
US-09-815-242-12611
; Sequence 12611, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
                                                                                                                                                                                                                                               E-----LDK----VQGNAIAKAEAEQLKQNIIDAQNALNGDQNLANAKDKANAFVN
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US-09-815-242-12611
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PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR TILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
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NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 12611
LENGTH: 3158
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Best Local Similarity 19.6%;
Matches 187; Conservative 13
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                                                     PVIETVELTDGILMDISPIEFSASNLIQDKLNLVAAKARHLYDMPDDRVLAINHDDGVNR
                                                                                                                                                                                                   AMETLKNKVDQVNTDKAQPNYTEASTD-----KKEAVDQALQAAESITDPTNGSNANKD
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                      PIAELVD-
                                                                                                    AVEQALTK --LQEKVNELNGNERVAEAKAQAKQTIDQLAHLNADQIATAKQNIDQATKLQ
                                                                                                                                                AV-RALSNDLIATRYFNMVNTEIVFPEREQIQN--DQVSFEQSSSSRTEPAQVDEST-LE
                                                                                                                                                                                                                                                                                                                              -----TKKNLIENASAEHGYFDGRWLDRSVDVILPD--NTA----DVSLIYDTGTQY-- 359
                                                                                                                                                                                                                                                                                                                                                                                        AAVQHAKDLINQTGNPT-LDKSQVEQL-----TQAVTTAKDNL------HGDQKLAR 1714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TEPYANIKAALEDITQE----SAMD-----LNGSIPRLRQTALVAARAVGYYDIDLSIIR
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                                                                                                                                                                                                                                                                                              DQQQAVTTVNALPN------LNHAQQQALTDAINAAPTRTEVAQHVQTATELDH 1762
                                                                                                                                                                                                                                                                                                                                                                                                                                    NSIGEVDVIIHDLGEPVYIDYRAVEVRGEGADDKAFTTVADEVPLLIGDVFHHGKYE---
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                                                                                                                                                                                                                                             ---RFDEVVFFTIDPKTNQLTTDPDKLPVKRELLEQLLTV-----NMGEAYNLQ 405
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Qy	Oy 522 SILGRISDAVSAVARAILPDESENEVIDLPERTALA 557

		2027	Db s
	DTKTGA 881	876	Q
2026	AQKGAVTGNINQAHTVAEVTQAIQTAQELNTAM-GNLKNSLNDK	1984	Db
875	GQVLAVGTAEYNYEFMKDLRLAVF	818	Qy
1983	VEAALSTYTTTKQALNGDRKVTDAKNNANQTLSTLDNLNN	1944	Db
817	ARAGISGYYSFGDNAYGSNRAHQMTGGIQAGYIWSDNFNHVPYRLRFFAGGDQ	765	Qy
1943	NQANGTNANQSQ	1907	рь
764	WQDLPVDFVNGKPSQEALLAGVAVHKTVADNLVNPMRGYRQRYSLEVGSSGLVSDANMAI	705	Qy
1906	KQDLNTQVTNAPNISTVNQVKTKAEQLDQAMERLINGIQDKDQVKQS	1860	Дb
704	QQEVFGHSTNGFDLSTRTLEHEISRSIIQNGGWNRTYSLRYRLDKLKTQAPPET	651	Qy
1859	ATSQPTLDPSAVTQAANQVSTNKTALNGAQNLANKKQETTANINQLSHLNNAQ	1807	рb
650	AELRLSEDKKGVKLYATKPLSHPLNDQLRATLGY	617	Qу
1806	VTGVQSVKDNATNLDNAMNQLRNSIANKDDVKASQPYVDADRDKQNAYNTAVTNAENIIN	1747	рь
616	GLGWGSDTGTRLVTKFEHNLINRDGYQAG	588	Qу
1746	TNAADVTAATQRVNNAETGLNGDTNLATAKQQAKDALRQMTHLSDAQKQSITGQIDSATQ	1687	DЬ
587	IDLPERTALANRKTPADVYQSKKVPLYVFVASDKPRDGQI	548	Qy
1686	NSATSLNNAMDQLKQAIADHDTIVASGNYTNASPDKQGAYTDAYNAAKNIVNGSPNVI	1629	Дb
547	DDRVLAINHDDGVNRSIL	507	Qy
1628	AIQSVTSTENALNGDANLQRAKTEAIQAIDNLTHLNTPQKTALKQQVNAAQRVSGVTDLK	1569	Db
506	FSASNLIQDKLNLVAAKARHLYDMP	463	Qy
1568	RLQSAIANKDQTKASENYIDADPTKKTAFDNAITQAESYLNKDHGANKDKQAVEQ	1514	рь
462		403	Qy
1513	RQAKSDAKANLGTLTHLNNAQKQDLTSQIEGATTVNGVNGVKTKAQDLDGAMQ	1461	Db
402		358	Qy
1460	DADQGKKDAYTNAVTNAQGILDKAHGQNMTKAQVEAALNQVTTAKNALNGDANV	1407	Db
357	IGDVFHHGKYETKKNLIENASAEHGYFDGRWLDRSVDVILPD-NTADVSLIYDTGT	303	Qy
1406	IDNATTVAGVTAAQNTANELNTAMGQLQNGINDQNTVKQQVNFT	1363	Db
302	EPVYIDYRAVEVRGEGADDKAFTTVADEVPLL	250	Qy
1362	ANETQ VQAALNQLNQ -AKNDLNGD-NKVAQAKESAKRALASYSNLNNAQSTAATSQ	1309	Db
249		203	Qy
1308		1283	Db
202	GSS	143	Qy
1282	NAQRTAANAEVDQAPNLAAVTAAKNKATSLNTAMGNLKHALAEKDNTKRSVNYTD	1228	Db
142	УΞЧ	89	Qy
1227	ISATNNPEMNPDTINQKASQVNSAKSALNGDEKLAAAKQTAKSDIGRLTDLN	1176	Db
88	PVLLTPEQIQARLNAAGLNAKPQSQALDVVN	29	Qy

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SEQ TPMARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1296

LENGTH: 6281

TYPE: PRT

ORGANISM: Staphylococcus aureus

US-09-815-242-1296
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Best Local Similarity 17.6%; Pr
Matches 181; Conservative 157;
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PRIOR FILING DATE: 2001-02-16
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
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PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
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                                             2240 RQA-----KSDAKANLGTLTHLNNAQKQDLTSQIEGATTVNGVNGVKTKAQDLDGAMQ 2292
                                                                                                                                        2186 DAD---QGKKDAYTNAVTNAQGILDKAHGQ---NMTKAQVEAALNQVTTAKNALNGDANV 2239
                                                                                                                                                                                                                                                                                                                          2088 ANETQ----VQAALNQLNQ-AKNDLNGD-NKVAQAKESAKRALASYSNLNNAQSTAATSQ 2141
                                                                                                                                                                                                                                                                                                                                                                                                                     2062 -ADQPKQQA-----TNANGSN 2087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2007 NAQRTAANAEVDQAPNLAAVTAAKNKATSLNTAMGNLKHALAEKDNTKRSVNYTD---- 2061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1955 ISATNNPEMNPDTINGKASQVNSAKSA-----LNGDE---KLAAAKQTAKSDIGRLTDLN 2006
403 NLQAVRALSNDLIATRYFNMVNTEIVFPEREQIQNDQVSFEQSSSSRTEPAQVDESTLEP 462
                                                                                        358 QYRFDEVVFFTIDPKTNQLTTDPDKLPVKRELLEQL---LTVN------MGEAY 402
                                                                                                                                                                                             303
                                                                                                                                                                                                                                                                                                                                                         203 HQKTEPYANIKAALEDITQESAMDLNGSIPRLRQTALVAARAVGYY------D 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                143 QGEQPNSEVVVPPTLEPEKPGLIKRLYARLFNDGVNKVPRLKAKFYQSSQSGETSAIGSS 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89 FDDQSPISRIGEQSPPLGLDMSVIEETTPLSL-----EELFAQESTEMGINPNDYIPEY 142
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APPLICATION NUMBER: 60/242,578
FILING DATE: 2000-10-23
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                                                                                                                                                                            IGDVFHHGKYETKKNLIENASA----EHGYFDGRWLDRSVDVILPD-NTADVSLIYDTGT 357
                                                                                                                                                                                                                                                                            ID-----LSIIRNSIGEVDVIIHDLGEPVYIDYRAVEVRGEGADDKAFTTVADEVPLL 302
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Zyskind, Judith W.
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Yamamoto, Robert T.
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OV Db	2293	RLQSAIANKDQTKASENYIDADPTKKTAFDNAITQAESYLNKDHGANKDKQAVEQ
B	4	:: ;       NLQRAKTEAIQAIDNLTHLNTPQKTALKQQVN
Qy	507	ILGRISDAV
Db	2408	
Qy	548	IDLPERTALANRKTPADVYQSKKVPLYVFVASDKPRD
Db	2466	TNAADVTAATQRVNNAETGLNGDTNLATAKQQAKDALRQMTHLSDAQKQSITGQ
Qy	588	GLGWGSDTGTRLVTKFEHNLINRDGYQAG
Дb	2526	VTGVQSVKDNATNLDNAMNQLRNSIANKDDVKASQPYVDADRDKQNAYNTAVTNAENI
Qy	617	
Db	2586	ATSQPTLDPSAVTQAANQVSTNKTALNGAQNLANKKQETTANINQLSHLNNAQ
Qy	651	QQEVFGHSTNGFDLSTRTLEHEISRSIIQNGGWNRTYSLRYRLDKLKTQA
Db	2639	:  :::: NQVKTKAEQLDQAMER
Qy	705	WQDLPVDFVNGKPSQEALLAGVAVHKTVADNLVNPMRGYRQRYSLEVGSSGLVSDANMAI
DЬ	2686	VNETDADPEKQTAYNNAVTAAENIINQANG
Oy	765	ARAGISGVYSFGDNAYGSNRAHQMTGGIQAGYIWSDNFNHVPYRLRFFAGGDQ
Db	2723	VEAALSTVTTTKQALNGDRKVTDAKNNANQTLSTLDNLNN
Qy	818	TGGQVLAVGTAEYNYEFMKDLRLAVFGD
Db	2763	AQKGAVTGNINQAHTVAEVTQAIQTAQELNTAM-GNLKNSLN-
Qy	876	DTKIGA 881
ДЬ	2806	DTTLGS 2811
RESUI US-0	ULT 20 09-815	-242-5229
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	APPLICANT APPLICANT	ANT: Haselbeck, Robert
	APPLICANT	: Zyskind, Judi
 22	APPLICANT	: Trawick, Joh
 ≥ ≥	APPLICANT APPLICANT	ICANT: Carr, Grant J. ICANT: Yamamoto, Robert T.
	E	Xu, H. Howard
; TIT	EE	OF INVENTION: Identification of Essential Genes in OF INVENTION: Prokaryotes
	FILE RI	FERENCE: ELITRA.011A
 Q Q	CURRENT	APPLICATION NUMBER: US/09 FILING DATE: 2001-03-21
יי יי קים		ION NUMBER: 60/1
ייי יי		TION NUMBER: 6
 	PRIOR A	APPLICATION NUMBER: 60/207,727
 g g		: 2000-05-26
		DATE: 2000-10-23
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 PI		NUMBER

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RESULT 21

US-09-815-242-12125

: Sequence 12125, Application US/09815242

: Patent No. US20020061569A1

: GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: F8SLSEQ for Windows Version
SEQ ID NO 5229
LENGTH: 1184
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Best Local Similarity
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                                                                                                                                                                                        KHANELARAIKYRTRIVT-LEGDIVNPGGSMTGGGARKSKSILSQKDELT-TMRHQLEDY
                                                                                                                      LROTESFEQOFKELKIKSDQLSELYFEKSQKHNTLK----EQVHHFEMELDRLTTQ 741
                                                                                                                                                                                                                             ----LGWGSDTGTRLVTKFEHNLINRDGYQAGAELRLSEDKKGVKLYATKPLSHPLNDQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RLDNHSKKLSVDE--NEVIVTRRLYRSGESEYYINNDRARLKDIADLFLDSGLGKEAYSI 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NPNDYIPEYQGEQPNSEVVVPPTL----EPE------KPGLIKRLYAR 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GPNGSGKSNITDAIKW------VLGEQSAK-SLRGSKMEDIIFSGAEHRKAQNYAEVQL 82
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131; Mismatches
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TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.O11A
CURRENT APPLICATION UNMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION UNMBER: 60/219,078
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
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PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
PRIOR PRIOR BATE: 2001-02-16
PRIOR PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2000-12-22
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Best Local Similarity 18.4%; Pred. No. 0.98;
Matches 143; Conservative 131; Mismatches
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LENGTH: 1188
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EFSASNLIQDKLNLVAAKARH---LY-----DMPDDRV--LAINHDD-----
                                                                                                          NNDIRFLKHTIEENEAKKSRL----DSRLVEVFEQLKDIQGQIKTTKKEYQQTNKELSAV
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                                                                                                                                                                         QND----QVSFEQSSSSRTEPAQVDESTLEPVIETVELTDGIL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EGRVEPLKEEAAIAK-----EYKTLSHQMKHSDIVVTVHDIDQYTNDNRQLDQRLND 251
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Ohlsen, Kari L.
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Yamamoto, Robert T.
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7 1 9 1 6 60 3 3 5 5 1 7 1 7 1	US-09-815-242-5834 US-09-815-242-5834 Sequence 5834, Application US/09815242 Patent No. US20020061569A1 GENERAL INFORMATION: APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L. APPLICANT: Trawick, John D. APPLICANT: Trawick, John D. APPLICANT: Yamamoto, Robert T. CURRENT FILING DATE: 2001-03-21 PRIOR APPLICATION NUMBER: 05/19/815,242 CURRENT FILING DATE: 2001-03-21 PRIOR APPLICATION NUMBER: 05/19/815,242 PRIOR APPLICATION NUMBER: 05/19/815 PRIOR APPLICATION NUMBER: 05/206,848 PRIOR FILING DATE: 2000-05-23 PRIOR APPLICATION NUMBER: 05/207,727 PRIOR APPLICATION NUMBER: 05/207,727 PRIOR FILING DATE: 2000-15-23 PRIOR APPLICATION NUMBER: 05/24,576 PRIOR APPLICATION NUMBER: 05/25,625 PRIOR APPLICATION NUMBER: 05/25,625 PRIOR APPLICATION NUMBER: 05/25,931	Qy 520NRSILGRISDAVSAVARAILPDESENEVID
RESULT 23 US-09-881-752A-308 : Sequence 308, Application US/09881752A : Patent NO. US20020115078A1 : GENERAL INFORMATION: APPLICANT: Kleanthous, Harold APPLICANT: Miller, Charles : APPLICANT: Miller, Charles : APPLICANT: Miller, Charles : APPLICANT: Oomen, Raymond P. : TITLE OF INVENTION: Identification of Polynucleotides : TITLE OF INVENTION: Genome : FILE OF INVENTION: Genome : FILE OF INVENTION: Genome : FILE REFERENCE: 06132/041002 : CURRENT APPLICATION UNMBER: US/09/881,752A : CURRENT APPLICATION NUMBER: US/09/881,752A : CURRENT FILING DATE: 1907-04-01 : NUMBER OF SED ID NOS: 370 : SOFTWARE: FastSEO for Windows Version 4.0 : SEQ ID NO 308 : LENGTH: 1797	OY 374 NQLTTDPDKLEVKRELLEOLLTVNNGEAYNLOAVRALSNDLIATRYEN 421    1	Db 211 HAMELLRNSVADNQTTLASEDYHDATAQRQNDYNQAVTAANNIINQTTSPTWNP 264  Qy 162 PGLIKRLYARLFNDGVNKVPRLKAKFYQSSQSGETSAIGSSHQKTEPYANIKAALE 217

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Best Local Similarity 19.2
Matches 193; Conservative
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ORGANISM: Helicobacter F
FENTURE:
NAME/KEY: VARIANT
LOCATION: 85
                                    1324 HKVHKGGSIADII----QEGWNVPNRIPYASELLVKD-NDPIAQDVYAKEKGVIKY----Y
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                                                                                                                                                                                                                                             619 LRLSEDKKGVKLYATK------PLSHPLNDQLRATLGYQQEVFGHSTNGFDLSTRT 668
                                                                           726 VAVHK--TVADNLVNPMRGYRQRYSLEVGSSGLVSDANMAIAR---AGISGVYSFGDNAY 780
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GSNRAH-QMTGGIQAGYIWSDNFNHVPYRLRFFA-----GGDQSIRGY-AHDSLSPISDK 833
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                                                                                                                                                             LEHEISRSIIQNGGWNRTYSLRYRLDKLKTQAPPETWQDLPVDFVNGKPSQEALL---AG 725
                                                                                                                                                                                                      LRTYTNKEGKNIIANRRNASILVVEPKIKAPFDGELRIETVYEEVVVS-------
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                                                                                                                      ---VKNGDQEAKFVLR-RSDIVK---PSE----LAGVGGKIEGKVYLPYASG
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2%; Pred. No. 3;
147; Mismatches 354; Indels 309;
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US-09-815-242-11410
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US-09-815-242-11410
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
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SEQ ID NO 11410
LENCTH: 2890
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
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    ET - - KKNLIENASAEHGYFDGRWLDRSVDVILPD-----
                                                                                                                                                                                        DVIIHDLGEPVYID------YRAVEVRGEGADDKAFTTVADEVPLL-IGDVFHHGKY 312
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                                                                                              NILLPASGKAVAIPSQDMVLGLYYLSLEKSGVKGEHKLFSSVNEIITAIDTKELDIHAKI 1937
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                                                                                                                                                                                                                                                                                       LHKQSIQAFHPKLIDGKAIQLHPLVCSAFNADFDGDQMAVHVPLSQEAIAECKVLMLSSM 1877
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Xu, H. Howard
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    -NTADVSLIYD----
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APPLICANT: Behr, Regine
APPLICANT: Sloma, Alan
TITLE OF INVENTION: Plapptides Having Gamma-Glutamyl
TITLE OF INVENTION: Transpeptidese Activity And Nucleic /
FILE REFERENCE: 10157.200-US
CURRENT APPLICATION NUMBER: US/10/107,649
CURRENT APPLICATION NUMBER: 60/279,374
PRIOR APPLICATION NUMBER: 60/279,374
PRIOR APPLICATION NUMBER: 60/279,374
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 604
TYPE: PRT
ORGANISM: Bacillus agaradhaerens
US-10-107-649-2
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US-10-107-649-2
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    Query Match
Best Local Similarity
Matches 116; Conserv
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/10107649 Publication No. US20030044949A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2521 SEVSTNSVISKPTTNTFKTIATWDPYNTPIIADFK----GKVG
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    Conservative
                    2.7%;
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  87;
                    Score 127; DB 9; Length 604; Pred. No. 0.61;
  Mismatches 226;
                                                                                                                                                                                                                                                                                                                Nucleic
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  Indels
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122;
Gaps
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CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.0
SEQ ID NO 16
LENGTH: 1616
TYPE: PRT
ORGANISM: M. genitalium
FEATURE:
                                                                                                                                                          ; NAME/KEY: misc_feature
; OTHER INFORMATION: cytadherence-accessory protein
; NAME/KEY: misc_feature
; OTHER INFORMATION: gi|1046097
US-09-820-843A-16
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                                    Qy
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US-09-820-843A-16
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Publication No. US2003003993A1
GENERAL INFORMATION:
APPLICANT: Council of Scientific and Industrial
TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR T
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
FILE REFERENCE: Q63915
      297
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                                          76
                                                                                                 Local Similarity
NTKSLASSL-----ENELLLENSSEEQP-----VIEEVKPRRNEVIFRNPVTKLHFEK 344
                                    NAKPQSQALDVVNFDDQSPISRIGEQSPPLGLDMSVIEETTPLSLEELFAQESTEMG--- 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GY--SVVGHSS
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                                                                               Conservative
                                                                                               2.7%; Score 125.5;
19.5%; Pred. No. 3.6;
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                                                                               Mismatches
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CURRENT APPLICATION NUMBER: US/10/108,605
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US 09/761,142
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR ETLING DATE: 2000-01-14
PRIOR FILING DATE: 2000-01-14
UMBER OF SEQ ID NOS: 361
SOFTMARE: PALENTIN Ver. 2.1
SEQ ID NO 103
LENGTH: 3712
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US-10-108-605-103
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APPLICANT:
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                                    2132 SYLEDFNSYTLAFFTSQKLNYYDQLADELEPKYKLLDPNSYDLSPS------KKAN 2181
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                                                                                                        / Match 2.6%; Score 124.5;
Local Similarity 20.1%; Pred. No. 15;
Nes 183; Conservative 117; Mismatches
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   ARLFNDG---VNKVPRLKAKFYQSSQSGETS---
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Bachmann, Jane
Kamdar, Kim
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US-09-995-542-10
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                                                                                                                                         Sequence 10, Application US/09995542 Patent No. US20020127647A1 GENERAL INFORMATION:
APPLICANT: Shutter, John
APPLICANT: Ulias, Laarni
APPLICANT: Ulias, Laarni
TITLE OF INVENTION: ATP-Binding Cassette Transporter-Like Molecules
TITLE OF INVENTION: Uses Thereof
FILE REFERENCE: 00-658-A
CURRENT APPLICATION NUMBER: US/09/995,542
CURRENT FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: 60/253,520
                                                                                                                                                                                                                                                                 2877 -- TGLRFKGN
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2783 LPNGDVVEHSKSGYLEGSQNILHVDKNSRLFVGGYPGISDFNAPPDLTTNSFSGDIEDLK
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                                                                                                                                                                                                                                                                                                                                                                            AQKNNDFVAVEIVNGYPILTIDLGNGPERITSDKYVADGRWYQAVVDRMGPNAKLTIREE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --ASDALEILKNYLEILEPVSVQTPKELEKAHGINRDL-------DLTNKDVSQANK 2617
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                                                                                                                                              VLAVGTAEYNYEFMKDLRLAVFGDIGNAYDKGFTNDTKIGA---GVGVRWASPVGQVRVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FNMVNTEIVFPEREQ------IQNDQVSFEQSSSSRTEPAQVDEST--LEPVIETVE 468
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PRIOR FILING DATE: 2000-1
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2
SEQ ID NO 10
LENGTH: 2310
TYPE: PRT
ORGANISM: Mus musculus
US-09-995-542-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              y Match 2.6%; Score 124;
Local Similarity 19.3%; Pred. No. 8;
                               TG-GQVLAVGTAEYNYEFMKDL
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SGLGQMMNVSGGPVTREASKEM 1601
                                                                                            YGSNRAHQMTGGIQAGYIWSDNFNHVPYRLRFFAGGDQSIRGYAHDSLSPISDK---GYL 836
                                                                                                                              TMLPECPEGAGGLPPPQRTQRSTEVLQDLTNRNISDYLVKTYPALIRSSLKSKFWVNEQR 1555
                                                                                                                                                                                               ---LKEEWLPEYPCINATSWKTPSV-----SPNITHLFQKQKWTAAHPSPSCKCSTREKL
                                                                                                                                                                                                                                                                  ---PFGEFPALTL--HPWMYGHQYTFFSMDEPNNEHLEVLADVLLNRPGFGNRC-----
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                                                                                                                                                                                                                                                                                                                               P----GVPFNTGARLILQHVQALLVKRFHHTIRSRKDFVAQIVLPATFVFLALMLSIIVP
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                                                                                                                                                               ----ADNLVNPMRGYRQRYSLEVGSSGLVSD----ANMAIARAGISGVYSFGDNA
                                                                                                                                                                                                                                LDKLKTQAPPE----TWQDLPVDFVNGKPSQEALL---AGVAVHKTV------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EGVCSCTSKGFSTRCPTRVDEITEEQVLDGDVQELMDLVYHHVPEAKLVECIGQELIFLL 1233
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APPLICANT: Milne, Todd
APPLICANT: NO. US20020128250Alman, Thea
APPLICANT: Royer, John
APPLICANT: Salama, Sofie
APPLICANT: Salama, Sofie
APPLICANT: Sharman, Amir
APPLICANT: Sharman, Amir
APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Se
FILE REFERENCE: 109272.147
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SOPTWARE: Patentin version 3.0
SEQ ID NO 364
LENGTH: 1250
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
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F----DGRWLDRSVDVILPDN-----TADVSLIYDTGTQYRFDEVVFFTIDPKTNQLTT
                                                                                                                                                                                                                                                                                     PELIQEGR--LVAGILRVNKKNRSDAWVSTD--GALDADIYICGSKDRNRALEGDLV---
                                                     DSDSLSSPTKSGVRRRSSLKQRPTQKKNDDVEVEGQSLLLVEEEEINDKYKPLYAGHVV-
                                                                                             DPDKL--PVK-----RELLEQLLTVNMGEAYNL--QAVRALSNDLIATRYFNMVNTEIVF
                                                                                                                                IPLNSSDDYHNDASYTAATSNNFLSSPSSSDSLSKDDLSVRR------KRSSTINN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----IDSVQADSGS--NSTTEQSDFKFPPPPNAHQGHRRATSNLSPPSFKFPPNSHGDND 246
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                                                                                                                                                                                                                                                 LGEPVYIDYRAVEVRGEGADDKAFTTVADEVPLLIGDVFHHGKYETKKNLIENASAEHGY
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Madden, Kevin
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20.0%; Pred. No. 3.4;
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Best Local Similarity

21.0%;

Pred. No. 2.6;

51;

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APPLICANT: IALLIAN, INCOM-
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: U$/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/37484
PRIOR APPLICATION NUMBER: JP 99/37484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR APPLICATION NUMBER: JP 00/280988
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN Ver. 3.0
SEQ ID NO 6999
LENGTH: 852
                                            ; ORGANISM: Corynebacterium US-09-738-626-6999
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US-09-738-626-6999
; Sequence 6999, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: NAKAGAWA, SATOSHI APPLICANT: MIZOGUCHI, HIROS
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OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
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Length 852;

RESULT 31 US-09-740-274-6 ; Sequence 6, Application US/09740274 ; Patent No. US20020031826A1

GENERAL INFORMATION:

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                                                                            745 VNRLDDVVIFDRLSPEQLTSIVDIQIKQLTDRLAG-----RRLNLRVSDS-----AKAW 793
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                                                                                                                                                                                                                                              MSEYGEKHSVARLVGAPPGYVGYDQGGQLTEAVRRPYTVVLFDEVEKAHP--DVFDILL
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                                                                                                                                                             QVLDE--GRLTDG---QGRTVDFRNTILILTSNLGAGG----TREQMMDAVKMAFKPEF
                                                                                                                                                                                                     GYQQEVFGHSTNGFDLSTRTLEHE----ISRSIIQNGGWNRTYSLRYRLDKLKTQAPPET
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                                                                                                                    WQDLPVDFVNGKPSQEALLAGVAVH-KTVADNLVNPMRGYRQRYSLEVGSSGLVSDANMA 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RWQNEKTAIDDVREMKEELEALR----SESDIAERDGNYGRVAELRYGRIPELEK----Q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DAIGILRGLKERYEV-HHGVRIQDSALVAAAELSNRYITSRFLPDKAIDLV--DEAASRL 403
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; TYPE: PRT
; ORGANISM: streptococcus mutans
US-09-740-274-6
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PRIOR FILING DATE: 1998-12-11
PRIOR PPLICATION NUMBER: 09/007,999
PRIOR FILING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: 08/478,704
PRIOR APPLICATION NUMBER: 08/478,704
PRIOR APPLICATION NUMBER: 09/009,620
PRIOR FILING DATE: 1998-01-20
PRIOR APPLICATION NUMBER: 08/485,243
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SEQ ID NO 6
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TITLE OF INVENTION: Glucan-containing Compositions and Paper FILE REFERENCE: 0357CRD
CURRENT APPLICATION NUMBER: US/09/740,274
CURRENT FILING DATE: 2000-12-19
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PRIOR FILING DATE: 1995-0
NUMBER OF SEQ ID NOS: 6
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FILING DATE: 1995-06-07
APPLICATION NUMBER: 09/
FILING DATE: 1998-01-16
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                                                                                                                     TVIAKIIKAQINPKTDGLTFTLDELKQAFKIYNEDMRQAKKKYTQSNIPTAYALM----L 644
                                                                                                                                              YRFDEVVFFTIDPKTNQLITDPDKLPV------KRELLEQLLTVNMGEAYNLQAVRAL 410
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44	2.6%; Score 121; DB 9; Length 1781; illarity 18.0%; Pred. No. 8.8; Conservative 119; Mismatches 326; Indels 344; Gaps 4	Match Local es 17	Query Best : Match	
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	entIn Ver.	TWARE: ID NO 2 ENGTH: 1	SEQ	
	APPLICATION NUMBER: EPO 00201871.1 FILING DATE: 2000-05-25 OE SEO ID NOS: 10	PRIOR FILIN		
	11-29 9/604,957	CURRENT FIL PRIOR APPLI		
	BO43388-CIP	FILE REFERENCE: CURRENT APPLICA		
	OBERT-JAN	APPLICANT:		
	VAN GEEL-SCHUTTEN, GERRITDINA HENDRIKA DIJKHUIZEN, LUBBERT	APPLICANT:		
	2 pplicat: 2002015; MATION:	32 )95- ence ence	(H) (N)	
	GYYSFDNDSK 1191	1182 GYYS	Db	
	FTNDTK 878	872 G	Qy	
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	RGYAHDSLSPISDKGYLTGGQVLAVGTAEYNYEFMKDLRLAVFGD	812 FAGG	Qy	
	TEYSTSGYQAKNSEVQDAKGNWYYFDNNGHMYY	96	Db	
	MAIARAGISGVYSFGDNAYGSNRAHOMTGGIOAGYIWSDNFNHVDYRLRF 811	754 SGLV	Qy	
	PSEKITAWKAKYFNGTNILGRGVGYVLKDNASDKYFELKGNGTYLPKQMTNKEAS 1	36	Db 2	
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	WNRTYSLRYRLDKLKTQAPPETWQDLPVDFVN 714		P. Oy	
	AMSKNNKYGSQQDMINAVKALHKSGIQVIADWVPDQIYNLPGKEVV-TATRVN 981	930 AMSK	Db	
	KKGVK	620 RLSED	Qy	
	KDSDYTNKKIAQNVQLFKSWGVTSFEMAPQYVSSEDGSFLDSIIQNGYAFEDRYDL 929	874 KDSD	Db	
	PRDGQIGLGWGSDTGTRLVTKFEHNLINRDGYQAGAEL 619	579 SDK-	Qy	
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	AHKNQEYRPLLITKDGLTSYTSDAAAKSLYRKTNDKGELVFDASDIQGYLNPQV 817	; 763 AHKN	DЬ	
	ASNLIQDKLNLVAAKARHLYDMPDDR-VLAINHDDGVNRSILGRISDAV 531	480 IEFSASN-	Qy	
	MDWDYTGVLTSVRYGTGANEATDQGSEATKTQGMAVITSN-NPSLK-LNQNDKVIVNMGA 762	705 MDWD	Db	

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RESULT 33
US-10-060-036-71
US-10-060-036-71
Sequence 71, Application US/10060036
Publication No. US20030073144A1
GENERAL INFORMATION:
APPLICANT: Benson, Darin R.
APPLICANT: Kalos, Michael D.
APPLICANT: Lodes, Michael J.
APPLICANT: Persing, David H.
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US-09-758-140-6

Sequence 6, Application US/09758140 Patent No. US20020012965A1

GENERAL INFORMATION:
APPLICANT: Strittmatter, Stephen M.
TITLE OF INVENTION: No. US20020012965Alo
FILE REFERENCE: 44574-5073-US

Receptor-Mediated Blockade of Axonal

Gro

CURRENT APPLICATION NUMBER: US/09/758,140

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version SEQ ID NO 71 LENGTH: 11192
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APPLICANT: Jiang, Yuqiu
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
FILE REFERENCE: 210121.566
CURRENT APPLICATION NUMBER: US/10/060,036
CURRENT FILING DATE: 2002-01-30
NUMBER OF SEQ ID NOS: 4560
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939 SKNGSATSKVLLLPPDVSALATQAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSA
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                                           ----SAVARAIL--PD-----ESENEVIDLPE-RTALANRKTPADVYQSKKVPLYVFVA
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RESULT 35
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Sequence 6, Application US/09972599A
PATCHIC NO. US20020077295A1
GENERAL INFORMATION:
APPLICANT: STRITTMATTER, STEPHEN M.
TITLE OF INVENTION: NOGO-RECEPTOR-MEDIATED BLOCKADE:
FILE REFERENCE: CO77 CIP US
CURRENT APPLICATION NUMBER: US/09/972,599A
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Best Local Similarity
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SOFTWARE: PatentIn Vo
SEQ ID NO 6
LENGTH: 1192
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PRIOR APPLICATION NUMBER: US 60/175,707
PRIOR FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: US 60/207,366
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/236,378
PRIOR FILING DATE: 2000-09-29
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                                                                                                                                                                                                         SKNGSATSKYLLLPPDVSALATQAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSA 998
                                                                                                                                                                                                                                          ----SAVARAIL--PD-----ESENEVIDLPE-RTALANRKTPADVYQSKKVPLYVFVA 578
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18.2%; Pred. No. 5.2;
ative 102; Mismatches 245;
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PRIOR APPLICATION NUMBER: PCT/US01/01041
PRIOR FILING DATE: 2001-01-12
PRIOR PPLICATION NUMBER: 09/758,140
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 60/236,378
PRIOR APPLICATION NUMBER: 60/236,378
PRIOR APPLICATION NUMBER: 60/207,366
PRIOR APPLICATION NUMBER: 60/207,366
PRIOR APPLICATION NUMBER: 60/207,366
PRIOR FILING DATE: 2000-09-29
PRIOR FILING DATE: 2000-09-29
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LENGTH: 1192
TYPE: PRT
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SKNGSATSKYLLLPPDVSALATQAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSA
                             ----SAVARAIL--PD-----ESENEVIDLPE-RTALANRKTPADVYQSKKVPLYVFVA
                                                                                    DSFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTELPHDLSL-KNIQPKVEEKISFSDDF
                                                                                                                               FSASNLIQDKLNLVAAKARHLYDMPDDR.----VLAINHDDGVNRSILGRISDAV.----
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                                                                                                                                                                          ----DLFISKEAQIRETE-TFSDSS-----
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RESULT 36
US-09-820-843A-15
; Sequence 15, Application US/09820843A
; Publication No. US20030039963A1
; GENERAL INFORMATION:

904 YLIIKKELQSELSRLIDQNENLNVQFNNAKNLTTLQKE---EMIRSLASDFAIAYKPS

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TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEI
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
FILE REFERENCE: Q63915
CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin version 3.0
SEQ ID NO 15
LENGTH: 1139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 2.5%;
Best Local Similarity 20.3%;
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OTHER INFORMATION: Cytadheren
NAME/KEY: misc_feature
OTHER INFORMATION: gi|1046012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FAQESTEMGINPNDYIPEYQGEQPNSEVVVPPTLEP--EKPGLIK------RLYARLF 173
                                                    YKIISELKRG-----ELNPTINFDAIFQMNDYQMSVKQSFIH-LNDFVTNYKNQISER 903
                                                                                     ---LSEDKKGVKLYATKPLSHPLN-DQLRATLGYQQEV---FGHSTNGF-----DLSTR 667
                                                                                                                           QPKIEVFVKAKEPVE-
                                                                                                                                                          -VPLYVFVASDKPRDGQIGLGWGSDTGTRLVTKFEHNLI-NRDGYQAGAELR------
                                                                                                                                                                                                                                                                                                      ISPIEFSASNLI------QDKLNLVAAKARHLYDMPDDRVLAINHDDGVNRSI-LGR 526
                                                                                                                                                                                                                                                                                                                                         QDQTTF--SSSFETQPTVEQFDQVNSEVNDQFKPEITKEPVLESSFNKQDVVETSNYTNN
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TLEHEISRSIIQNGGWNRTYSLRYRLDKLKTQAPPETWQDLPVDF-VNGKPS
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Pred. No. 5.7
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; ORGANISM: Staphylococcus aureus US-09-815-242-5480
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US-09-815-242-5480
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APPLICANT: Haselbeck,
APPLICANT: Ohlsen, Ke
APPLICANT: Zyskind,
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Matches
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PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
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PRIOR TILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
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les 169; Conser
QSSSSRTEPAQVDESTLEPVIETVELTDGILMDISPIEFSASNLIQDKLNLVAAKARHLY
                                                                   LNKLGGSEWKKT----KAKVQQSVEDIAEELID-------LYKEREM------
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                                                                                                          KREL--LEQLLTVNMGEAYNLQAVRALSNDLIATRYFNMVNTEIVFPEREQIQNDQVSFE
                                                                                                                                                                                               YFDGRWLDRSVDVILPDNTADVSLIYDTGTQYRFDEVVFFTID--PKTNQLTTDPDKLPV 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEVVVPPTLEPEKPGLIKRLYARLFNDGVNKVPRLKAKFYQSSQSGETSAIGSSHQKTEP 208
                                                                                                                                                          ---GRYLGVETLEVGQTHRDYIKL-----QYKGTDQLFVPVDQMDQVQKYVASEDKTPK
                                                                                                                                                                                                                                                  ----VHHGV-----
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PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR ELING DATE: 2000-05-23
PRIOR PELICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/259,308
PRIOR FILING DATE: 2000-12-2
PRIOR FILING DATE: 2001-02-16
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                          NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12151
LENGTH: 1168
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12151, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L. APPLICANT: Zyskind, Judith W.
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ORGANISM: Staphylococcus aureus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----AEGYQYGEDTAEQT--TFEL--DFPYELTPDQAKSIDEIKDDMQ----KSR---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yamamoto, Robert T.
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GUGLTY MATCH  2.5%; SCOTE 119.5; DB 10; Length 1168; Best Local Similarity 18.8%; Pred. No.5.9;  MATCHES 169; CORSELVALIVE 116; MISMATCHES 279; Indels 333; Gd  108 DMSVIETTPISJEELFACESTEMGINNDYI	VCEDIVCONIEENV	DINTEGAGNIJGKOOHGET-DT	965	7
QUETY MATCH  2.5%; SCOTE 119.5; DB 10; Length 1168; Best Local Similarity 18.8%; Pred. No. 5.9;  MATCHES 169; CORSETVALIVE 116; MISMATCHES 279; Indels 333; GB  108 DMSVIETTPLSLEELFACESTEMGINNDYI	90	YNYE	œ	Qy
QUELY MATCH  16.8%; SCOTE 119.5; DB 10; Length 1168; Best LOCAI SIMILIARITY 118.8%; SCOTE 119.5; DB 10; Length 1168; Best LOCAI SIMILIARITY 118.8%; SCOTE 119.5; DB 10; Length 1168; Best LOCAI SIMILIARITY 118.8%; SCOTE 119.5; Indels 333; Ga  108 DMSVLEETPLISCELFACESTEMGINNYI	96	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	21	DЪ
GUGLTY MAICH  Best Local Similarity 18.8%, prod. no. 5.9;  MATCHES 169; CONSETVATIVE 116; Mismatches 279; Indels 333; GS  108 DMSVIETTPLSLEELFAGESTEMGINNDYI	ISDKGYLTGGQVLAVGTA	- }	92	Qy
DOURTY MAICH  Best Local Similarity  18.8%, Pred. No. 5.9;  MRICHES 169; CONSERVATIVE 116; MISMATCHES 279; Indels 333; Ga  108 DMSVIEETTPLSLEELFAQESTEMGINPUDYIPEYOGE	R 92	GQMSERDLEETMLSFINNEYDILVTTTIE	61	日
DOURTY MAICH BEST LOCAL SIMILARITY 18.8%; PTECH. NO. 5.9; BEST LOCAL SIMILARITY 18.8%; PTECH. NO. 5.9; MARICHES 169; CONSERVATIVE 116; MISMATCHES 279; INDELS 333; GA  108 DMSVIEETTPLSLEELFAQESTEMGINPNDYIPEYGGE	G	AGISGVYSFGDNAY	67	Qy
GUGLTY WAICH  BEST LOCAL SIMILARITY  BEST LOCAL SIMILARITY  BEST LOCAL SIMILARITY  BOST LOC	LMPDANIAVAH 8			Db
GUGLTY MATCH  BOST LOCAL SIMILARITY  BOST LOC	_	LPVDFVNGKPSQEALLAGVAVHKTVADNLV	0	Qy
Query Match  2.5%; Score 119.5; pb 10; Length 1168; Best Local Similarity 18.8%; Pred. No. 5.9; Matches 169; Conservative 116; Mismatches 279; Indels 333; Ga  108 DMSVIEETTPLSLEELFAQESTEMGINPNDYIPEYOGE	SRD 82	LGVRDL	8	Db
Query Match  Query Match  Best Local Similarity 18.8%; Score 119.5; DB 10; Length 1168;  Best Local Similarity 18.8%; Pred. NO. 5.9;  Matches 169; Conservative 116; Mismatches 279; Indels 333; Ga  108 DMSVIEETTPLSLEELFAQESTEMGINPNDYI	TYSLRYRLDKLKTQAPPETWQD	EVFGHSTNGFDLSTRTLEHEISR	ū	Qy
QUORTY MATCH  Best LOCAL Similarity 18.8%; SCORE 119.5; DB 10; Length 1168;  Best LOCAL Similarity 18.8%; Pred, NO. 5;  MATCHES 169; CONSETVATIVE 116; Mismatches 279; Indels 333; Ga  108 DMSVIEETTPLSLEELFAQESTEMGINPNDYI	7	HKLLSKDIQYKDLGLLIVDEEQRFGVRHKE	729	B
QUORTY MATCH  2.5%; SCORE 119.5; DB 10; Length 1168; Best LOCAL Similarity 18.8%; Pred. NO.5.9; MATCHES 169; CONSERVATIVE 116; Mismatches 279; Indels 333; G8  108 DMSVIEETTPLSLEELFAQESTEMGINPNDYI	PLNDQLRATLGYQ	HNLINRD-GYQAGAELRLSEDKK-GVK-LY	605	Qy
Query Match  2.5%; Score 119.5; DB 10; Length 1168; Best Local Similarity 18.8%; Pred. No. 5.9; Matches 169; Conservative 116; Mismatches 279; Indels 333; Ge  108 DMSVIEETTPLSLEELFAQESTEMGINPNDYI	T 7	RMQDFPVEIQLMSRFRTPKEIKQTKE	690	В
Query Match 2.5%; Score 119.5; DB 10; Length 1168; Best Local Similarity 18.8%; Pred. No. 5.9; Matches 169; Conservative 116; Mismatches 279; Indels 333; Ga 110 DMSVIEETTPLSLEELFAQESTEMGINPNDYI	E 60	DLPERTALANR-	4	Qy
Query Match 2.5%; Score 119.5; DB 10; Length 1168; Best Local Similarity 18.8%; Pred. No. 5.9; Matches 169; Conservative 116; Mismatches 279; Indels 333; Ga  140 SEVVPPTLEEFRAGESTEMGINPNDYI	E 68	-PMDRLLCGDVG	639	Db
Query Match  2.5%; Score 119.5; DB 10; Length 1168; Best Local Similarity 18.8%; Pred. No. 5.9;  Matches 169; Conservative 116; Mismatches 279; Indels 333; Ga  10		DMPDDRVLAINHDDGVNRSILGRISDAVS	504	Qy
Query Match 2.5%; Score 119.5; DB 10; Length 1168; Best Local Similarity 18.8%; Pred. No. 5.9; Matches 169; Conservative 116; Mismatches 279; Indels 333; Ga  169; Conservative 116; Mismatches 279; Indels 333; Ga  180; Conservative 116; Mismatches 279; Indels 333; Ga  181; Conservative 116; Mismatches 279; Indels 333; Ga  182; Conservative 116; Conserva	:   KSR	AEGYQYGEDTAEQTTFEL-	596	В
Query Match 2.5%; Score 119.5; DB 10; Length 1168; Best Local Similarity 18.8%; Pred. No. 5.9; Best Local Similarity 18.8%; Pred. No. 5.9; Best Local Similarity 18.8%; Pred. No. 5.9; Matches 169; Conservative 116; Mismatches 279; Indels 333; Ga 108 DMSVIEETTPLSLEELFAQESTEMGINPNDYI	PIEFSASNLIQDKLNLVAAKARHLY	SSSSRTEPAQVDESTLEPVIETVELT	444	Qy
Query Match 2.5%; Score 119.5; DB 10; Length 1168; Best Local Similarity 18.8%; Pred. No. 5.9;  Matches 169; Conservative 116; Mismatches 279; Indels 333; Ga  Matches 169; Conservative 116; Mismatches 279; Indels 333; Ga  169; Conservative 116; Mismatches 279; Indels 333; Ga  170; Indels 333; Ga  170; Indels 333; Ga  171; Indels 333; Ga  172; Indels 333; Ga  173; Indels 333; Ga  174; Indels 333; Ga  175; Indels 333; Ga  176; Indels 333; Ga  177; Indels 333; Ga  178; Indels 333; Ga  179; Indels 333; Indels 33	::           59		560	В
QUETY MATCH  2.5%; SCOTE 119.5; DB 10; Length 1168;  Best LOCAL SIMILARITY 18.8%; Pred. NO. 5.9;  Matches 169; Conservative 116; Mismatches 279; Indels 333; Ga  169; Conservative 116; Mismatches 279; Indels 333; Ga  180; Ganthes 279; Indels 333; Ga  181; III	ਲ		89	Qy
Query Match  2.5%; Score 119.5; DB 10; Length 1168; Best Local Similarity 18.8%; Pred. No. 5.9;  Matches 169; Conservative 116; Mismatches 279; Indels 333; Ga  108 MSVIEETTPLSLEELFAQESTEMGINPNDYI	PK 55	GRYLGVETLEVGQTHRDYIKL	509	Ф
QUETY MATCH QUETY MATCH QUETY MATCH BEST LOCAL SIMILARITY 18.8%; Pred. No. 5.9; Best LOCAL SIMILARITY 18.8%; Pred. No. 5.9; MATCHES 169; CONSERVATIVE 116; MISMATCHES 279; Indels 333; Ga local description of the property of	-PKTNQLTTDPDKLPV	FDGRWLDRSVDVILPDNTADVSLIYDTG	N	Qy
Query Match 2.5%; Score 119.5; DB 10; Length 1168; Best Local Similarity 18.8%; Pred. No. 5.9; Matches 169; Conservative 116; Mismatches 279; Indels 333; Ga 108 DMSVIEETTPLSLEELFAQESTEMGINPNDYI	5		0	B
QUETY MATCH  2.5%; SCORE 119.5; DB 10; Length 1168; Best Local Similarity 18.8%; Pred. No. 5.9; Matches 169; Conservative 116; Mismatches 279; Indels 333; Ga  108 MSVIEETTPLSLEELFAQESTEMGINPNDYI	(L)	DLGEPVYIDYRAVEVRGEGADDKAFTTVAL	6	QУ
Query Match 2.5%; Score 119.5; DB 10; Length 1168; Best Local Similarity 18.8%; Pred. No. 5.9; Matches 169; Conservative 116; Mismatches 279; Indels 333; Gap Matches 169; Conservative 116; Mismatches 279; Indels 333; Gap Matches 169; Conservative 116; Mismatches 279; Indels 333; Gap Matches 169; Conservative 116; Mismatches 279; Indels 333; Gap Matches 169; Conservative 116; Mismatches 279; Indels 333; Gap Matches 169; Conservative 116; Mismatches 279; Indels 333; Gap Matches 169; Conservative 116; Mismatches 279; Indels 333; Gap Matches 169; Conservative 116; Mismatches 279; Indels 333; Gap Matches 169; Conservative 116; Mismatches 279; Indels 333; Gap Matches 169; Conservative 116; Mismatches 279; Indels 333; Gap Matches 169; Conservative 116; Mismatches 279; Indels 333; Gap Matches 169; Conservative 116; Mismatches 279; Indels 333; Gap Matches 169; Conservative 116; Mismatches 279; Indels 333; Gap Matches 169; Conservative 116; Mismatches 279; Indels 333; Gap Matches 169; Conservative 116; Mismatches 279; Indels 333; Gap Matches 169; Conservative 116; Mismatches 279; Indels 333; Gap Matches 169; Conservative 116; Mismatches 279; Indels 333; Gap Matches 169; Conservative 116; Mismatches 279; Indels 333; Gap Matches 169; Conservative 116; Mismatches 279; Indels 333; Gap Matches 169; Conservative 116; Mismatches 279; Indels 333; Gap Matches 169; Conservative 116; Mismatches 279; Indels 333; Gap Matches 169; Conservative 116; Mismatches 279; Indels 333; Gap Matches 169; Conservative 116; Mismatches 279; Indels 333; Gap Matches 169; Conservative 116; Mismatches 279; Indels 333; Gap Matches 169; Conservative 116; Mismatches 279; Indels 333; Gap Matches 169; Conservative 116; Mismatches 279; Indels 169; Mismatche	HAIAG	FELPDMGLVVITERELFKSKQKKQRKRTK <i>I</i>	Ci	B
Query Match 2.5%; Score 119.5; DB 10; Length 1168; Best Local Similarity 18.8%; Pred. No. 5.9; Matches 169; Conservative 116; Mismatches 279; Indels 333; Gap  10 MSVIEETTPLSLEELFAQESTEMGINPNDYIPEYGE	IIRNSIGEVDVIIH		209	VΩ
Query Match  2.5%; Score 119.5; DB 10; Length 1168; Best Local Similarity 18.8%; Pred. No. 5.9; Matches 169; Conservative 116; Mismatches 279; Indels 333; Gaps  108 DMSVIEETTPLSLEELFAQESTEMGINPNDYIPEYQGE	:   ::    :     :  ITKLHRSMSSGQAVIIEGSLSEG 4	-	403	В
Query Match 2.5%; Score 119.5; DB 10; Length 1168; Best Local Similarity 18.8%; Pred. No. 5.9; Matches 169; Conservative 116; Mismatches 279; Indels 333; Gaps Matches 169; Conservative 116; Mismatches 279; Indels 333; Gaps Matches 169; Conservative 116; Mismatches 279; Indels 333; Gaps Matches 169; Conservative 116; Mismatches 279; Indels 333; Gaps Matches 169; Conservative 116; Mismatches 279; Indels 333; Gaps Matches 169; Conservative 116; Mismatches 279; Indels 333; Gaps Matches 169; Conservative 116; Mismatches 279; Indels 333; Gaps Matches 169; Conservative 116; Mismatches 279; Indels 333; Gaps Matches 169; Conservative 116; Mismatches 279; Indels 333; Gaps Matches 169; Conservative 116; Mismatches 279; Indels 333; Gaps Matches 169; Conservative 116; Mismatches 279; Indels 333; Gaps Matches 169; Conservative 116; Mismatches 279; Indels 333; Gaps Matches 169; Conservative 116; Mismatches 279; Indels 333; Gaps Matches 169; Conservative 116; Mismatches 279; Indels 333; Gaps Matches 169; Conservative 116; Mismatches 279; Indels 333; Gaps Matches 169; Conservative 116; Mismatches 279; Indels 333; Gaps Matches 169; Conservative 116; Mismatches 279; Indels 333; Gaps Matches 169; Conservative 116; Mismatches 279; Indels 333; Gaps Matches 169; Conservative 116; Mismatches 279; Indels 333; Gaps Matches 169; Conservative 116; Mismatches 279; Indels 333; Gaps Matches 169; Conservative 116; Mismatches 279; Indels 169; Mismatches 279; Mismatches 279; Mismatches 279; Mismatches 279; Mismatches 279; Mismatches 279; Mismatches 2	AIGSSHOKTEP 20	SEVVVPPTLEPEKPGLIKRLYARLFNDGV	149	Qγ
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uery Match 2.5%; Score 119.5; DB 10; Length 1168; est Local Similarity 18.8%; Pred. No. 5.9; atches 169; Conservative 116; Mismatches 279; Indels 333; Ga	IPEYQGEQPN 14	DMSVIEETTPLSLEELFAQESTEMGINPNI	108	Qy
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RESULT 39
US-09-789-386-2
; Sequence 2, Application US/09789386
; Patent No. US20020010324A1
; GENERAL INFORMATION:
; APPLICANT: MICHALOVICH, DAVID

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TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP-30165-C1
CURRENT APPLICATION NUMBER: US/09/789,386
CURRENT FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: U.K. 9916898.1
PRIOR APPLICATION NUMBER: U.K. 9916024.5
PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: US 09/359,208
PRIOR APPLICATION NUMBER: US 09/359,208
PRIOR APPLICATION NUMBER: US 09/359,208
PRIOR FILING DATE: 1999-07-22
NUMBER OF SEO ID NOS: 6
SOFTWARE: FASTSEQ for Windows Version 3.0
SEO ID NO 2
US-09-93-348-23

; Sequence 23, Application US/09893348

; Patent No. US20020072493A1

; GENERAL INFORMATION:
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; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-789-386-2
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Best Local Similarity 18.0%;
Matches 116; Conservative 9
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                                                                                                                                                                                                                                                                                                                                                                   QVSFEQSSSSRTEPAQVDESTLEPVIETVELTDGILMDISPIEFSASNLIQDKLNLVAAK 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SALATQAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSA 998
                                                                                                                                                                                                   ----ESENEVIDLPE-RTALANRKTPADVYQSKKVPLYVFVA 578
                                                                                                                                                                                                                                               KSEIANAPDGAGSLPCTELPHDLSL-KNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDV 955
                                                                                                                                                                                                                                                                                         ARHLYDMPDDR-----VLAINHDDGVNRSILGRISDAV------SAVARAIL--PD-
                                                                                                                                                                                                                                                                                                                                     E-TFSDSS-----
                                                                                                                                                                                                                                                                                                                                                                                                                            KKEKIPLQ --- MEELSTA ---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAEHG--YFDG--RWLDRSVDVILPDNTADVSLIYDTGTQYRFDEVVFFTIDPKTNQLTT 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPVDL-----FSDDSIPDVPQKQDETVMLVKESLTETSFESMIEYENKEKLSAL 791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EPVYIDYRAVEVRGEGADDKAFTTV---ADEVPLLIGDVFHHGKYET-----KKNLIENA 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ETEAPYISIACDL-----IKETKLSAEPAPDFSDYSEMAKVEQPVPDHSELVEDSSPDS 742
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPLEASSVN--YESIKHEPENPPP-----YEEAMSVSLKKVSGIKEEIKEPENINAALQ 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MDLVQTSEVMQESLYPAAQLCPSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSS 636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-----QSQALDVVNFDDQSPISRIGEQSPPLGLDMSVIEETTPLSLEEL------ 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AYITCAPFNPAATESIATNIF---PLLGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSN 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EPEKPGLIKRLYARLFNDGVNKVPRLKAKFYQSSQSGETSAIGSSHQKTEPYANIKAALE 217
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                                                                                                                                                                                                                                                                                                                                                                                                                            ----VYSND----
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Best Local Similarity
Matches 116; Conserv
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PRIOR APPLICATION NUMBER: IL 124500
PRIOR FILING DATE: 1998-05-19
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CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: US 09/314,161
PRIOR FILING DATE: 1999-05-19
PRIOR FILING DATE: 1998-12-22
PRIOR FILING DATE: 1998-12-22
PRIOR FILING DATE: 1998-12-22
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: US 09/218,277
PRIOR FILING DATE: 1998-12-22
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APPLICANT: MOSCNEGO, Alon
APPLICANT: MOSCNEGO, Alon
APPLICANT: MOALEM, Gila
TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR
FILE REFERENCE: EIS-SCHWARTZ=2A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: EISENBACH-SCHWARTZ, Michal APPLICANT: COHEN, Irun R.
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SALATQAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSA
                                                                                                                                                                     E-TFSDSS------PIEIIDEFPTLISSKTDSFSKLAREYTDLEVSH
                                                                                                                                                                                                               QVSFEQSSSSRTEPAQVDESTLEPVIETVELTDGILMDISPIEFSASNLIQDKLNLVAAK
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                                     ----ESENEVIDLPE-RTALANRKTPADVYQSKKVPLYVFVA 578
                                                                                  KSEIANAPDGAGSLPCTELPHDLSL-KNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDV
                                                                                                                          ARHLYDMPDDR----VLAINHDDGVNRSILGRISDAV----
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149.5	152.5	159	159.5	168	170.5	171	171.5	177.5	177.5	178	178	178	183.5	190.5	193.5
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ALIGNMENTS

Qγ 밁 Qγ Вb Ş Вb Qy Вþ Ω Ъ ρ Ş A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pa A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: F83327
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-579 <STO>
A;Cross-references: GB:AE004682; GB:AE004091; NID:g9948598; PIDN:AAG05931.1; GSPDB:GN
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA2543 C;Accession: F83327
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, ; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000 C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: F8327 밁 conserved hypothetical protein PA2543 [imported] - Pseudomonas aeruginosa (strain C;Species: Pseudomonas aeruginosa Query Match 13.0%; Score 615.5; DB 2; Best Local Similarity 24.5%; Pred. No. 1.8e-27; Matches 178; Conservative 117; Mismatches 220; 555 ALANRKTPADVYQSKKVPLYVFVASDKPRDGQIGLGWGSDTGTRLVTKFEHNLINRDGYQ 614 495 239 435 198 375 146 315 266 210 ANIKAALEDITQESAMDLNGSIPRLRQTALV----AARAVGYYDIDLSIIRNSIGEVDVI 265 87 41 IQNDQVSFEQSSSSRTEPAQVDESTLEPVIETVELTDGILMDISPIEF\$ASNLIQDKLNL | : | : | : | QLTTDPDKLPVKRELLEQLLTVNMGEAYNLQAVRALSNDLIATRYFNMVNTEIVFPEREQ 434 IHD------LGEPVYIDYRAVEVRGEGADDKAFTTVADEVPLLIGDVFHHGKYET 314 ANIEAYVGSLGERD----EAALQRFRRNAEAQAEKAAQALGYFQ-----AQIDSE VAAKARHLYDMPDDRVLAINHDDGVNRSILGRISDAVSAVARAILPDESENEVIDLPERT AKRLIQNQASRYGFFQGRFSTQRLSIDPRAGIADIDLVYDSGQRYTFGKVSF-----VKDGKPPKLTLKVVPGEPVRLRQVNIQVLGEAASLESFRLPSGK-QLKPGAKLNQGVYED ----DGDSI-IEEELLRRMVPFKAGQPYDSELIAELNQNLQSSGYF---------DGARQAI - - --EGVRVDAAPTQAQA Indels 213; Length 579; Gaps 494 374 86 259 252 238 197 17; × × ...

260

PVAVRLEARKPRTMGVGLGFSTDVGARARFNWTRHWVNAEGHS 302

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R.Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001

A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A;Reference number: AB0001; MUID:21470413; PMID:11586360

A;Accession: AE0428

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-578 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC92753.1; PID:g15981448; GSPDB:GN00175
C;Genetics:
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C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Accession: AE0428
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                                                MPDDRVLAINHDDGVNRSILGRISDAVSAVARAILPDESENEVIDLPERTALANRKTPAD
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                                                                                                                                       SSSSRTEPAQVDESTLEPVIETVELTDGILMDISPIEFSASNLIQDKLNLVAAKARHLYD
                                                                                                                                                                                                                                 VKRELLEQLLTVNMGEAYNLQAVRALSNDLIATRYFNMVNTEIVFPEREQIQNDQVSFEQ 444
                                                                                                                                                                                                                                                                                 RRGYFDANMIKSQLGVAAQLHEAFWDIDFDSGQRYRFGKVIF-
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23.4%; Pred. No. 1.6e-20;
htive 105; Mismatches 255;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable exported protein ytfM [imported] - Salmonella enterica subsp. enterica (;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001 C;Accession: AD1055 C;Accession: AD1055 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Chart, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.;
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A;Gene: ytfM
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A; Residues: 1-577 < PAR>
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Best Local Similarity
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KLNLVAAKARHLYDMPDDRVLAINHDDGVNRSILGRISDAVSAVARAILPDESENEVIDL
                                                                                            EREQIQNDQVSFEQSSSSRTEPAQVDESTLEPVIETVELTDGILMDISPIEFSASNLIQD 490
                                                                                                                                                                                                                                 DYDNFKKSLTSVSLRKGYFDSEFIKSQLGIALGRHQAFWDIDYDSGERYRFGPVTF----
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                                                                                                                                                                                                                                                                                                                                                                        SIIRNSIGEVDVIIHDL--GEPVYIDYRAVEVRGEGADDKAFTTVADEVPLLIGDVFHHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FNHVPYRLRFFAGGDQSIRGYAHDSLSPISDKGYLTGGQVLAVGTAEYNYEFMKDLRLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GDSQRYSIDVSDTTWGSDVDFGIFQAQNVWIRTLGEK-----NRFVARGNVGWIETNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QRAINLRWSLD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NRTYSLRYRLDKLKTQAPPETWQDLPVDFVNGKPSQEALL--AGVAVHKTVADNLVNPMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EQTLDFSYRIPLLRNPLEQYYLIQGGFRR-----TDLNDTNSDTTTLNVARFWDLSSGW
                                                                                                                                                                                   PKTNOLTTDPDKLPVKRELLEQLLTVNMGEAYNLQAVRALSNDLIATRYFNMVNTEIVFP
                                                                                                                                                                                                                                                                                                                               DLLPPPAKGRQVLIARVTPGQPVLIGGTEVILRGGARTDKDYLALLKTRP-AIGTVLNQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FDRVPPSLRFFAGGDRSIRGYKFRNISPRDSDGKLTGASKLATGSLEYQYNFTGRWWGAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KKGVKL-YATKPLSHPLNDQLRATLGYQQEVFGHSTNGFDLSTRTLEHEISRSIIQNGGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative 104;
                                                                                                                                          EGSQIRDEYLQNLLPFKEGDEYESKDLAELNRRLSATGWFNSV---VVAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.1%; Score 479; DB 2; 22.7%; Pred. No. 1.1e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----HFTQGRVTDTTMLLYPGVSINRTRQRGGAMPVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----AVGYYD--IDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bowd, L.; Wain, J.; Church
Dowd, L.; White, N.; Farr
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GSPDB:GN00176

Stevens,

Gaps

17;

81

252

430 196

243

140

916

serov

406

459

362 683

D 60 1 0 1 H	etical protein VC2548 [imported] - Vibrio choolerae 000 #sequence_revision 20-aug-2000 #text_cha 064 F: Eisen, J.A.; Nelson, W.C.; Clayton, R.A. molaeva, M.D.; Vamathevan, J.; Bass, S.; Qir 08, J.J.; Venter, J.C.; Fraser, C.M. 483, 2000 uence of both chromosomes of the cholera pat er: A82035; MUID:20406833; PMID:10952301 linary DNA 2 <hei> 2 <hei> 9.6%; Score 454; DB 2; Length conservative 104; Mismatches 237; Indel EDITOESAMDLNGSIPRLRQTALVAARAVGYYDIDLSII  </hei></hei>	F82064 Cconserved hypoth C:Species: Vibric C:Species: Vibric C:Species: Vibric C:Accession: F82 C:Accession: F82 C:Accession: F82 C:Accession: F82 C:Accession: F82 C:Accession: F82 A:Fittle: DNA Seq A:Reference numb A:Reference reference C:Genetics: 1-58 A:Coss-reference A:Experimental sice C:Genetics: 164; C:G
787 444 444 905 504 905 564  rain N16961 serog -2001 .L.; Dodson, R.J. oi, I.; Sellers, io Cholerae. io Cholerae. 689.1; GSPDB:GN00 689.20;	cha. Qin Qin Qin pat	rB2064 conserved C:Species C:Species C:Accession I, R.R.; Inteledable Chardson, I, R.R.; Nature 40) A;Title: Nature 40 A;Title: A;Refactus: A;Refactus: A;Refactus: A;Residue: A;Conserim A;Residue: A;Conserim A
787 444 444 905 504 905 564 1.; Dodson, R.J. 1.; Sellers, 10 cholerae. 10 cholerae. 10 cholerae. 10 cholerae.	chachachachachachachachachachachachachac	rB2064 conserved C:Species C:Species C:C;Accession L:R:Heidelbi chardson, L:R:Heidelbi chardson, R:Heidelbi A;Rittle: A;Refersion A;Residue A;Cross-r A;Coss-r A;C
787 444 444 905 504 905 564 564 1.: Dodson, R.J. 1.: Sellers, 10 cholerae. 10 cholerae.	cha cha Qir pat	F82064 CCONSERVED C: Species C: Date: 1 C: Date: 1 C: Pate: 1 R. R.; I R
787 444 444 905 564 564 561, I.; Dodson, R.J. L.; Dodson, R.J. Lo; Cholerae.	hypothetical protein VC2548 [imported] - Vibrio chos: Vibrio cholerae 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_char ion: F82064 berg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, McKalanos, J.J.; Venter, J.C.; Fraser, C.M. 06, 477-483, 2000 DNA Sequence of both chromosomes of the cholera pati noe number: A82035; MUID:20406833; PMID:10952301 ion: F82064	F82064 cconserved c:Species C:Spate: 11 C:Accessi
787 444 444 905 564 564 564 561, Dodson, R.J. 51, I.; Bellers,	d hypothetical protein VC2548 [imported] - Vibrio chos: Vibrio cholerae 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_char ion: F8204 berg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. 06, 477-483, 2000	F82064 conserved C; Species C; Spate: 1: C; Accessi C; Heidelb R; Heidelb Chardson, 1, R.R.; J
787 444 444 847 504 905 564	<pre>d hypothetical protein VC2548 [imported] - Vibrio cho s: Vibrio cholerae 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_char ion: F82064</pre>	F82064 conserved C; Species C; Date: 1: C; Accessi
		RESULT 4
	5 HGLOFYIG 572	Db 565
	GNPIKLHE	Оу 906
	8 EYNYEFMKDLRLAVFGDIGNAYDKGFTNDTKIGAGVGVRWASPVGQVRVDVATGVKEE	Qy 848 Db 505
	8 MTGGIQAGYIWSDNENHVPYRLREFAGGDQSIRGYAHDSLSPISDKGYLTGGQVLAVGTA   :   :	Qy 788 Db 445
		Db 392
	VHKTVADNLVNPMRGYRQRYSLEVGSSGLVSDANMAIARA	
EALLAGVA 727 :     TTMLFYPGVM 391	0 EHEISRSIIQNGGWNRTYSLRYRLDKLKTQAPPETWQDLPVDFVNGKPSQEALLAGVA 	Qy 670 Db 350
-DINDTEQDSTTL 349	YGHSLTTSTSISAPEQVLDFSYKMPLLKNPLEQYYLVQGGFKRT	Db 294
		Db 269
TKFEHNLINR 610	PERTALANRKTPADVYQSKKVPLYVFVASDKPRDG	
- :: :   : -LKGVVSPRTENTI 268		

Qy	432 REQIQNDQVSFEQSSSSRTEPAQVDESTLEPVIETVELTDGILMDISPIEFSASNLIQDK 491	
рь	252 LSQL 255	
Qy	492 LNLVAAKARHLYDMPDDRVLAINHDDGVNRSILGRISDAVSAVARAILPDESENEVIDLP 551	
Db	256 258	
Qy	552 ERTALANRKTPADVYQSKKVPLYVFVASDKPRDGQIGLGWGSDTGTRLVTKFEHNLINRD 611	
Db	259	
Qy	612 GYQAGAELRLSEDKKGVKLYATKPLSHPLNDQLRATLGYQQEVFGHSTNGFD-LSTRTLE 670	
Db	302 GHSFDSSFSLSIPEQTITAGYKIPLEDALNEYYRIQYGMKHLDKRDTESLE 352	
Qy	671 HEISRSIIQNGGWNRTYSLRYRLDKLKTQAPPETWQDLPVDFVNGKPSQEALLAGVAV 728	
DЪ	353 SNLSLERHWOLDGGWHRTVFIRYLLENYRQGLQDDNSQFLLPGMTY 398	
Qy	729 HKT-VADNLVNPMRGYRQRYSLEVGSSGLVSDANMAIARAGISGVYSFGDNAYGSNRAHQ 787	
Db	399 TRTRTRSNSGLLTWGDKQTITLEYGDPALLSETRVLRLQTGSSWLRTYARN	
Qy	788 MTGGIQAGYIWSDNENHVPYRLRFFAGGDQSIRGYAHDSLSPISDKGYLTGGQVLAVGTA 847	
Db	452 ALVRVDGGANLVDEFDQLSPSLRFFAGGDNNLRGYGYKSISPQDASGALTGAKYIATSSI 511	
Qy	DKGFTNDT	
Db	512 EYQYRLTGNWWAAMFMDVGDAFNDNPEWKKGVGTGIRWISPVGPIRLDFAWGLDA 566	
Qy	904 EEGNPIKLHFFIG 916	
Вb	567 APGDEFKIHETLG 579	

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RESULT 6

S56445

S56445

S56445

hypothetical 64.8K protein (msra-chpbi intergenic region) - Escherichia coli (strain K-l hypothetical faceli protein o577

C;Specles: Escherichia coli
C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 01-Mar-2002
C;Accession: S56445; G65233

R;Burland, V.; Plunkett III, G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R.
Nucleic Acids Res. 23, 2105-2119, 1995
A;Title: Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.
A;Reference number: S56344; MUID:95334362; PMID:7610040
A;Reference number: S56344
A;Rocession: S56445
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-577 <BUR>
A;Rote: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
A;Bota: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
A; Rose, D.J.; Mau, B; Shao, Y.
Crience 777 1453-1462 1997
                                                                                                                                                A;Gene:
A;Start
                                                                                                                                                                                                      A;Status; F. A. A;Status A; Aratus A; A; Status A; Molecule type: DNA A; Molecule type: 
                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: The complete genome sequence of Escherichia coli K-12
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: G6523
A;Status: preliminary; nucleic acid sequence not shown; transla
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                                                                            Query Match
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       Matches
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                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GVRWASPVGAIKFDIATPIRDKDNSKNIQFYIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QEALLAGVAVHKTVADNLVNPMRGYR-------QRYSLEVGSSGLVSDANMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VTKFEHNLINRDGYQAGAELRLSEDKKGVK-LYATKPLSHPLNDQLRATLGYQQEVFGHS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YKKIAPKNRNGKLVGGSRLLTTSLEYQYQVYPNWWAATFADSGLAADNYTAKELRYGTGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HDSLSPISDKGYLTGGQVLAVGTAEYNYEFMKDLRLAVFGDIGNAYDKGFTNDTKIGAGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EN--DINTRYLTLSALRYWNNAHGWQYFGGLRMRYDSF-TQAD---
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   164;
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                                      9.2%;
22.9%;
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100;
                                      Score 433.5; DB 2; Pred. No. 4.4e-17;
   Mismatches
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   262;
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                                                                            577;
   189;
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   Gaps
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R;Hayas... Yasu... gasawara, N.; Yasu...
                                                                                                                                                                                                                                                                                                           hypothetical protein ECs5198 [imported] - Escherichia coli (strain C;Species: Escherichia coli (c;Species: Bscherichia coli C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-C;Accession: F91278
                                                       A; Experimental source: C; Genetics: A; Gene: ECs5198
                                                                                                                                                                                            DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: F91278
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                                                                                              A;Cross-references: GB:BA000007; PIDN:BAB38621.1; PID:g13364675; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
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A; Residues: 1-577 <HAY>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DSGEAVSDIRRSDFKTGTGVGVRWESPVGPIKLDFAVPVADKDEHG----LQFYIG
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                                                                                                                                                                                                                                                      Yasunaga,
1-22, 2001
                                                                                                                                                                                                                                                                    Makino, K.; Ohnishi,
Yasunaga, T.; Kuhara,
9.2%;
22.9%;
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Score 433.5; DB 2
Pred. No. 4.4e-17;
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Shiba, T.; Hattori, I
                  DB 2;
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Matches

164;

Conservative

100;

Mismatches

Indels

189;

Gaps

18;

Best Local Similarity

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A; Experimental:
C; Genetics:
A; Gene: ytfM
                                                                                                                                                                                  A;Title: Genome sequence of enterchemorrhagic Escherichia coli 0157:H7 A;Reference number: A85480; MUID:21074935; PMID:11206551 A;Accession: F86119
                                                                                                                                                                                                                                                                            hypothetical protein ytfm [imported] - C;Species: Escherichia coli C;Date: 16-Feb-2001 *sequence_revision C;Accession: F86119 R;Perna, N.T.; Plunkett III, G.; Burlar
                                                                                                  A;Cross-references: GB:AE005174; NID:g12519219; PIDN:AAG59418.1; A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-577 <STO>
                                                                                                                                                                                                                                            iller, L.; Grotbeck, E.J.
Nature 409, 529-533, 2001
                                                                                                                                                                         A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYSLRYRLDKLKTQAPPETWQDLPVDFVNGKPSQEALL--AGVAVHKTVADNLVNPMRGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TLDFSYKMPLLKNPLEQYYLVQGGFKRT----DLNDTESDSTTL--VASRYWDLSSGWQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GVKL-YATKPLSHPLNDQLRATLGYQQEVFGHSTNGFDLSTRTLEHEISRSIIQNGGWNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QSKKVPLYVFVASDKPRDGQIGLGWGSDTGTRLVTKFEHNLINRDGYQAGAELRLSEDKK
        164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DDRVLAINHDDGVNRSILGRISDAVSAVARAILPDESENEVIDLPERTALANRKTPADVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSRTEPAQVDESTLEPVIETVELTDGILMDISPIEFSASNLIQDKLNLVAAKARHLYDMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RELLEQLLTVNMGEAYNLQAVRALSNDLIATRYFNMVNTEIVFFEREQIQNDQVSFEQSS 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GYFDSEFTKAQLGIALGLHKAFWDIDYNSGERYRFGHVTF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GYFDGRWLDRSVDVILPDNTADVSLIYDTGTQYRFDEVVFFTIDPKTNQLTTDPDKLPVK 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VTPGVPVLIGGTDVVLRGGARTDKDYLKLLDTRP-AIGTVLNQGDYENFKKSLTSIALRK 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NVRAQLSTIESDEVTPDRRFRARVDDAIREGLKALGYYQPTIEFDLRPPPKKGRQVLIAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIKAALEDITQESAMDLNGSIPRLRQTALVAARAVGYY----DIDLSIIRNSIGEVDVII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEYLQNLVPFKEGDEYESKDLAELNRRLSATGWFNSV---VVAPQ-----FDKAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HDLGEPVYIDYRAVEVRGEGADDKAFTTVADEVPLLIGDVFHHGKYETKKNLIENASAEH
                      Similarity
                                                                                                                                                                                                                                                     Plunkett III, G.; Burland, V.; Mau, B.; Glasner, beck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.;
       Conservative
                   9.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----ETGVGYSTDVGPRVKATWKKPWMNSYGHSLTTSTSISAPEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----HFTQGEITNTTMLFYPGVMISRTRSRGGLMPTWGD
       100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -LT-GV---VSP
Score 433.5; DB 2;
Pred. No. 4.4e-17;
0; Mismatches 262;
                                                                                                                                                                                                                                                                                                   16-Feb-2001 #text_change 14-Sep-2001
                                                                                                                                                                                                                                                                                                                                        Escherichia coli (strain 0157:H7, substrain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----RTENTI--
 Indels
                                 Length 577;
 189;
                                                                                                                                                                                                                                                     J.D.; Rose, D.J.;
Potamousis, K.; Ap
                                                                                                                  GSPDB:GN00145; UWGP:Z58
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521
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                        DIGNAYDKGFTNDTKIGAGVGVRWASPVGQVRVDVATGV--KEEGNPIKLHFFIG
DSGEAVSDIRRSDFKTGTGVGVRWESPVGPIKLDFAVPVADKDEHG---LQFYIG
                                                                                 KVPPDLRFFAGGDRSIRGYKYKSIAPKYANGDLKGASKLITGSLEYQYNVTGKWWGAVFV
                                                                                                                        HVPYRLRFFAGGDQSIRGYAHDSLSPISDKGYLTGGQVLAVGTAEYNYEFMKDLRLAVFG 863
                                                                                                                                                                                                       RQRYSLEVGSSGLVSDANMAIARAGISGVYSFGDNAYGSNRAHQMTGGIQAGYIWSDNFN 803
                                                                                                                                                                                                                                                          AINLRWSLD
                                                                                                                                                                                                                                                                                           TYSLRYRLDKLKTQAPPETWQDLPVDFVNGKPSQEALL--AGVAVHKTVADNLVNPMRGY 743
                                                                                                                                                                                                                                                                                                                                    TLDFSYKMPLLKNPLEQYYLVQGGFKRT----DLNDTESDSTTL--VASRYWDLSSGWQR 363
                                                                                                                                                                  SQRYSIDYSNTAWGSDVDFSVFQAQNVWIRTLYDR-----HRFVTRGTLGWIETGDFD
                                                                                                                                                                                                                                                                                                                                                                                GVKL-YATKPLSHPLNDQLRATLGYQQEVFGHSTNGFDLSTRTLEHEISRSIIQNGGWNR 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                             QSKKVPLYVFVASDKPRDGQIGLGWGSDTGTRLVTKFEHNLINRDGYQAGAELRLSEDKK 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DDRVLAINHDDGVNRSILGRISDAVSAVARAILPDESENEVIDLPERTALANRKTPADVY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RELLEQLLTVNMGEAYNLQAVRALSNDLIATRYFNMVNTEIVFPEREQIQNDQVSFEQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GYFDSEFTKAQLGIALGLHKAFWDIDYNSGERYRFGHVTF------EGSQIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GYFDGRWLDRSVDVILPDNTADVSLIYDTGTQYRFDEVVFFTIDPKTNQLTTDPDKLPVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VTPGVPVLIGGTDVVLRGGARTDKDYLKLLDTRP-AIGTVLNQGDYENFKKSLTSIALRK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HDLGEPVYIDYRAVEVRGEGADDKAFTTVADEVPLLIGDVFHHGKYETKKNLIENASAEH
                                                                                                                                                                                                                                                                                                                                                                                                                          ---ETGVGYSTDVGPRVKATWKKPWMNSYGHSLTTSTSISAPEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LT-GV---VSP----
                                                                                                                                                                                                                                                       -HFTQGEITNTTMLFYPGVMISRTRSRGGLMPTWGD
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                                       916
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RESULT G82706

B 20 밁 Qy

В Q B δÃ 밁 Qy 밁 Q Вb Š Дb Ω Вþ δÃ 뫄 ΩV Вþ Qy 멍 Q

C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_ch
C;Accession: G82706
R;Anonymous, The Xylella fastidiosa Consortium of the Organ
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number
A;Accession: G82706 conserved hypothetical protein XF1231 [imported] C:Species: Xylella fastidiosa #text_change 20-Aug-2000 Xylella fastidiosa (strain number Organization for A59328 below Nucleotide 9a5c) Sec

GSPDB:GN

A;Ktatus; preliminary
A;Molecule type; DNA
A;Molecule type; DNA
A;Molecule type; DNA
A;Residues; 1-617 <51M>
A;Cross-references: GB:AE003957; GB:AE003849; NID:g9106207; PIDN:AAF84041.1; GSPDB:
A;Experimental source; strain 9a5c
A;Experimental source; strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga,
Briones, M.R.S.; Bueno, M.R.P.; Canargo, A.A.; Canargo, L.E.A.; Carraro, D.M.; Carr
Briones, M.R.S.; Bueno, M.R.P.; Facincani, A.P.; Ferreira, A.J.S.
as-Neto, E.; Docenna, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
as-Neto, E.; Docenna, C.; Callory, H.; Facincani, A.P.; Ferreira, A.J.S.
Submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.;
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.;
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marrino, C.L.; Marques, M.V.; Marti Franco, M.C.; Fr Kuramae, E.E.; La es, M.V.; Martins æ

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RESULT 10
D82000

Outer membrane protein OMP85 NMA0085 [imported] - Neisseria meningitidis (strain c:Species: Neisseria meningitidis
C:Species: Neisseria meningitidis
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C:Accession: D82000
C:Accession: D82000
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.
R:Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Raja
Nature 404, 502-506, 2000
Nature 404, 502-506, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Ollveira, M.A.; de Ollveira, M.C.; de Oliveira, R.C.; Palmieri, D.P. Rodrigues, V.; Rosa, A.J. de M.; de Ar., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z A;Reference number: A59328
A;Contents: annotation
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 21.6 nes 149; Conservative
                                                                                                                                                                                                      PRTAKPDAFALGAKHVFSAGAEFEYYYKGGPFGGAVFVDSGSAFNR--YPDWHTGVGIGL
                                                                                                                                                                                                                                                                                                                                                           DFVNGKPSQEALLAGVAVHKTV--ADNLVNPMRGYRQRYSLEVGSSGLVSDANMAIARAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LRAGVERRYMNARGHKMNARLDYAQNLKSL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LPDESENEVIDLPERTALANRKTPADVYOSKKVPLYVFVASDKPRDGQIGLGWGSDTGTR 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIEFSASNLIQDKLNLVAAKARHLYDMPDDRVLAINHDDGVNRSILGRISDAVSAVARAI 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YFH------EGLFNPLVYWDEGS-----YFHEGKLDRLRES------LT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YFNMYNTEIVFPEREQIQNDQVSFEQSSSSRTEPAQVDESTLEPVIETVELTDGILMDIS 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FKPKLGETFNHPTYEASKVRITRRLAERGYFDADFTHRRVEVTRAAHAADIDLIWESGRR 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VPLLIGDVFHHGKYETKKNLIENASAEHGYFDGRWLDRSVDVILPDNTADVSLIYDTGTQ 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALEPFGYYAPTIRIDAPRQNDHITVVIYVDKGEPVRVRQAHVAMTGAAAQDHYLQRDLED 162
                                                                                                                                                                                                                                       RWASPVGQVRVDVATGVKEEGNPIKLHFFIG
                                                                                                                                                                                                                                                                                                       PISDK--GYLTGGQVLAVGTAEYNYEFM-KDLRLAVFGDIGNAYDKGFTNDTKIGAGVGV 885
                                                                                                                                                                                                                                                                                                                                        LRWFHGLGASSRLILRG-----EAGTTWASDLVAMPPSLRFFAGGVNSIRGYAFREVG
                                                                                                                                                                                                                                                                                                                                                                                                         DGTNTVAYQQSTLVYPQLEASYVDVDDATFPRNGSAATVLLRGGASALGSKSNFTQLHGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DGWYIFFARAYDEQTKYIDLRNVKLSAARSGQINRHLTATASLNALRGR-----WRYRAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----HSTNGFDLSTRTLE-HEISRSIIQNGGWNRTYSLRYRLDKLKTQAPPETWQDLPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LVTKFEHNLINRDGYQAGAELRLSEDKKGVKLYATKPLSHPLNDQLRATLGYQQEVFG--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.3%; Score 347; DB 2;
21.6%; Pred. No. 4.3e-12;
tive 96; Mismatches 252
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A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: D82000
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-797 <PAR>
A;Residues: 1-797 <PAR>
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C;Superfamily: protect
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A; Experimental source: serogroup
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TPLSLEELFAQESTEMGINPND-----YIPEYQGEQPNSEVVVPPTLEPEKPGLIKRLY
LRLAVFGDIGNAYD
                                                                                                                                                                                                                                                                                   N--GK-PSQEALLAGVAVHKTV-----ADNLVNPMRGYRQRYSLEVGSSGLVSDANMAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DKLPVKRELLEQLLTVNMGEAYNLQAVRALSNDLIATRYFNMVNTEIVFPEREQIQNDQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DFYQNNGYFDFRILDTDIQTNEDKTKQTIKITVHEGGRFRWGKV---SIEGDTNE----
                                               ENFYGGGLGSVRGYESGTLGP---KVYDEYGEKISYGGNKKANVSAELLFPMPGAKDART
                                                                                                                                                                                                                                                    KKYGKTDGTDGSFKGWLYKGTVGWGRNKTDSALWPTRGY------LTGVNAEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAGVSQDNLFGTGKSAALRASRSK--TTLNGSLSFTDPYFTADGVSLGY--DVYGKAFDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENEVIDLPERTALANRKTPADVYQSKKVPLYVFVASDKPRDGQIGL--GWGSDTGTRLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NLVAAKARHLYDMPDD------RVLAINHDDGVNRSILGRISDAVSAVARAILPDES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SFEQSSSSRTEPAQVDESTLEPVIETVELTDGILMDISP-----IEFSASNLIQDKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NASAEHGYFDGRWLDRSVDVILPDNTADVSLIYDTGTQYRFDEVVFFTIDPKTNQLTTDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GNQVYSDRKLMR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GEPVYIDYRAVEVRGEGADDKAFTTVADEVPLLIGDV-----FHHGKYETKKNLIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FNQATLNQAVAGLKEEYLGRGKLNIQITPKVTKLARNRVDIDITIDEGKSAKITDIEFE- 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MD---LNGSIPRLRQ------TALVAARAVGYYDIDLSIIRNSIGEVDVIIHDL 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDA---IKKNLESFGLAQSQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARLFNDGVNKVP---RLKAKFYQSSQSGETSAIGSSHQKTEPYANIKAALED--ITQESA
                                                                                                 LRFFAGGDQSIRGYAHDSLSPISDKGYLTGGQVLAVG---TAEYNYEFM-----KD
                                                                                                                                                   ALPGSKLQY-----YSATHNQTWFFPLSKTFTLMLGGEVGIAGGY---GRTKEIPFF
                                                                                                                                                                                                  ARAGISGVYSFGDNAYGSNRAHQMTG-------GIQAGYIWSDNFNHVPYR
                                                                                                                                                                                                                                                                                                                                                        RKASTSIKQYKTTTA----GAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHYADFI
                                                                                                                                                                                                                                                                                                                                                                                                    FDLSTRTLEHEISRSIIQNGGWNR----TYSLRYRLDKLKTQAPPETWQDLP----VDFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KFEHNLINRDGYQAGAELRLSEDKKGVKLYATKPLSHPLNDQLRATLGYQQEVFGHSTNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----VDL--NMSLTERST---------GSLDLSAGWVQDTG--LVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -VVRRELRQMESAPYDTSKLQRSKERVELLGYFDNVQ-----FDAVPLAGTPDK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----VPKAELEKLLTMKPGKWYERQQMTAVLG----------EIQNRMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 259; DB 2;
Pred. No. 6.9e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
  --KGFTNDTKIGAGVGVRWAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 797;
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890 PVGQVRVDVATGVKEEGNPIKLHFFIGTPF 919	PVGQVRVDVAT	890	Qy	
GKTYDDNSSSATGGRVQNIYGAGNTHKST	5 VRLSLFADAGS	706	Db	
LRLAVFGDIGNAYD		857	QY	Ve
649 ENFYGGGLGSVRGYESGTLGPKVYDEYGEKISYGGNKKANVSAELLFPMPGAKDART 705	9 ENFYGGGLGSV	649	Db	
809 LRFFAGGDQSIRGYAHDSLSPISDKGYLTGGQVLAVGTAEYNYEFMKD 856	) LRFFAGGDQSI	809	QY	ъ . . А
600 ALPGSKLQYYSATHNQTWEFPLSKTFTLMLGGEVGIAGGYGRTKEIPFF 648	) ALPGSKLQY	600	Db	
765 ARAGISGVYSFGDNAYGSNRAHQMTGGIQAGYIWSDNFNHVPYR 808	5 ARAGISGVYSF	765	ОУ	Se
553 KKYGKTDGTDGSFKGWLYKGTVGWGRNKTDSALWPTRGYLTGVNAEI 599	3 KKYGKTDGTDG	553	Db	
YSLEVGSSGL	NGK-PSQEA	714	Qy	
497 RKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHYADFI 552	7 RKASTSIKQYK	497	Db	
662 FDLSTRTLEHEISRSIIQNGGWNRTYSLRYRLDKLKTQAPPETWQDLPVDFV 713	2 FDLSTRTLEHE	662	Qy	

olecule type: DNA esidues: 1-617 <KUR> ross references: GB:AE008688; PIDN:AAL43596.1; PID:g17741114; GSPDB:GN00186 xperimental source: strain C58 (Dupont) itle: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58. eference number: AB2577; PMID:11743193 ccession: AF2897 tatus: preliminary ene: Atu2615 uthors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam r, E.W. ap position: circular chromosome enetics: 141 NVRLEGDVTGRNLDEYGLIAGGDAGSLAIIRAGNKLIDDLKAEGRPLAKLTKREAVANHA 200 259 IGEVDVIIHDLGEPV-YIDYRAVEVRGEGADDKAFTTVADE---VPLLI----GDVFHHG 310 200 GSSHQKTEPYANIKAALEDITQESAMDLNGSI-PRLRQTALVAARAVGYYDIDLSIIRNS 258 81 RDDRDRLIAALYENARYGGIVNVTVAGKNVDDLPPNPVFDHSTPVPMVITVTPGPKFTLG 140 y Match
5.0%; Score 236.5; DB 2;
Local Similarity 20.3%; Pred. No. 8.8e-06;
hes 162; Conservative 107; Mismatches 246; 25 GSEEPEVEVINPVKYA---VTLDAA-DADKSLKSSLENSSLLLADKDKPASGDLGLLIKA 80 -NTADVSLIYDTGTQYRFDEVVFFTIDPKTNQLTTDPDKLPVKRELLEQLLTVNMGEAYN 403 Indels Length 617; 283; Gaps 344 31;

404 LQAVRALSNDLIATRYFNMVNTEIVFPEREQIQNDQVSFEQSSSSRTEPAQVDESTLEPV 463

PEKLRKAADRLRQLGVF------SSLTIKEAGTLARDGTIPL

283

201 TNTVDITMAAEGGPVAPLGAVTV-----TGEKTVDGD-----FIRRYSRLNGGEPYS 247

OY 461 EVELTHOLIADISPITESSNILLOKINIMAKARHILIDHAPDERVIATHEDOV	310 164 344 224	259 IGEVDVIIHDLGEPV-YIDYRAVEVRGEGADDKAFTTVADEVPLLIGDVFHHG	0	
NLIQDKNILVAAKARHLYDMPDDRVLAIMDOCY 519	8 4	162: Conservative 107; Mismatches 246; Indels 283; Garshoktepyanikaaleditoesamblugsi-prirotalvaaravgyydiblsiirns	Matc Oy :	
464 IEWELTOGILMDISPIERSASNILIONAKARHLYDMPDDRVLAINIDOCY	N00169	.1; PID:g1515 DB 2; Leng	A; Status: A; Molecule A; Residues A; Cross-re C; Genetics A; Gene: AG A; Map posi Query Ma	
IEYELTOSILMDISPIEFSASNILTORKINLVAAKARHLYDMPDDRVLAINHDOGY	ain C58, C B.; Goldm Markelz, bacterium	13  atical protein AGR_C_4742 (imported) - Agrobacterium tumefaciens ies: Agrobacterium tumefaciens: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-ssion: H97672  ner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurcker, Hinkle, G.; Gattung, S.; Miller, D.; Scott, C.; Lappas, P.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, 294, 2323-2328, 2001  segenome Sequence of the Plant Pathogen and Biotechnology Agent ssion: H97672	RESULT H97672 hypothe C; Spec: C; Date C; Acces R; Goodr R; Goodr A; L: Science A; Title A; Refe	
IETVELTBOILMDISPIEFSASNILTORKINLVAAKARHLYDMPDDRVLAINHDOGY		-EEGNPIKLHFFIGTPF :    ::      YDGGNNFGIYAGIGQSF	Qу	
IEYVELTOGILMDISPIEFSASNLIQDKLNLVAAKARHLYDMPDDRVLAINHDDGY	99		Оy	
IEYVELTOGILMDISPIEFSASNLIQDKLNLVAAKARHLYDMPDDRVLAINHDOGV	146		ОУ	
ISTVELTPOCILMDISPIEFSASNLIQDKLNLVAAKARHLYDMPDDRVLAINHDOCY	83		Db Oy	
IETVELTOGILMDISPIEFSASNLIQDKLNLVAAKARHLYDMPDDRVLAINHDDGV	¹ 26		ОУ	
ISTVELTPGILMDISPIEFSASNLIQDKLNLVAAKARHLYDMPDDRVLAINHDOGV	45	GHSTNGFDLST	ОУ	
ISTVELTPOCILMDISPIEFSASNLIQDKLNLVAAKARHLYDMPDDRVLAINHDOCY	515		ДУ	
IETVELTDGILMDISPIEFSASNLIQDKLNLVAAKARHLYDMPDDRVLAINHDDGV	355 5	TFTKPGMENPRTTEKTS	ОУ	
	519 811	ETVELTDG1LMDISPIEFSASNLIQDKLNLVAAKARHLYDMPDDRVLAI  : :::  -TIEVSEGKHRYFGVGAQY	ОУ	

RESULT D97527 Ompl p C;Spec	ОУ	Db	Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qу	DЬ	Qy	Ф	Qy	рь	Qy	Db	Qy	Db	Qy
14  rotein precursor (U51683) [imported] des: Agrobacterium tumefaciens	904 EEGNPIKLHFFIGTPF 919 :    :      624 KYDGGNNFGIYAGIGQSF 641	565 VEARIKYTDTIGLVPFFDAGVVSD-GVTPDFSDIRAGAGIGLRYATPFGPLRLDVAMPLE	847 AEYNYEFMKDLRLAVFGDIGNAYDKGFTNDTKIGAGVGVRWASPVGQVRVDVATGVK	508 KLSGGVLVGGSDLQDIPTTRRFFAGGGGSVRGYSYQEISPYNAAGDATGGRSYVVGS	787 QMTGGIQAGYIWSDNFNHVPYRLRFFAGGDQSIRGYAHDSLSPISDKGYLTGGQVLAVGT	480NGTFFSSFEGSITGYKGLGAEDRLIM	727 AVHKTVADNLVNPMRGYRQRYSLEVGSSGLVSDANMAIARAGISGVYSFGDNAYGSNRAH	470	667 RTLEHEISRSIIQNGGWNRTYSLRYRLDKLKTQAPPETWQDLPVDFVNGKPSQEALLAGV	425 GLEVQWADTEDAFGKNEYLTTSIPLEFVRDTRDDKLNPTEGFRAS-	616 GAELRISEDKKGVKLYATKPISHPINDQLRATIGYQQEVFGHSTNGFDLST	391 LIAKTENPDTYRAKTL	556 LANRKTPADVYQSKKVPLYVEVASDKPRDGQIGLGWGSDTGTRLVTKFEHNLINRDGYQA	336 YWGHRNLFGQAESLRIEGSVSRIAEASS	520NRSILGRISDAVSAVARAILPDESENEVIDLPE	308TIEVSEGKHRYFG	464 IETVELTDGILMDISPIEFSASNLIQDKLNLVAAKARHLYDMPDDRVLAINHDDGV	272 PEKLRKAADRLRQLGVF	404 LQAVRALSNDLIATRYFNMVNTEIVFPEREQIQNDQVSFEQSSSSRTEPAQVDESTLEPV	225 TNTVDITMAAEGGPVAPLGAVTVTGEK	345 - WTADVSLIYDTGTQYRFDEVVFFTIDPKTNQLTTDPDKLPVKRELLEQLLTVNMGEAYN
- Agrobacterium tumefaciens (						AG	ANMAIARAGISGVYSFGDNAYGSNRAH 7	:				TGTAGFAYELNDTDTAAA 4		SSVEGMDYSAGITETKPGMENPRTTEKTS	RTA	KHRYFGVGAQYSTTEGIGLQG		SSLTIKEAGTLARDGTIPL		TGEKTVDGDFIRRYSRLNGGEPYS	
(strain		623	903	564	846	507	786	479	726	469	666	424	615	390	555	335	519	307	463	271	403

Ompl protein precursor (U51683) [imported] - Agrobacterium tumefaciens (strain C58, C ;Species; Agrobacterium C; Allinger, M; Discort, C; Lappas, C, Markelz, A; Liu, F; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldm R; Conmerce C914, 2323-2328, 2001

A; Fittle: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium A; Reference number: A97359; PMID:11743194

A; Apcession: D97527

A; Status: preliminary A; Molecule type: DNA
A; Residues: 1-774 (KUR>
A; Rolecule type: DNA
A; Residues: 1-774 (KUR>
A; Rolecule type: DNA
A; Residues: 1-774 (KUR>
A; Rolecule: 1-794 (KUR

39;

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group 1 outer membrane protein precursor omp1 [imported] - Agrobacterium tumefaciens C:Species: Agrobacterium tumefaciens C:Species: Agrobacterium tumefaciens C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002 C:Accession: AE2746 R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Wooderage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McCl; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam
                                                                                                                                                                                                                                       RESULT 15
AE2746
ster, E.W.

A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58
A;Reference number: AB2577; PMID:11743193
A;Accession: AE2746
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A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-774 <KUR>
A;Cross-references: GB:AE008688; PIDN:AAL42387.1; PID:917739796; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
C;Genetics:
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           EEQRFRFG
                                             IKLHFFIG
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                                                                                                                  LRLAVFGDIGNAYDKGFT-----
                                                                                                                                                    VFD-QFKFGGRQ-VRGFKNDGIGPRIGSDS---IGGTTYFAASAEVTAPMPGVPEDF--G
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                                                                               LRLAGFVDAGTMYGNKVSTSQTVKDDNSIRASAGIGVMWASPFGPIRVDYAIPIAKEDYD
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21.0%;
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Pred. No. 2.2e-05;
9; Mismatches 310;
                                                                                                                NDTKIGAGVGVRWASPVGQVRVDVATGVKEEGNP
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C;Specles: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C;Accession: $77409
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajin O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecho
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A;Accession: S77409
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-861 <KAN>
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Best Local Similarity
Matches 189; Conserv
                                                                                                                                                                                                                                                              417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 422 MVNTEIVFPEREQIQNDQVSFEQSSSS-----RTEPAQ------VDESTLE- 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        362 DEVVFFTIDPKTNOLTTDPDKLPVKRELLEQLLTVNMGEAYNLQAVRALSNDLIATRYFN 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    267
                                                                       524
                                                                                                                                                                464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        312 YETKKNLIENASAEHGYFDGRWLDRSVDVILPDNTAD-----VSLIYDTGTQYRF 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          212 IKAALEDITQESAMD-----LNGSIPRLRQTALVAARAVGYYDIDLSIIRNSIGEVDVII 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   152 VVPPTLEPEKPGLIKRLYARLFNDGVNKVPRLKAKFYQSSQSGETSAIGSSHQKTEPYAN 211
                        666 TRTLEHEISRSIIQNG---
                                                                                                                                                                                                                                                                                                                                                       366 YGKILNLRELQEG----IKTINEWYSNQGYDLAQVVGSP-----QVGADGQVTLVIAEGI 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93 SPISRIGEQSPPLGLDMSVIEETTPLS-LEELFAQESTEMGINPNDYIPEYQGEQPNSEV 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----EPQSPLMAQAAVEEEVEAVEMEATEETTGVTEETPEETPSFTPDAPPTNTEGTPGP 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LDVGVDDLPPMAPVDSAELAQANELPHGNAVAQVAPRVAQVEQENLIAETKTDNQTDHV- 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELLVY-----NAIRTQPGRTTTRTQLQEDV------NAIYATGYFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TQTLPSFTPPAS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HDLGEP-----VYIDYRAVEVRGEGADDKAFTTVADEVPLLIGDV-----FHHGK 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNYSTLQEAAPSVINALNGE--NGEISVIPP-EIEQIDGDRLGQTMEISA-----GN 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPYYRLLLITSGLVLGASPAQATQAFSPLNMLADGDNTELLVSPSSEL-NFPGPTSESEA 69
                                                                                                                                                                                                                                                              VENIQVRFFD------SEDEPVQGRTRDFIITREMRLKPGDVFNRNRAQTDLQ 463
                                                                                                                                                                                                                                                                                                                                                                                     --PVIETVELTDGILMDISPIEFSASNLIQDKLNLVAAKARHLYDMPDDRVLAINHDDGV 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NVR----VAPSDTPL-GVRVTFEVQANPVFTGLNIRTVPETAEGKERILPQEVVDETFGEQ 365
                                                                     LGGNNQTIGVEAQVGQRELLFDVSFTDPWIGGDPFRTSYTANL-FRRRTISLVFDGADSS 582
                                                                                                                 INRDGYQAGAELRLSEDKKGVKLYATKPL -- SHPLNDQLRATLGYQQEVFGHSTNGFDLS 665
                                                                                                                                                                RVYSLGLFEDVRLSFNPGSDPTEVIVNVDVVEGNTGSIAAGGGISSSSGLFGTISYQERN 523
                                                                                                                                                                                                          NRSILGRISDAVSAVARAILPDESENEVIDLPERTALANRK---TPADVYQSKKV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.8%; Score 225; DB 2; Length 861; nilarity 19.7%; Pred. No. 6.9e-05; Conservative 130; Mismatches 399; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------GWNRTYSLRYRLDKLKTQAPPETWQDL 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   399; Indels 242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              274
                                                                                                                                                                                                                                                                                                             571
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601	550 LPERTALANRKTP	
549 429	Qy 499 ARHLYDMPDDRVLAINHDDGVNRSILGRISDAVGAVARAILPDESENEVID	
498 377	QY 440 VSFEQSSSSRTEPAQVDESTLEPVIETVELTD-GILMDISPIEFSASNLIQDKLNLVAAK :  : :   :   :                     : : :   :	
439 329	Qy 380 PDKLPVKRELLEQLLTVNMGEAYNLQAVRALSNDLIATRYENMVNTEIVFPEREQIQNDQ	
379 290	OY 321 NASAEHGYFDGRWLDRSVDVILÞDNTADVSLIYDTGTQYRFDEV-VFFTIDÞKTNQLTTD	
320 239	Qy 272 PVYIDYRAVEVRGEGADDKAFTTVADEVPLIGDVFHHGKYETKKNLIE	
271 183	Qy 212 IKAALEDITQESAMDLNGSIPRLRQTALVAARAVGYYDIDLSIIRNSIGEVDVIIHDLGE   :  :	
211 136	Qy 165 IKRLYARLENDGVNKVPRLKAKFYQSSQSGETSAIGSSHQKTEPYAN	
Gaps 45;	Ouery Match 4.7%; Score 223.5; DB 2; Length 781; Best Local Similarity 20.9%; Pred. No. 7.1e-05; Matches 180; Conservative 116; Mismatches 302; Indels 263; Ga	
GSPDB:GN00190	patnogen 75; GSPDB	
(strain 16M)  01-Feb-2002  , C.; Los, T.; Ivanov  O'Callaghan, D.; Let		
	RESULT 17	d101824
919 861	Qy 868AYDKGFTNDTKIGAGVGVRWASPVGQVRVDVATGVKEEGNPIKLHEFIGTPF   ;   ;	
867 805	QY 812 FAGGDQSIRGYAHDSLSPISDKGYLTGGQVLAVGTAEYNYEFMKDLRLAVFGDIGN	Yasuda ocystis
811 754	QY 762 MAIARAGISGVYSFGDNAYGSNRAHQMTGGIQAGYIWSDNFNHVPYRLRF :	ma, N.;
761 700	709 PVDEVNGKPSQEALLAGVAVHKTVADNLVNPMRGYRQRYSLEVGSSGLVSDAN  :: : : : : : : : : : : : : : : : : :	
042	Db 583 IRTFNGFDSPRVVRTGLGLTFFRPIADDVFAPPDWRLSAGFGYQNVKLENAAGALSFFSA	_

QΥ

Qy 620RLSEDKKGVKLYATKPLSHPLNDQLRATLGYQQEVFGHSTNG 661	Db 228IAFGDFEITGTQRYPEQIVSGLARFQPGTPYDLDLLLDFQQAL-EQNGHYSGASVQ 282	583 RDGQ	168	AYTVHITPGPRTKIANVGVAILGDILSDGNLAEYYRNALEN	Oy 522 SILGRISDAVSAVARAILPDESENEVIDLPERTALAN 558	Db 48 PDTESVKLKPKFPVRIDTQDSEIKDMVEEHLPLITQQQEEVLDKEQTGFLAEEAPDNVKT 107	Macches	ery Match 4.78; st Local Similarity 22.38;	A;Gene: NMA0296	A;Molecule type: DNA A;Rolecule type: DNA A;Residues: 1-615 <par> A;Residues: 1-615 <par> A;Cross-references: GB:AL162752; GB:AL157959; NID:g7378778; PIDN:CAB83602.1; PID:g737905 A;Experimental source: serogroup A, strain Z2491 C:Genetics:</par></par>	Accession: A82025 Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churche Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; ture 404, 502-506, 2000 Title: Complete DNA sequence of a serogroup A strain of Neisse Reference number: A81775; MUID:20222556; PMID:10761919 Accession: A82025	[imported] - Neisseria meningit	Db 761 PVAKADTDKVQNFNFGVSTKF 781	Qy 901 GV-KEEGNPIK-LHFFIGTPF 919	QY 854MKDLRLAVFGDIGNAYDKGFTNDTKIGAGVGVRWASPVGQVRVDVAT 900	OY 800 DNFNHVPYRLRFFAGGDQSIRGYAHDSLSPISDKGYLTGGQVLAVGTAEYNYEF 853	622	OY 740 MRGYRQRYSLEVGSSGLVSDANMAIARAGISGVYSFGDNAYGSNRAHQMTGGIQAGYIWS 799	OY 686TYSERY-REDKEKTQAPPETWQDEPVDFVNGKPSQE-ALLAGVAVHKTVADNEVNP 739	516 YD	Oy         643QLRATLGYQQEVFGHSTNGFDLSTRTLEHEISRSIIQNGGWNR- 685           I         I::::::::::::::::::::::::::::::::::::	461ERNELGRGQYIRISAGAGQDDMRNYGLSFTEPYELGYRLSAGEDVERRSYRVNDD	Db 430 VVEKST
Оу 365 V	Db 290 H	Оу 305 г	Qy 251 I Db 233 (	Db 177 <i>i</i>	ОУ 204 (	Qy 174 I Db 117 I	Db 62 1	Оу 120 г	Db 13	Query Mat Best Loca Matches	A; Scatus: A; Molecule A; Residues A; Cross-re A; Experime C; Genetics A; Gene: Cj	Nature 403 A; Title: Ti A; Reference A; Accession	C;Date: 31 C;Accessio R;Parkhill	Outer memb C;Species:	RESULT 19 A81430	Qy 873 Db 571	Db 511		Qy 760 Db 463	Db 403	Qy 719	Db 343	Dh 283

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: preliminary
le type: DNA
les: 1-739 <PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The genome sequence of the food-borne pathogen Campylobacter jejuni reveals noe number: A81250; MUID:20150912; PMID:10688204 on: \frac{1}{100}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nbrane protein Cj0129c [imported] - Campylobacter jejuni (strain NCTC 11168)
s: Campylobacter jejuni
s1-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  eferences: GB:AL139074; GB:AL111168; NID:96967505; PIDN:CAB72613.1; PID:9696
ental source: serotype O2, strain NCTC 11168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chil
il, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Bar
3, 665-668, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               atch 4.6%; Score 216.5; DB 2; Length 739; cal Similarity 18.1%; Pred. No. 0.00016; 172; Conservative 142; Mismatches 317; Indels 317; Gaps
                                                                 KTINIEDIRKDVKTIETQSADLGY---AFVEVYPDIQKNDQTQEATVVFKV---IPHDKV 343
                                                                                                                                                                                                                                                                            DLS-----IIRNSIGEVDVIIHDLGEPVYIDYRAVEVRGEGADDKAFTTVADEVPLLIG 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        j0129c
VFFTIDPKTNQLTTDPDKLPVKRELLEQLLTVNMGEAYNLQAVRALSNDLIATRYFNMVN 424
                                                                                                                                      DVFHHGKYETKKNLIENASAEHGYFDGRWLDRSVDVILPDNTADVSLIYDTGTQYRFDEV 364
                                                                                                                                                                                                       QVSSPYLKTYTDTYQANLTYFIKE-GKPYKI--KSISIENPLFDDKQNAQTVKDLRSSAG 289
                                                                                                                                                                                                                                                                                                                                              NDGVNK--VPRLKAKFYQSS-------------QSGETSAIGSSH--- 203
                                                                                                                                                                                                                                                                                                                                                                                                                       QKTEPYANIKAALEDITQE------SAMDLNGSIPRLRQTALVAARAVGYYDI 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEGNIKEAIERIKAYYEAKSYFDTIVEYKKKTLENTDGLELEFIVNRGENIIIDNVHLSG 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KQNYFENIAVE---NNNGILEIIVTEKPTIAKVTITGIASNDRKQVESILGIKR--GTLL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AMANAATIKDIKFIGLNHLSNTSAINIAGL-----KIGEEINPAKINTAILN----LY 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ARLNAA-----GLNAKPQSQALDVVNFDDQSPISRIGEQSPPLGLDMSVIEETTPLS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEELFAQESTEMGINPNDYIPEYQGEQPN-SEVVVPPTLEPEKPGL----IKRLYARLF 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KRMKLKHGSGLGVRWFSPLAPFSFDIAYGHSDK--KIRWHISLGTRF 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FINDTKIGAGVGVRWASPVGQVRVDVATGVKEEGNPIKLHFFIGTPF 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TALIRTSARAG-----YFFTPENKKLGTFIIRGQAGYTVARDNAN-VPSGLMFR 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANM--AIARAGISGVYSFGDNAYGSNRAHQMTGGI----QAGY-IWSDNFNHVPYRLRFF 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AEFLAEGRKIPGSDIDLGNSHATMLTASWKRQLLNNVLHPENGHYLDGKIGTTLGAFLSS 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QEALLAGVAV-----HKT-----VADNLVNPMRGYRQRYSLEVGSSGLVSD 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MDKYETTLAAGISQPRNYRGNYWTSNVSYNRSTTQNLEKRAFSGGIWYVRDRAGIDARLG 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FDLSTRTLEHEISRSIIQNGGW----NRTYSLRYRLDKLKTQAPPETWQDLPVDFVNGKPS 718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43;
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A;Gene: CC1603  Ouery Match Best Local Similarity 21.8%; Pred. No. 0.00013; Matches 110; Conservative 87; Mismatches 236; Indels 72; Gaps 17;  Oy 456 DESTLEPVIETVELTDGILMDISPIEFSASNLIQDKLNLVAAKARHLYD 504	C;Species: Caulobacter crescentus C;Datc: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001 C;Accession: B87448 C;Accession: B87448 R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001 A;Title: Complete Genome Sequence of Caulobacter crescentus. A;Reference number: A87249; MUID:21173698; PMID:11259647 A;Accession: B87448 A;Stacus: preliminary A;Molecule type: DNA A;Residues: 1-628 <sto> A;Cross-references: GB;AE005673; NID:g13423000; PIDN:AAK23582.1; GSPDB:GN00148 C;Genetics:</sto>	Qy 770 SGVYSFGDNAYGSNRAHQMTGGIQAGYIWSDNFNHVDYRLRFFAGG 815	Db 467	Db 344 YIRNVIISGNSRTVDRVIRRELYITEGNLYNRTDLSESKNALKRTSYFDDVN 395  Qy 425 TEIVFPEREQIQNDQVSFEQSSSSRTEPAQVDESTLEPVIETVELTD 471  Db 396
Qy 522 SILGRISDAVSAVARAILPDESENEVIDLPERTALAN 558	A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-635 <tet> A; Cross-references: GB: AE002561; GB: AE002098; NID: g7227384; PIDN: AAF42442.1; PID: g722 A; Cross-references: GB: AE002561; GB: AE002098; NID: g7227384; PIDN: AAF42442.1; PID: g722 A; Cross-references: GB: AE002561; GB: AE002098; NID: g7227384; PIDN: AAF42442.1; PID: g722 A; Cross-references: GB: AE002581 C; Genetics: A; Genetics: A; Gene: NNB2134  4.5%; Score 215; DB 2; Length 635; Best Local Similarity 22.1%; Pred. No. 0.00016; Best Local Similarity 22.1%; PID: g7227384; PIDN: AAF42442.1; PID: g722</tet>	hypothe Neisss -Mar-21 n: G810 K.; H.; K.; H.; T, 1800 7, 1800 Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Grando Gr	Db 430 ATLAGLAAYAWDFSDDILDPRRGWRLETRAEPTYVAGDTSVPYLKLAGQGSAYL 483  Qy 779 AYGSNRAHOMTGGIQAGYIWSDNFNHYPYRLEFFAGGDQSIRGYAHDSLSPISDKGYLTG 838    1	Db 263 ELERRLDTAVYDSISVSLAGTDKASAEGYRPVVVTLSDRRARTIELGAGYSTSEGAGVD 322  Qy 601 TKFEHNLINRDGYQAGAELRLSEDKKGVKLYATKPLSHPLNDQLRATLGYQQEVFGHSTN 660  1:

	AFFINENNUELERLÆTTEGGØF /84	102
	ATGVKEEGNPIKLHPEIGTPF 919	899
898 761	GTAEYNYEFMKDLRLAVFGDIGNAYDKGF-TNDTKIGAGVGVRWASPVGQVRVDV 898  :  :    :       :      :    :    :	845 702
844 701	GTQAGYIWSDNENHYPYRLRFFAGGDQSIRGYAHDSLSPISDKGYLTGGQVLAV       :   :     :     :     :     :       :	791 648
790 647		752 598
751 597	PSQEALLAGVAVHKTVAD	717 538
716 537	NGGWNRTYSLRYRLDKLKTQAPPETWODLPVDFVNGK	680 479
679 478	ATKPLSHPLNDQLRATLGYQQEVFGHSTNGFDLSTRTLEHEISRSIIQ	632 423
631 422	LGWGSDTGTRLVTKFEHNLINRDGYQAGAELRLSEDKKGVKLY :	589 369
588 368	VSAVARAILPDESENEVIDLPERTALANRKTPADVYQSKKVPLYVFVASDKPRDGQIG	531 325
530 324	ILMDISPIEFSASNLI-QDKL-NLVAAKARHLYDMPDDRVLAINHDDGVNRSIIGRISDA	473 270
472 269	IQNDQVSFEQSSSSRTEPAQVDESTLEPVIETVELTDG	435 210
434 209	LTTDPDKLPVKRELLEQLLTVNMGEAYNLQAVRALSNDLIATRYFNMVNTEIVFPEREQ-:	376 157

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B 64

04 04 05 05 06 07 07 07 07

RESULT 23
ACO129

Probable surface antigen YPO1052 [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C;Accession: ACO129
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G 11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: ACO129
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-795 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC89894.1; PID:g15979119; GSPDB:GN00175
C;Genetics:
A;Gene: YPO1052
C;Superfamily: protective surface antigen D-15

Query Match 4.5%; Score 211.5; DB 2; Best Local Similarity 19.1%; Pred. No. 0.00036; Matches 172; Conservative 139; Mismatches 306;

Length 795; Indels 283;

Gaps

42;

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RESULT 24
AI3488
Outer membrane protein BMEI1895 [imported] - Brucella melitensis (Strain ..., C:Species: Brucella melitensis
C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C:Accession: AI3488
R:DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; IV.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D. Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella **Peference number: AD3252; PMID:11756688
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A;Accession: AI3488
A,Status: preliminary
A;Molecule type: DNA
A;Residues: 1-623 <KUR>
A;Cross-references: GB:AE008917; PIDN:AAL53076.1; PID:g17983939;
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEI1895
A;Map position: I
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                                                        VGGGLRYLTSLGPIRLDVAVPLNRRSGDPNYGFYVG
                                                                                           AGVGVRWASPVGQVRVDVATGVKEEGNPIKLHFFIG
                                                                                                                              YRNIGVSAGNGNIIGGRSLVEANGEVRTRITDSIGAVAFVDAGYVGEKSFPDFSEQMRVG
                                                                                                                                                                    HDSLSPISDKGYLTGGQVLAVGTAEYNYEFMKDLRLAVFGDIGNAYDKG----FTNDTKIG
                                                                                                                                                                                                                                        GD------NAYGSNRAHQMTGGIQAGYIWSDNFNHVPYRLRFFAGGDQSIRGYA 823
                                                                                                                                                                                                                                                                                 -RDFTTAG-----IEGNLL----YDSRNNKPDPSSGFYLVGN-----IQPFYEFHY
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                                                                                                                                                                                                                                                                                                                  SQEALLAGVAVHKTVADNLVNPMRGYRQRYSLEVGSSGLVSDANMAIARAGISGVYSF--
                                                                                                                                                                                                                                                                                                                                                         ----LDAYTET-----SINAKTGFTQIFS-----DELSGALYANASQGHFVDDVFGK- 421
                                                                                                                                                                                                                                                                                                                                                                               STNGFDLSTRTLEHEISRSIIQNGGWNRTYSLRYRLDKLKTQAPPETWQDLPVDFVNGKP 717
                                                                                                                                                                                                                                                                                                                                                                                                                                   -GERLRFDAKVSGIGGSQDNSFDPKNYTYLLGASFAKPGVYTPDTDFVATLDAKREV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----IEPDGSLPITLNVQERKPRRFGFGAEYSTIDGFGVTSYWMHRNLLGR----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -YD-PDDIENA--
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; Pred. No. 0.00033;
79; Mismatches 263; Indel
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RESULT 25
G64601
protective surface antigen D15 - Helicobacter pylori (strain 26695)
C.Species: Helicobacter pylori
C.Species: Helicobacter pylori
C.Species: Helicobacter pylori
C.Accession: G64601
C.Accession: G64601
C.Accession: G64601
C.Ferlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McK Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McK son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey Nature 388, 539-547, 1997

Db	Qy	Оy	Оy	ду С.У	?	\$ \$ \$	ОУ	р ОУ	дь Оу	94 04	р <b>у</b>	Db	Оу	Db Qy	Qy Db	Query Best I Matche	A; Aut A; Tit A; Refi A; Acc A; Sta A; Mol A; Res A; Cro
670 SYDNTDDYYFPRNGVIFSSYATMSGLPSSGTLNSWNGLGGNVRNTKVYGKFAAYH 724	ANMAI	716 KPSQEALLAGVAVHKTVADNLVNDWRGYRQRYSLEV 751	670 -EHEISRSIIQNGGWNRTY-SLRYRLDKLKTQAPPETWQDLPVDFVNG 715 ::		CONNYELLY EYASUN FRUGUT - G	31		402 YNLQAVRALSNDLIATRYFNMVNTEIVFPEREQIQNDQVSFEQSSSSRTEPAQVDES 458	345 -NTADVSLIYDTGTQYRFDEVVFFTIDPKTNQLTTDPDKLPVKRELLEQLLTVNMGEA 401 :	317 NLIENASAEHGYFDGR	260 GEVDVIIHDLGEPVYIDYRAVEVRGEGADDKAFTTVADEVPLLIGDVFHHGKYETKK 316	201 SSHQKTEPYANIKAALEDITQESAMDLNGSIPRLRQTAL-VAARAVGYYDIDLSIIRNSI 259 : :	143 QGEQPNSEVVVPPTLEPEKPGLIKRLYARLFNDGVNKVPRLKAKFYQSSQSGETSAIG 200	83 ALDVVNFDDQSPISRIGEQSPPLGLDMSVIEETTPLSLEELFAQESTEMGINPNDYIPEY 142     :	24 MTSQALAQQNNPANIINHVPAHDTAINQAKAGNPPVLLTPEQIQAR-LNAAGLNAKPQSQ 82	Query Match 4.4%; Score 206.5; DB 2; Length 916; Best Local Similarity 19.3%; Pred. No. 0.00087; Matches 202; Conservative 143; Mismatches 318; Indels 383; Gaps 51;	A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori. A;Reference number: A64520; MUID:97394467; PMID:9252185 A;Accession: G64601 A;Status: prellminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-916 <ton> A;Cross-references: GB:AE000511; TIGR:HP0655</ton>

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A;Accession: D71726
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-768 <AND>
A;Residues: 1-768 <AND>
A;Cross-references: GB:AJ235270; GB:AJ235269; NID:93860572; PIDN:CAA14627.1; PID:9386
A;Experimental source: strain Madrid E
C;Genetics:
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D71726
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446 RNLVG-TGKLLNAGVQVSKNSTSYYGCITDPHFLDRDLSLSVNAFRNYTGRGASVLNTTD 504
                                                 605 HNLINRDGYQAGAELRLSEDKKGVKLYATKP--LSHPLNDQLRATLGY------Q
                                                                                                                                                                                                  349 INKINII -- NNLKTEDHVIRRAFKIEEGDVMNRSYIEK--
                                                                                                                                                                                                                                                   489
                                                                                                                                                                                                                                                                                           324 YPD-----IKKNDNHTADIKFIIEKADKVY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            165 IKRLYAR-----LFNDG-----VNKVPRLKAKFYQSSQSGETSAI-----GSS 202
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                                                                                                                                                                                                                           QDKLNLVAAKARHLYDMPDDRVLAINHDDGVNRSILGRISDAVSAVARAILPDESENEVI 548
                                                                                                                                                DLPERTALANRKTPA-DVYQSKKVPLYVFVASDKPRDGQIGLGWGSDTGTRLVTKF---E 604
                                                                                                                                                                                                                                                                                                                                                                                       NKLTN----INIKQLNKIVNIKQGKIFNMKTVDDIAEKI--GEYFTANGYPAVN---V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KNLIENASAEHGYFDGRWLDRSVDVILPDNTADVSLIY--DTGTQYRFDEVVFFTIDPKT 373
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                                                                                                                                                                                                                                                                                                                                        FPEREQIQNDQVSFEQSSSSRTEPAQVDESTLEPVIETVELTDGILMDISPIEFSASNLI 488
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                                                                                                   VNVEVDEKSTSSIGFDLGYNTAGGLFGRFSFLE
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                                                                                                                                                                                                                                                                                                               VIKRLYATSLFRNINMHITNDGNLIVNVTETPFISSVVFSGNSKIKTNMLAKEIYTMSGE 123
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                                                                                                                KTNQLTTDPDKLPVKRELLEQLLTVNMGEAYNLQAVRALSNDLTATRYFN-----MVNTE 426
                                                                                                                                            DKELLRDFYQSVGFADFRVISASAEL - - - NNTKEYFTLTYSIEEGEKYSFGNI - - - TIDN
                                                                                                                                                                       KKNLIENASAEHGYFDGRWLDRSVDVILPDNTAD-VSLIY--DTGTQYRFDEVVFFTIDP
                                                                                                                                                                                                   --KVIFDIAEGPKTGINYIYFSGNENYSDSELKSIVLTKESRWFRFLESNDTYDPDRMEY
                                                                                                                                                                                                                            VDVIIHDL--GEPVYIDYRAVEVRGEGADDKAFTTVADEVP-----LLIGDVFHHGKYET
                                                                                                                                                                                                                                                        SLSQAKIELDVKKILE-IYKRSGRFATTVTPKIE-----------NLENNRV--
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LIQDKLNLVAAKARHLYDMPDDRVLAINHDDGVNRSILGRISDAVSAVARAILPDESENE
                                                        IVFPEREQIQNDQVSFEQSSSSRTEPAQVDESTLEPVIETVELTDGILMDISPIEFSASN
                                                                                                                                                                                                                                                                                                                                                                     4.3%; Score 202.5; DB 2; ilarity 20.1%; Pred. No. 0.0011; Conservative 122; Mismatches 301;
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                                                                                     -LNKIVNIKQGKVFNMKKVDDIAEKI--GEYFTANGYPAVN--
                             -----IMKNANHT----ADIKFIIEKADK
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                                                                                                                                                                                                                                                                                                                                                                                               Length 768;
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RESULT
AF2089
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                                                                                                                                                                                                                                                                                                                                                                               693 LDKLKTQAPPETWQDLPVDFVNGKPSQEALLAGVAVHKTVADNLVNPMRGYRQRYSLEVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               444 LERNLVGTGKLLNAGVQVSKNTTSYYGGITAPHFLDRDLSLGVNTFRNYTGRGASVLNTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   547 VIDLPERTALANRKTPA-DVYQSKKVPLYVFVASDKPRDGQIGLGWGSDTGTRLVTKF--
                                                                    747 FPIKKKKYDDTQHFHL
                                                                                                                                       689 F--NLTGTVFMDLGSVGGVGLNKKQYQTPNGFYNDTSLRASIGFGFIWVTRFAPIRMDWG 746
                                                                                                                                                                          853 FMKDLRLAVFGDIGNA------YDKGFTNDTKIGA--GVGVRWASPVGQVRVDVA 899
                                                                                                                                                                                                                                                                               591 GVG----GNNKYIKHEVDGKYYKSFIHNKLTLKLSASGGN----ITG--LGGKIIRISDR
                                                                                                                                                                                                                                                                                                                                                   504 DQSYKLHSIGVKTSLGYEIKEDLGHE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                        635 PLSHPLND-QLRATLGYQ-QEVFGHSTNGFDLSTRTLEHEISRSIIQNGGWNRTYSLRYR
              28
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                                                                                                                                                                                                                                           FNHVPYRLRFFAGGDQSIRGYAHDSLSP---ISDKGYLTGGQVLAVGTAEYNY-----E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -EHNLI - - -
                                                                                                      TGVKEEGNPIKLHFFI
                                                                                                                                                                                                                                                                                                                  SSGLVSDANMAIARAGISGVY--SFGDN-----AYGSNRAHQMTGGIQAGYI--WSDN
                                                                                                                                                                                                              -----GDYSLRGFANGGVGPREKVTNEG--LGGERYYKFSTELNFPTPIPEE
                                                                      762
                                                                                                      915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -NRDGYQAG-----AELRLSEDK-----KGVKLYATK 634
                                                                                                                                                                                                                                                                                                                                                                                                                            ---IDYLIKRDILSAPTPSSSIFLKEQ
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Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabati DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AF2089
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein alr2269 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp.
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C;Accession: AF2089
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.;
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.;
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A; Gene: alr
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A;Residues: 1-833 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB73968.1; PID:g17131360; GSPDB:GN00179
A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                QY
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                 Matches 134;
                                                                                                                                                                                                                                              210
                                                                                                                                                                                                                                                                                371 PKTNQLTTDPDKLPVKRELLEQLLTVNMGEAYNLQAVRALSNDL---IATRYFNMVNTEI 427
                                                             484 ASNLIQDKLNLVAAKARHLYDMPDDRVLAINH-DDGVNRSILGRISDAVSAVARAI-LPD 541
                                                                                                                                                                                428 VFP----EREQIQNDQVSFEQSSSSRTEPAQVDESTLEPVIETVELTDGILMDISPIEFS 483
                                                                                                                           251 --PGRTTTRSQLQEDINAIFGTGFFSNVQASPEDTPLGVRVSFIVQPNPVL---SKVEIQ 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alr2269
ANPGTNVPSVLPQATADEIFRAQYGKILNLRDLQEGI-KELTKRYQDQGYVLANVVGAPQ 364
                                                                                                                                                                                                                                           PNATPETTEP-----RVLVSEVL------VRPQSGQLTPELETQVYNVIRTQ-
                                                                                                                                                                                                                                                                                                                                                       4.2%; Score 197.5; DB 2; ilarity 19.7%; Pred. No. 0.0024; Conservative 104; Mismatches 255;
                                                                                                                                                                                                                                                                                                                                                                    255;
                                                                                                                                                                                                                                                                                                                                                                    Indels 187;
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Query Best Matcl	Oy 54  Db 30  Oy 55  Db 41  Oy 64  Oy 64  Oy 65  Oy 65  Oy 66  Ob 66  Db 66  Db 67  Oy 77  Oy
Query Match  4.1%; Score 194.5; DB 2; Length 906; Best Local Similarity 19.9%; Pred. No. 0.0041; Matches 192; Conservative 131; Mismatches 311; Indels 333; Gaps 49;  116 TPLSLEELFAQESTEMGINPNDYIP-EYQ	OY 581 ESENRYIDLO
RESULT 30 AE2417 Apporthetical protein alr4893 [imported] - Nostoc sp. (strain PCC 7120) C;Species: Nostoc sp. A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 C;Accession: AE2417 R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata DNA Res. 8, 205-213, 2001 A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840 A;Accession: AE2417 A;Status: preliminary A;Molecule type: DNA	Qy 271 EPVYIDYBAVEVRGEGADKAPITVADEVPLLIGOVEHBGKYETKKNLIENASAEH-

		854	
	RWASPVG 892	886	
885 853	KAAKMILAWFEDDEGELTEKTPTRGSEFYNAPTTTANFKDYGVVGAGFERATWRASTGLQI	855 794	
793		734	
854	YRLRFFAGGDQSIRGYAHDSLSPISDKGYLTGGQVLAVGTAEYNYEFM	796	
733	SYATMSGLPSSGTLNSWNGLGGNVRNTKVYGKFAAYHHLQKYLLIDLIARFKTQGG	678	
795		761	
677	RTPLVPESCSSPGAITTSPEIKGIWDRDYHTPITSSFTLDVSYDNTDDYYFPRNGVIFS-	619	
760	VGSSGLVSDA	731	
618	VGRMLGNRTHVSLGYNLNVTKLLGFSSPLYNRYYSSVNEVASPRQCSTPASVIINRLSGG	559	
730		683	
558	FAGNLSLTNPRIFDSWYSSTINLYADYRISYQYIQQGGGFGVN	516	
682	HPLNDQLRATLGYQQEVFGHSTNGFDLSTRTLEHEISRSIIQNGG	636	
515	QLQFGLGYGSYGGLMLNGSVSERNLFGTGQSMSLYANIATGGGRSYPGMPKGAGRM	460	
635	INRDGYQAGAELRLSEDKKGVKLYATKP	586	
459	FFSKVKIEEKRVNSSLMDLLVSVEEGRTG	431	
585	RISDAVSAVARAILPDESENEVIDLPERTALANRKTPADVYQSKKVPLYVFVASDKPRDG	526	
430	VGDMVHINDVIISGNQRTSDRIIRRELLLGPKDKYNLTKLRNSENSLRRLG	380	
525	PIEFSASNLIODKLNLVAAKARHLYDMPDDRVLAINHDDGVNRSILG	469	
379	ILKTEIADKGYAFAVVKPDLDK	344	
468	DQVSFEQSSSRTEPAQVDEST-LEPVIETVE	413	
343	VKEGIQYRISDIL	296	
412	RELLEQLLTVNMGEAYNLQAVRALSN	355	
295	RDFMGWMWGLNDGKLRLDQLEYDSLRIQDVYMRRGYLDAHISSPFLKTDFSTHDAKLHYK	236	
354	GYFDGRTADRSVDVILPD-NTADVSLIVD	327	
235	VEVRTEKVSEGALLIVFDVNRGDSIYIKQSIYEGSDKLKRRVIESLSANKQ	185	
326	EPVYIDYRAVEVRGEGADDKAFTTVADEVPLLIGDVFHHGKYETKKNLIENASAEH-	271	

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A;Cross-references: GB:BA000019; PIDN:BAB76592.1; PID:g17134030; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr4893
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Best Local Similarity
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                                                                                             GYAHDSLSPISDKGYLTGGOVLAVGTAEYNYEFMKDLRLAVFGDIGNAYDKGFT-----
                                                                                                                                                                                                                                                                                              LRATLGYQQEVFGHSTNGFDLSTRTLEHEISRSIIQNGGWNRTYSLRYRLDKLKTQ---A
GVRGKPGSGFCYGAGIRVDSPLGLIRADY - - GINDQGES - RVHLGIGQRF
                                                              GY-----DAGNVGSGRSYVLASAEYRFPIVPIVGGVLFADFASDLGSGDTVLGNPA
                                                                                                                                                                                               PPETWQDLPVDFVNGKPSQEALLAGVAVHKTVADNLVNPMRGYRQRYSLEVGSSGLVSDA 760
                                                                                                                                                                                                                                                                                                                                                             GLGWGSDTGTRLVTKF--EHNLINRD--GYQAGAELRLSEDKKGVKLYATKPLSHPLNDQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASANVN-----SRTTPSGLNVVYQ--VQPVIV--RSLQLTGA----KALTYSVAQ--
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                               ----NDTKIGAGVGVRWASPVGQVRVDVATGVKEEGNPIKLHFFIGTPF
                                                                                                                              NISMNRLKADYSQYVPVNIFNSQTPQVFALNVQAGTVLG---NLPPYE-TFNLGGSNSVR
                                                                                                                                                              NMAIARAGISGVYSFGDNAYGSNRAHQMTGGIQAGYIWSDNFNHVPYRLRFFAGGDQSIR 820
                                                                                                                                                                                                                                                             IKLANGDKVRE-GKVGTGISLQ-RPID------GWNASLGFNYSRTSIRDRQGNI
                                                                                                                                                                                                                                                                                                                             GL---SRTDLQFDTKFISPYRDTNSDRLGYTVNA-----FRRREISETFDDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TDGILMDISPIEFSASNLIQDKLNLVAAKARHLYDMPDDRVLAINHDDGVNRSI--LGRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LSNDLIATRYFNMVNTEIVFPEREQIQNDQVSFEQSSSSRTEPAQVDESTLEPVIETVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VSD--IKFRFVNDDGKTIDSNGNPVGGRTKPD-----FLRQQLKLQPGQVFQENIVKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IYDTGTQYRFDEVVFFTIDPKTNQL--TTDPDKLPVKRELLEQLLTVNMGEAYNLQAVRA 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRFQSQI----GKPISPEGLKQAVAQVNQWYADNGYNLARVLSIEPNRQGILNINVAE-GL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLLIGDVFHHGKYETKKNL-----IENASAEHGYFDGRWL--DRSVDVILPDNTADVSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QETIRQVIKTQTGGDTS------QTQLQRDVAAILE-----TGLF 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                K---AKFYQSSQSGETSAIGSSHQKTEPYANIKAALEDITQESAMDLNGSIPRLRQTALV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INPNDYIPEYQGEQPNSEVVVPPTLEPEKPGLIKRLYARLFND------GVNKVPRL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGLNAKPQSQALDVVNFDDQSPISRIGEQSPPLGLDMSVIEETTPLSLEELFAQESTEMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MRISSAALLTLTTLVA------SNATQQAIAA-PHTASTPSK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AARAVGYYDIDLSIIRNSIGEVDVIIHDLGEPVYIDYRAVEVRGEGADDKAFT-TVADEV 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----QNENL-VIPVVEETPV-QLGNVTPP-----ET----EVTPQFSTKSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     191;
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                                                                                                                                                                                                                                                                                                                                                                                                 ----YQDQNIGGKNDTLLAN----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.1%; Score 193.5; DB 2; 20.1%; Pred. No. 0.0029; ative 119; Mismatches 323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----ATKLDMIYELKENGARAINLGGSYNGDVGLMGTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  323;
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676
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Q
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A;Title: Complete Genome Sequence of Caulobacter crescentus. A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: F87486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            outer membrane protein CC1915 [imported] - Caulobacter crescentus C;Species: Caulobacter crescentus C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001 C;Accession: F87486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ъ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-769 <STO>
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Best Local
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662 NSMGAKLYAISTFELTVPTFLPEQYGIKAALFSDVGTA---GLLDDVDRQRSPGVFDPNI 718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     250 IDLSIIRNSIGEVDVI-IHDLGEPVYI--DYRAVEVRGEGADDKAFTTVADEVPLLIGDV 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  y Match
4.0%; Score 190.5; DB 2;
Local Similarity 20.0%; Pred. No. 0.0053;
hes 151; Conservative 94; Mismatches 250;
                                        YLTGGQVLAVGTAEYNY-EFMKD----LRLAVFGDIGNAYDKGFTNDT-----
                                                                                            YWGFTKDLVFSATGSF--GYIEGWGGDNVRINDRFYRGG-TSFRGFEIAGIGPRDISSSF
                                                                                                                                                                                         IDKRNDPINPTRGW-----
                                                                                                                                                                                                                                                                                GGDVRFGFPLTNDSSMSLRYTVRQDEVSVADSLCASGSVSQILCLQRGAYITSLIGYGLR
                                                                                                                                                                                                                                                                                                                                   WQDLPVDFVNGKPSQEALLAGVAVHK-TVADNL------
                                                                                                                                                                                                                                                                                                                                                                                SVGSLRQQIDFGFSEPRF-----LGRNLV--AGVN-LYTFRYDLSEFAAYDTKSV 504
                                                                                                                                                                                                                                                                                                                                                                                                                             TLG--YQQEVFGHSTNGFDLSTRTLEHEISRSIIQNGGWNRTYSLRYRLDKLKTQAPPET
                                                                                                                                                                                                                                   ----VNPMRGYRQRYSLEVGSSGLVSDANMAIARAGISGVYSFGDNAYGSNRA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LSFSAGYSSIDKLV--LDVGITERNFRGRGQNLR------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---PRVYVDRIDIV-GNTRTL-DYVLRRELEVAEGDAYNR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FFTIDPKTNQLTTDPDKLPVKRELLEQLLTVNMGEAYNLQAVRALSNDLIATRYFNMVNT 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FHHGKYETKKNLIENASAEHGYFDGRWLDRSVDVILPD-NTADVSLIYDTGTQYRFDEVV 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IGLGWGSDTGTRLVTKFEHNLINRDGYQAGAELRLSEDKKGVKLYATKPLSHPLNDQLRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ESEN-----EVID----LPERTALANRKTPADVYQSKKVPLYVFVASDKPRDGQ 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FSASNLIQDKLNLVAAKARHLYDMPDDRVLAINHDDGVNRSILGRISDAVSAVARAILPD 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --TVETELKKLDGN------LLAQILPVRTGQLYE-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----DERIEQATDALTFAAGAAGFAFVDVRPRYVPNRETKTVDVVFQVREG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EIVFPEREQIQNDQVSFEQSSSS-----RTEPAQVDESTLEPVIETVELTDGILMDISPIE 481
                                                                                                                                         --HQMTGGIQAGYIWSDNFNHVPYRLRFFAGGDQSIRGYAHDSLSP--ISDKG
                                                                                                                                                                                    -----FADLNQDLAGVG-----GDVKYLKTEADAGW
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Qy	9 KLYATKPLSHPLNDQLRATLGYQQEVFGHST-NGFDLSTRTLEHEISRSIIQNGGWNRTY 687	629	Оy
Db	TYGLSVQRDQIDTGRYTVDEI-YDFLDKEGDNETNFKASIGWSES	Ñ	Db .
Qy	2 PLYVEVASDKPRDGOIGLGWGSDTGTRLVTKFEHNT.TNRDGVOAGAELBIGEDKKGV	57:	ογ
Db	9 VDGVSLGYNAFYRKTDYDELDVDVASYSVNSLGAGMSIGYPISETSRL 526	479	B 2
Oy Oy		431	DB
Qy		455	δ .
Db	NMGEAYNIQAVRALSNDLIATRYFNMVNTBIVFPEREQIQNDQVSFEQSSSSSRTEPAQ	397	P 29
Db &	17 SVDVILPDNTADVSLIYDTGTQYRFDEVVFFTIDPKTNQLTTDPDKLPVKRELLEQLLTV 396 :         :     :     :	337 324	D Q
מם מם גא	11 EVRGEGADDKAFTTVADEVPLLIGDVFHHGKYETKKNLIENASAEHGYFDGRWLDR 336 	281 271	DP QA
Bes Mat	11 IPHURQTALVAARAVGYYDIDLSIIRNSIGEVDVIIHDLGEPVYI	222	дь d
A; Exp C; Sup Que		166	, p 64
A; Sta A; Mol A; Res A; Cro	34 NPNDYIPEYOGEQPNSEVVVPPTLEPEKPGLIKRLYARLFNDGVNKVPRLKAKFY 188	134 114	Оу
Scier A; Tit	90 DDQSPISRIGEQSPPLGLDMSVIEETTPLSLEELFAQESTEMGI 133     :             : :  :   :    :  54 DDQALVQATRSLFKTGFFQDIQLGRDGNVLVVTVVERPSISSIEIEGNKAISKEDLLKGL 113	51 90	Db
C; Dat C; Dat C; Acc R; Bla	y Match Local Similarity 20.0%; Pred. No. 0.014; Local Similarity 20.0%; Pred. No. 0.014; hes 185; Conservative 111; Mismatches 327; Indels 302; Gaps 42;	Query M Best Lo Matches	
Qy Db RESUI A647 hypol	A;Status: preliminary A;Molecule type: DNA A;Residues: 1-797 <sto> A;Cross-references: GB:AE004784; GB:AE004091; NID:g9949799; PIDN:AAG07036.1; GSPDB:GN00 A;Experimental source: strain PA01 C;Genetics: A;Gene: PA3648 C;Superfamily: protective surface antigen D-15</sto>	A; Status: p A; Molecule A; Residues: A; Cross-ref A; Experimen C; Genetics: A; Gene: pA3 C; Superfami	0202222
Оу	A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path A;Reference number: A82950; MUID:20437337; PMID:10984043 A;Accession: H83190	Title: Refere Access	D D D 2
y Qy Cd	RESULT 32   RESULT 32 H83190 probable out C; Species: P C; Date: 15-S C; Accession: R; Stover, C. adman, S.; Y adman, S.; Y Native AG 66;	A · B R C C · P H R E	
Db Oy	78KIGAGVGVRWASPVGQVRVDVATGVKEE 905 :   ::    :  :    :: :  19 KDNLGLRASAGISIDWKSPMGPIRFDISRILSKE 752	87 71	Qy Db

	Db 571FINKGVLATRGHSQSUTLETTLPGSDLSFY 600
	QY 688 SLRYRLDKLKTQAPPETWQDLPVDFVNGKPSQEALLAGVAVHKTVADNLVNPMRGYRQRY 747
	Db 601 KIDYRGQVFAPLTDNYTMRF 620
v01)	748 SLEVGSSGLVSDANMAIARAGISGVYSFGDNAYGSNRAHOMTGGIQAGYIWSDNFNHVPY
1	Qy 808 RLRFFAGGDQSIRGYAHDSLSPISDKGYLTGG 839
Br ,im,	Db 639 YENYYAGGENSVRGFKDSTLGPRSTPSVARNPDGTPMKNQGPDSKGRYTDPDQDPBAFGG 698
thd	840
	Db 699 NILITGGAELLFPLPFVKDQRQLRTVLFWDVGSTFDTDCPTKTTTNCDGIKTDNLASSVG 758
	Qy 883 VGVRWASPVGQVRVDVATGVKEEGN 907
1001	Db 759 VGLTWITALGPLSFSLATPIKKPDN 783
	coli (strain K-12)
	17-Sep-1997 #text. och, C.A.; Perna, N of Escherichia coli 517; PMID:9278503 own; translation nc 1096; NID:91786370; ostrain MG1655 gen D-15
	Query Match 3.8%; Score 178; DB 2; Length 810; Best Local Similarity 17.7%; Pred. No. 0.03; Matches 161; Conservative 133; Mismatches 311; Indels 304; Gaps 37;
	QY 139 IPEYQGEQPNSEVVVPPTLEPEKPGLIKRLYARLFNDGVNKVPRLKA 185 :   :
	Qy 186 KFYQSSQSGETSAIGSSHQKTEPYANIKAALEDITQESAMDLNGSIPRL 234 : ::  : :  :  :    :
	Qy 235 RQTALVAARAVGYYDIDLSIIRNSIGEVDVIIHDLGEPVYIDYRAVEVRGEGAD 288
	ннс
	Db 180 INIVGNHAFTTDELISHFQLRDEVPWWNVVGDRKYQKQKLAGDLETLRSYYLDRGY 235
	QY 334 LDRSVDVILPDNTADVSLIYDTGTQYRFDEVVFFTIDPKTNQLTTDPDKLPVKRE 388
	Db 236 ARENIDSTQVSLTPDKKGIYVTVNITEGDQYKLSGVEVSGNLAGHSA 282
	389 LLEQLLTVNMGEAYNIQAVRALSNDLIATRYFNMVNT
	SSRTEPAQVDESTLEPVIETVELTDGILMDISPIEFSASNLIQ : :  :  : : :
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A; Experimental source: strain 015	QY 235 RQTALVAARAVGYYDIDLSIIRNSIGEVDVIIHDLGEPVYIDYRAVEVRGEGAD 288
A; Residues: 1-810 <sto></sto>	Db 97 ITFSGNKSVKDDMLKQNLEASGVRYGESLDRT-TTADIEKGLEDF 140
A; Status: preliminary	Oy 186 KFYQSSQSGETSAIGSSHQKTEPYANIKAALEDITQESAMDLNGSIPRL 234
A; Title: Genome sequence of enter A; Reference number: A85480; MUID: A:Accession: C85502	Db 46 MPVRTGDTVNDEDISNTIRALFATGNFEDVRVLRDGDTLLVQVKERPTIAS 96
<pre>iller, L.; Grotbeck, E.J.; Davis, Nature 409, 529-533, 2001</pre>	OY 139 IPEYQGEQPNSEVVVPPTLEPEKPGLIKRLYARLFNDGVNKVPRLKA 185
sion N.N.	Best Local Similarity 17.7%; Pred. No. 0.03; Matches 161; Conservative 133; Mismatches 311; Indels 304; Gaps 37;
C:Species: Escherichia coli	Gene: ECs0179 Superfamily: protective surface antigen D-15
ມ ກ	A:Cross-references: GB:BA000007; PIDN:BAB33602.1; PID:g13359635; GSPDB:GN00154 A:Experimental source: strain 0157:H7, substrain RIMD 0509952 C:GenetLcs:
Db 785 FSYAODFKK 793	A; Molecule type: DNA A; Residues: 1-810 <hay></hay>
006	A; Accession: C90651 A; Status: preliminary
	A: Reference number: A99639; WIID:21156231; PMTD:11258796
665	R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Bes 8 11-2 200
Qy 824 HDSLSPISDKGY	-Jul-2001 #text_cha
Db 605 DNEYYKVTLDTATYVPIDDDHKK	hypothetical protein ECs0179 [imported] - Escherichia coli (strain 0157:H7, substrain RIC; Species: Escherichia coli
Qy 777 DNAYGSNRAF	RESULT 34 C90651
Db 547 RYLYSMGEHPSTSDQDNSFK	
Qy 744 RQRYSLEVGSSGLVSDANMAI-	785 FSYAOPEKK
Db 509 YG	VDVATGVKE 904
Oy 687 YSLRYRLDKLKTQAPPETWQDLE	725 ISDKYANSYRTSFFWDMGTVWDTNWDSSQYSGYPDYSDPSNIRWSAGIALOWMSPLGPLY
Db 464 DYQTYAELSVTNPYFTVDGVSLC	. 00
Qy 627 GVKLYATKPLSHPLNDQLRATLO	:::   :
Db 417 KVKERNTGSFNFG	
Qy 567 QSKKVPLYVFVASDKPRDGQIGI	
Db 374 GAWLGSDLVDQGKERLNRLGI	777 DNAYGSNRAHOWTGGTOAGYTWSDNENHVDYRLREEAGGDOSTRGVA
Qy 507 DDRVLAINHDDGVNRSILGRISI	547 RYLYSMGEHDSTSDODDNSFKTDDFTENYGWTYNKLDRGYFDTDGSRVNLTGKVTIDGS
Db 331 ADKTVKLRVN	744 RORYSLEVGSSGLVSDANMAT
Oy 447 SSRTEPAQVDESTLEPVIETVE	509
Db 283 EIEQLTKIEPGELYNGTKVTKM	687 VST.BVRT.DKT.KTOADDETWODT DVDTVAGEDEDEATTACVA-VILKTVADVIT VADVEDOV
Qy 389 LLEQLLTVNMGEAYNLQAVRAL	
Db 236 ARFNIDSTQVSLTPDKKGIYVT	627 GVKLYATKDI SHPI NDOL RATI GYOO EVERGHST NGEDI STETT EHET SESTITONGGUNDT
Qy 334 LDRSVDVILPDNTADVSLIXDT	417 KVKERNTGSFNFGTGYGTESGYSFOAGVOODNWTGTGYAVGTNGTKN
Db 180 INIVGNHAFTTDELISHFQLRD	567 OSKKVPLYVEVASDKPRDGOIGLGWGSDTGTRLVTKFEHNLTNRDGYOAGAELBLSEDKK
Qy 289DKAFTTVADI	374 GAWLGSDLVDQGKERLNRLGFFETVDTDTORVPGSPDQVDVVY
Db 141YY	507 DDRVLAINHDDGVNRSILGRISDAVSAVARAILPDESENEVIDLPERTALANRKTPANVV
Ξ	Db 331 ADKTVKLRVNVDAGNRFYVRKIRFEGNDTSKDAVLRREMROME 373

	FSYAQPEKK 793	785	Ŭ
	VDVATGVKE 904	896	1
895 784	-NYEFMKDLRLAVFGDIGNAYDKGFTNDTKIGAGYGYRWASPYGQVR::::	850 725	•
724	ECATQDGAKDLCKSDDAVGGNAMAVASLEFITPTPF	665	0
84.0		824	•
823 664	DNAYGSNRAHQMTGGIQAGYIWSDNENHVPYRLRFFAGGDQSIRGYA	777 605	0 ~
604	RYLYSMGEHPSTSDQDNSFKTDDFTFNYGWTYNKLDRGYFPTDGSRVNLTGKVTIPGS	547	0
776		744	_
546	YGTDVTLGFPINEYNSLRAGLGYVHNSLS-NMQPQVAMW	509	0
743		687	_
508	DYQTYAELSVTNPYFTVDGVSLGGRLFYNDFQADDADLSDYTNKS	464	U
686	RSIIQNGGWNRT	627	~
463	KVKERNTGSFNFGIGYGTESGVSFQAGVQQDNWLGTGYAVGINGTKN	417	O
626	GTRLVTKFEHNLINRDGYQAGAELRLSEDKK	567	~
416	GAWLGSDLVDQGKERLNRLGFFETVDTDTQRVPGSPDQVDVVY	374	O
566	DDRVLAINHDDGVNRSILGRISDAVSAVARAILPDESENEVIDLPERTALANRKTPADVY	507	~
373	ADKTVKLRVNAVDAGNRFYVRKIRFEGNDTSKDAVLRREMRQME	331	0
506	SPIEFSASNLIQDKLNLVAAKARHLYDMP	447	~
330		283	0
446	LLEQLLTVNMGEAYNLQAVRALSNDLIATRYFNMVNTEIVFPEREQIQNDQVSFEQSS	389	~
282	ARENIDSTQVSLTPDKKGIYVTVNITEGDQYKLSGVEVSGNLAGHSA	236	0
388	DPKTNQLTTDPDKLPVKRE	334	~
235	INIVGNHAFTTDELISHFQLRDEVPWWNVVGDRKYQKQKLAGDLETLRSYYLDRGY	180	σ
333		289	~
179		141	σ

hypothetical protein yaeT [imported] - Escherichia coli (strain O157:H7, substrain ED C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: C85502
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: C85502
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-810 <STO>
A;Cross-references: GB:AE005174; NID:912512902; PIDN:AAG54479.1; GSPDB:GN00145; UWGP: A;Experimental source: strain O157:H7, substrain EDL933

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A;Gene: yaeT
C;Superfamily: protective surface antigen D-15
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Best Local Similarity
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FSYAQPFKK 793
                                                                                                           SNTIGPKAVYFPHQASNYDPDYDYECATQDGAKDLCKSDDAVGGNAMAVASLEFITPTPF '724
                                                                                                                                               HDSLSPIS----
                                                                                                                                                                        DNEYYKVTLDTATYVPIDDDHKWVVLGRTRWGYGDGLGGKEMPFYENFYAGGSSTVRGFQ 664
                                                                                                                                                                                                    DNAY------GSNRAHQMTGGIQAGYIWSDNFNHVPYRLRFFAGGDQSIRGYA 823
                                                                                                                                                                                                                                   RYLYSM--GEHPSTSDQDNSFKTDDFTFNYGWTYNKLDRGYFPTDGSRVNLTGKVTIPGS
                                                                                                                                                                                                                                                                    RQRYSLEVGSSGLVSDANMAI -----
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                                                                                                                                                                                                                                                                                                                                                                                   GVKLYATKPLSHPLNDQLRATLGYQQEVFGHSTNGFDLSTRTLEHEISRSIIQNGGWNRT 686
                                                                                                                                                                                                                                                                                                                                                                                                                                            QSKKVPLYVFVASDKPRDGQIGLGWGSDTGTRLVTKFEHNLINRDGYQAGAELRLSEDKK 626
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                          VDVATGVKE 904
                                                   ISDKYANSVRTSFFWDMGTVWDTNWDSSQYSGYPDYSDPSNIRMSAGIALQWMSPLGPLV 784
                                                                                 -NYEFMKDLRLAVFGDIGNAYDKGF-----TNDTKIGAGVGVRWASPVGQVR 895
                                                                                                                                                                                                                                                                                                                                                        DYQTYAELSVTNPYFTVDGVSLGGRLFYNDFQADDADLSDYT
                                                                                                                                                                                                                                                                                                                                                                                                                   KVKERNTGSF-----NFGIGYGTESGVSFQAGVQQDNWLGTGYAVG----INGTKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----DKAFTT------VADEVPL--LIGDVFHHGKYETKKNLIENASAEHGYFDGRW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MPVRTGDTVNDEDI------SNTIRALFATGNFEDVRVLRDGDTLLVQVKERPTIAS
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                                                                                                                                                                                                                                                                                             ---DKGY---
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                                                                                                                                            ---LTGGQVLAVGTAEY-----
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A;Molecule type: DNA
A;Residues: 1-778 <AQF>
A;Cross-references: GB:AE000733; NID:g2983720; PIDN:AAC07292.1; PID:A;Experimental source: strain VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             outer membrane protein - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C;Accession: C70412
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A; Gene: omp
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V.
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Local Similarity 19.9%; Pred. No. 0.03;
nes 179; Conservative 122; Mismatches
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NMAIARAG-----ISGVYSFGDNAYGSNRAHQMTGGIQAGYIWSDNFNHVPYRLRF
                                        QRVKYSDIDPEASTYVKEQ----AGRRDSRKIFFTLTRDTRDY---YLLPTKGSLFVFRN
                                                                              PPETWQDLPVDFVNGKPSQEALLAGVAVHKTVADNLVNPMRGYRQRYSLEVGSSGLVSDA
                                                                                                                                                               LRATLGYQQEVFGHSTNGFDLSTRTLEHEISRSIIQNGGWNRTYS---LRYRLDKLKTQA
                                                                                                                                                                                                        QFSVGLSYNEVTGLAGFIELRKGNFRGTGDIAGISVSYG-----SLYRNNAIS-----
                                                                                                                                                                                                                                              DGQIGLGWGSDTGTRLVTKFEHNLINRDGYQAGAELRLSEDKKGVKLYATKPLSHPLNDQ
                                                                                                                                                                                                                                                                                                                             VSAVARAILPDESENEVIDLPERTALANRKTPADVYQSKKVP-----LYVFVASDKPR
                                                                                                                                                                                                                                                                                                                                                                    -GKPVYVKKIKIKGNYETRD--YVIRREMR-----VQENELALK--KGIERS------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PER------EQIQN------DQVSFEQSSSS---RTEPAQVDESTLEPVIETVELT
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                                                                                                                         ----YTRKWFLKKPVDLDLSAFDRRIEYDTYTVERTGFSVALSKELSEYWRASIGTSI
                                                                                                                                                                                                                                                                                       -----QIEPVPRRDAWWDLLVKIRERFTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NERKGRYFRREVIEKIKNRIREKYAEIGFLNTSVEERVNVNPEKKEVSVLLKIIE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KNEGFLEVEVSYEVKEEGPARKVIVKVKEGPRYKLKEIKIEGNTLFA--YSELVDNILKK 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----KLPVKRELLEQ-----LLTVNMGEAYNLQAVRALSNDLIATRYFNMVNTEIVF
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surface antigen VC2252 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C;Species: Vibrio cholerae
C;Date: 1B-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: B82099
C;Accession: B82099
C;Accession: B82099
C;Accession: B82099
C;Accession: Day F:; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R. Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers
C, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: B82099
A;Accession: B82099
A;Accession: B82099
A;Accession: B82095
A;Accession: B82095
A;Accession: GB:AE004297; GB:AE003852; NID:99656810; PIDN:AAF95396.1; GSPDB:GNA;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
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C:Superfamily: protective surface antigen D-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genetics:
391 RLGFFETVEVQTVRVPGSEDQV-DL------VYSVKEA-----NSG
                                                                                                                                                                      338 VVHVEAGKRVYVRDIRFVGNNSTRDEV-----LRREMRQMEGSWLNSKDIETGKTR--LN
                                                                                                                                                                                                                                                                    300 AVTRLEESV-------KKVLGESGYAYPQ---VRTIPEFDDEK--QOVSL 337
                                                                                                                                                                                                                                                                                                                  406 AVRALSNDLIATRYFNMVNTEIVFPEREQIQNDQVSFEQSSSSRTEPAQVDESTLEPVIE 465
                                                                                                                                                                                                                                                                                                                                                                                                              347 -ADVSLIYDTGTQYRFDEVVFFTIDPKTNQLTTDPDKLPVKRELLEQLLTVNMGEAYNLQ 405
                                                                                                                                                                                                                                                                                                                                                                     253 GVYITLNLNEGEPYTVSKVQF-------RGELMGKEAEFTSLIPFEIGETYNGS 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               294 TVADE---VPLLIGDVFHHGKYETKKNLIENASAEHGYFDGRWLDRSVD----VILPDNT 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  148 NATVKAVVTPLPRNRADLKFVFTEGVSAKIQQINFIGNQVFSDEELLSRFNLNVDVAWWN 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             139 IPEYQGEQPNSEVVVPPTLEPEKPGLIKRLYA-----RLFNDGVNKVPRLK----- 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           722 ADK--WSDFKLSNFRGGYGIGVRIITPFAPIRIDWAFKTKTVPGDTNRSRIHFVLGTFF 778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         869 YDKGFTNDTKI-----GAGVGVRWASPVGQVRVDVATGVKE---EGNPIKLHFFIGTPF 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        605 SYGYGLLGGDEKFYKFEVEGAKYFSDTYFDTGIILSLKG--EYGFVEGYGGKKVPIDERF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
                                                                                                                     RISDAVSAVARAILPDESENEVIDLPERTALANRKTPADVYQSKKVPLYVFVASDKPRDG 585
                                                                                                                                                                                                                   TVELTDGILMDISPIEFSASNLIQDKLNLVAAKARHLYDMPDDRVLAINHDDGVNRSILG 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FLADDKYKKOVLAGDIEALRTY------YLDRGYLKFQVDSTQVAISPDKK 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RQTALVAARAVGYYDIDLS-IIRNSIGEVDVIIHDLGEPVYIDYRAVEVRGEGADDKAFT 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VSFSGNKAIKEEQLKQNLEASSIRVGEALDRT-TLSNIEKGLEDFYY-----SVGKY 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------AKFYQSSQSGETSAI--GSSHQKTEPYANIKAALEDITQESAMDLNGSIPRL 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MPVRVGDSVDSQDVA-----NTIKALYSSGNFEDVKVLRDGNTLMVQVKERPTIAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.8%; Score 177.5; DB 2; Length 803; liarity 19.4%; Pred. No. 0.032; Conservative 128; Mismatches 340; Indels 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 0.03
B; Mismatches
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S, F	VGLQQDNFLGSGNRVGVNAN LGYQQEVFGHS-TNGFDLS1 :	
7.S., T	627 LLRGRLGYGNGYGOTDGKDNLFPPYENFYAGGFTSLRGFGSNSAGPKAVYRDYSGSNNGS  836 LTGQVLAVGTAEYNYEFMKDLRLAVF	
N001	surface antigen D-15 precursor - Haemophilus influenzae (type Haemophilus influenzae type b Jun-1995 *sequence_revision 14-Jul-1995 *text_change 29-Sep-195.; JC005more, S.; Chong, P.; Thomas, W.R. [7-99, 1995] [8 esquencing of the 80-kDa D15 protective surface antigen of Homber: JC4078; MUID:95255676; PMID:7737523] [8 esquencing of the 80-kDa D15 protective surface antigen of Homber: JC4078; MUID:95255676; PMID:7737523] [8 esquencing of the 80-kDa D15 protective surface antigen D-15 *surface antigen D-15 surface antigen D-15 surface antigen D-15 surface antigen b-15 *status predicted <mat></mat>	<b>⊬</b>
	Query Match Query Match Query Match Query Match Best Local Similarity 19.8%; Pred. No. 0.069; Matches 158; Conservative 121; Mismatches 305; Indels 215; Gaps 39;  Qy 263 DVIIHDLGEPVYIDYRAVEVRGEGA-DDKAFTTVADEVPLLIGDVFHHGKYETK 315	
	Qy 426 EIVFPEREQIONDQVSFEQSSSSTTEPAQVDESTLEPVIETVELTDG 472	

Qy	\$ 8	Qу	Qу	Que Bes Mat	A;Reference A;Accession A;Status: p A;Molecule A;Residues: A;Cross-ref A;Experimen C;Genetics: A;Gene: aq_	V. Nature 3	RESULT D70304 hypoth C; Spec C; Date C; Acces	Qy Db	Db Qy	ОУ	Db Qy	Оy	Оy	Db Qy	Db Qy	ДЬ
335	7	222 91	169 39	Query Matc Best Local Matches 1	Reference no Accession: D Accession: D Status: prel Molecule typ Residues: 1- Cross-refere Experimental Genetics: Gene: aq_050	e 392,	T 39 4 hetic cies: cies: e: 08 e: 08 kert,	903 779	863 719	828 661	770 608	714 566	665 518	609 458	565 409	4-
NLYFLEDIQFEGVKKLQKKELIKASGLVIGSIFDIDKVEDAEENLENFYRKKGFFE 205 DRSVDVILPDNTADVSLIYDTGTQYRFDEVVFFTIDPKTNQLTT 378	YRAVEVRGEGADDKAFTTVADEVPLLIGDVFHHGKYETKKNLIENASAEHGYFDGRWL	ESAMDLNGSIPRLRQTALVAARAVGYYDIDLSIIRNSIGEVDVIIHDLGEDV-YID 276 :: :     :   :   :   :   :   :   :   :	YARLFNDGVNKVPRLKAKFYQSSGETSATGSSHQKTEPYANIKAALEDITQ 221   :: ::  ::  :	Match 3.6%; Score 171; DB 2; Length 853; Ocal Similarity 19.4%; Pred. No. 0.082; s 179; Conservative 136; Mismatches 325; Indels 284; Gaps 47;	number: A70300; MUID:98196666; PMID:9537320 : D70304 reliminary; nucleic acid sequence not shown; translation type: DNA 1-853 <aof> erences: GB:AE000671; NID:g2982793; PIDN:AAC06430.1; PID: tal source: strain VF5</aof>	1990 Of the homest believed to the transfer of the homest believed to the transfer of the homest believed to the transfer of the homest believed to the homest b	S -1998 #text_change 05-Nov-1999	KEEGNPIKLHFFIGTPF 919	GDIGNAYDKGFTNDTKIGAGVGVRWASDVGQVRVDVATGV 902	SPISDKGYLTGGQVLAVGTAEYNYEFMKDLRLAVF 862	SGYYSFGDNAYGSNRAHQMTGGIQAGYIWSDNFNHVPYRLRFFAGGDQSIRGYAHDSL 827 	NGKPSQEALLAGVAVHKTVADNLVNPMRGYRQRYSLEVGSSGLVSDANMAIARAGI 769 	STRTLEHEISRSIIQNGGWNRTYSLRYRLDKLKTQAPPETWQDLPVDFV 713:	NRDGYQAGAELRLSEDKKGVKLYATKPLSHPLNDQLRATLGYQQEVFGHS-TNGFDL 664 ::	VYQSKKVPLYVFVASDKPRDGQIGLGWGSDTGTRLVTKF-EHNLI 608   :	LRFEGNTVSADSTLRQEMRQQEGTWYNSQLVELGKIRLDRTGFFETVENRIDPINGSNDE 408

Оу	Qy	Qу Дъ	Qy Db	Qу	Qy Db	Qy Db	Qу	Qу	Oy Db	Qy Db	Оy	Db
897 828	841 770	782 737	733 682	674 640	619 585	568 539	535 481	487 422	457 362	427 302	379 247	206
DVATGVKE-EGNPIKLHFFIGTPF 919  :  :::	VLAVGTAEYNYEFMKDLRLAVFGDIGNAYDKGFTNDTK-IGAGVGVRWASPVGQVRV 896 :	SNRAHOMTGGIOAGYIWSDNENHVPYRLRFFAGGDQSIRGYAHDSL-SPISDKGYLTGGQ 840 : :	ADNLVNPMRGYRORYSLEVGSSGLVSDANMAIARAGISGVYSFGDNAYG 781	SRSIIQNGGWNRTYSLRYRLDKLKTQAPPETWQDLPVDFVNGKPSQ-EALLAGVAVHKTV 732 :	LRLSEDKKGVKLYATKPLSHPLNDOLRATLGYQQEVFGHSTNGFDLSTRTLEHEI 673	SKKVPLYVFVASDKPRDGQIGLGWGSDTGTRLVTKFEHNLINRDGYQAGAE 618   :	ARA-ILPDESENEVIDLPERTALANRKTPADVYQ 567 : ::    ::     ::     : :     : :     ::     ::     ::	LIQDKLNLVAAKARHLYDMPDDRVLAINHDDGVNRSI-LGRISDAVSAV 534   :   :	ESTLEPVIESV 486	IVFPEREQIQND QVSFEQSSSSRTEPAQV 456	DPDKLPVKRELLEQLITVNMGEAYNLQAVRALSNDLIATRYFNMVNTE 426	:    :    :    :    :    :    :    :

RESULT 40
AD2445
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C; Species: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C; Species: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C; Accession: AD2445
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C; Accession: AD2465
C; Accession: AD2465
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamadda, M.; Yasuda, M.; Tabata
A, Res. 8, 205-213, 2001
A; Accession: AD2465
A; Residues: 1-588 KUR>
A; Cross-references: GB:BA000019; PIDN:BAB76815.1; PID:g17134254; GSPDB:GN00179
A; Experimental source: strain PCC 7120
C; Gene: al15116

Sear Job	B 6	99	B 5	P 64	PP Oy	Db Qy	g 64	DP OA	pp Oy	Db Qy	9 6	Ma Ma
ch cor time	861 519	814 464	781 408	730 362	686 321	627 267	567 248	507 200	148	396 88	338 28	Query Ma Best Loo Matches
Search completed: April 28, 2003, 16:24:05 Job time : 74 secs	VFGDIGNAYDKGFTNDTKIGAGVGVRW 887         ::     :  !  !    PFIDIGTGWNTQGSNPSPSTFVGTGLGLLW 548	GDDQSIRGYAHDSLSPISDKGYLTGGQV-LAVGTAEYNYEEMKDLRLA 860      :    :       :    :    :    :	GSNRAHQMTGGIQAGYIWSD-NFNHVPYRLREFA	KTVADNLVNPMRGYRORYSLEVGSSGLVSDANMAIARAGISGVYSFGDNAY 780	TYSLRYRLDKLKTQAPPETWQDLPVDFVNGKPSQEALLAGVAVH 729	GVKLYATKPLSHPLNDQLRATLGYQQEVFGHSTN-GFDLSTRTLEHEISRSIIQNGGWNR 685	QSKKVPLYVFVASDKPRDGQIGLGWGSDTGTRLVTKFEHNLINRDGYQAGAELRLSEDKK 626 :	DDRVLAINHDDGVNRSILGRISDAVSAVARAILPDESENEVIDLPERTALANRKTPADVY 566	RTEPAQVDESTLEPVIETVELTDGILMDISPIEFSASNLIQDKLNLVAAKARHLYDMP 506 	VNMGEAYNLQAVRALSNDLIATRYFNMVNTEIVFPEREQIQNDQVSFEQSSSS 448   : : : : : :	VDVILPDNTADVSLIYDTGTQYRFDEVVFFTIDPKTNQLTTDPDKLPVKRELLEQLLT 395	Query Match 3.6%; Score 170.5; DB 2; Length 588; Best Local Similarity 19.0%; Pred. No. 0.047; Matches 120; Conservative 87; Mismatches 234; Indels 189; Gaps 24;

8

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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length: 2000000000
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Gapop 10.0 , Gapext 0.
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4727
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     SwissProt_40:*
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      Length
   DB
                                                          FATZ_HUMAN
TRX_DROME
CLPB_HAEIN
YD86_SCHPO
HS75_KLUMA
RA50_THEAC
RPOB_UREPA
SCA4_RICFE
PGCV_RAT
SLAP_BACCI
                                                                                                                                                                                                                                       BCC1_ACEXY
YDF6_SCHPO
SCA4_RICAD
SCA4_RICPR
ACE7_HUMAN
G6PD_STRPN
IF38_ARATH
FRPA_NEIMC
MAPX_DROME
DPO1_BACSU
DSG3_HUMAN
RBP1_PLAVB
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BCSC_PSEFL
P200_MYCPN
ASA1_ENTFA
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           P44038
P39320
O32629
P39170
 200798
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                                B thermoplasm
cureaplasma
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rickettsia
rattus norv
bacillus ci
neisseria m
drosophila
                                                                                                                                homo sapien
drosophila
haemophilus
schizosacch
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7 streptococc
0 arabidopsis
9 b tyrocidin
                                                                                                                                                                                                                                                                      8 haemophilus
0 escherichia
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0 escherichia
4 haemophilus
5 haemophilus
5 acetobacter
8 acetobacter
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8 rickettsia
9 rickettsia
          bacillus su
homo sapien
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enterococcu
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This SWISS-PROT entry is copyright between the Swiss Institute of Bilthe European Bioinformatics Institutes by non-profit institutions; modified and this statement is not entities requires a license agreem or send an email to license edsb-silones.  EMBL; U32752; AAC22357.1;  EMBL; U32752; AAC22357.1;  TIGR; HI0698;  TIGR; HT0698;  TIGR; HT060184; Bac_surfag_D1: pfam; PF01103; Bac_surface_Ag; 1.  Signal; Complete proteome. POTENT CHAIN 23 578 PROTEST CHAIN 23 578 PROTEST CHAIN 34F3	[1] SEQUENCE FROM N.A. STRAIN-Rd / KW20 / ATCC 51907 MEDLINE-95350630; PubMed-7547 Fleischmann R.D., Adams M.D., Kerlavage A.R., Bult C.J., TG MCKenney K., Sutton G., Fitzl Scott J.D., Shirley R., Liu I Weidman J.F., Phillips C.A., Utterback T.R., Hanna M.C., N Fine L.D., Fritchman J.L., Fr Gnehm C.L., McDonald L.A., Sn Venter J.C.; "Whole-genome random sequenci Rd."; Science 269:496-512(1995). [2] IDENTIFICATION BY MASS SPECTF MEDLING-20137488; PubMed-1067 Langen H., Takacs B., Evers S Gray C., Fountoulakis M.; "Two-dimensional map of the p Electrophoresis 21:411-429(20) -1-SIMILARITY: STRONG, TO E.	LT 1  _HAEIN _YTFM_HAEIN _P44038; 01-NOV-1995 ( 01-NOV-1995 ( 15-JUN-2002 ( 15-JUN-2002 ( 16-JUN-2002 ( 16-JUN-2002 ( 16-JUN-2002 ( 16-JUN-2002 ( 16-JUN-2002 ( 18-JUN-2002 ( 18-JUN-200	126.5 126.5 126.5 126.5 126.5 125.5 125.5 125.5 125.5 125.5 125.5 125.5
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Query Match

9.2%; Score 436.5;

DB 1; Length 578;

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Hypothetical protein ytfM precursor.
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MEDLINE-21156231; PubMed=11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoya Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T IIda T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunag Kuhara S., Shiba T., Hattori M., Shinagawa H.;

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DNA Res. 8:11-22(2001).
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Hypothetical protein; Signal; Complete proteome.

SIGNAL 1 21 POTENTIAL.
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MEDLINE-21074935; PubMed-11206551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE000493; AAC77177.1; -. EMBL; AE005654; AAG59418.1; -. EMBL; AP002568; BAB38621.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U14003; AAA97116.1; -.
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Nucleic Acids Res. 23:2105-2119(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                   GYFDGRWLDRSVDVILPDNTADVSLIYDTGTQYRFDEVVFFTIDPKTNQLTTDPDKLPVK 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VTPGVPVLIGGTDVVLRGGARTDKDYLKLLDTRP-AIGTVLNQGDYENFKKSLTSIALRK 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HDLGEPVYIDYRAVEVRGEGADDKAFTTVADEVPLLIGDVFHHGKYETKKNLIENASAEH 326
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                               DDRVLAINHDDGVNRSILGRISDAVSAVARAILPDESENEVIDLPERTALANRKTPADVY
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                                                                                                                                                                                                                                          DEYLQNLVPFKEGDEYESKDLAELNRRLSATGWFNSV----VVAPQ
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00; Mismatches
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  Matches
                            Query Match
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STRAIN-PAK 12085;
MEDLINE-97427952; Pubmed-9284140;
MEDLINE-97427952; Pubmed-9284140;
                                                                              InterPro: IPR000184; Bac_surfAg_D15.
Pfam; PF01103; Bac_surface_Ag; 1.
Antigen; Outer membrane; Signal.
SIGNAL 1 19 POTENTI
                                                        SEQUENCE
                                                                                                                                     EMBL; U60834; AAB61977.1; -
                                                                                                                                                             use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                              species and may represent a universal protective antigen invasive disease.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Protective surface antigen D15 precursor (80
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (D-15-Ag) (Outer membrane protein D15). Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                         Outer membrane protein D15 is conserved among
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                Local Similarity
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                                                                                                                                                                                                                                                                 act. Immun. 65:3701-3707(1997).
SUBCELLULAR LOCATION: Outer membrane.
SIMILARITY: BELONGS TO THE SURFACE ANTIGEN D15 FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DIGNAYDKGFTNDTKIGAGVGVRWASPVGQVRVDVATGV--KEEGNPIKLHFFIG
  159;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DSGEAVSDIRRSDFKTGTGVGVRWESPVGPIKLDFAVPVADKDEHG----LQFYIG 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KVPPDLRFFAGGDRSIRGYKYKSIAPKYANGDLKGASKLITGSLEYQYNVTGKWWGAVFV
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793 AA;
  Conservative
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87511 MW;
               20.1%;
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  121;
              Score 180.5;
Pred. No. 0.
                                                  POTENTIAL.

PROTECTIVE SURFACE ANTIGEN D15.

5 518FDB2036801A14 CRC64;
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  Mismatches
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               0.015;
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207;
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Gaps
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                                                                                                       UP05_ECOLI STANDARD; PRT; 810 AA. P39170; P39181; P77465; 01-FEB-1995 (Rel. 31, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Unknown protein from 2D-page spots M62/M63/O3/O9/T35 YAET OR B0177 0.7 2018 OR ECS0179.
                                                                                                                                                                                                                                        ECOLI
                                                                               Escherichia coli, and Escherichia coli 0157:H7.
SEQUENCE FROM N.A.
                               NCBI_TaxID=562,
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                                                             Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                                                                                                       NPIKLHFFIGTPF
                                                                                                                                                                                                                                                                                                                                                                       WNTKWKSDKNGLESKVLKDLPDYGKSSRIRASTGVGFQWQSPIGPLVFSYAKPIKKYEND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SP---ISDKGYLT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGVYSFGDNAYGSNRAHQ--MTGGIQAGYIWSDNFNHVPYRLRFFAGGDQSIRGYAHDSL 827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRT----LEH---EISRSIIQNGGWNRT---YSLRYRLDKLKTQAPPETWQDLPVDFV 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TKNDYGTSVNLGYTEPYFTKDGVSLGGNIFFENYDNSKSDTSSNYKRTTYGSNVTLGFPV 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NRDGYQAGAELRLSE---DKKGVKLYATKPLSHPLNDQLRATLGYQQEVFGHS-TNGFDL 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VDVVYKVK-----ERNTGSINFGIGYGTESGISYQTSIKQDNFLGTGAAVSIAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GNE-SYSSSTLQEQMELQPDSWWKLWGNKFEGAQFEKDLQAIR-----DYYLNNGYA 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NGKPSQEALLAGVAVHKTVADNLVNPMRGYRQRYSLEVGSSGLV----SDANMAIARAGI 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NENNSYYVGLGHTYNKISNFALE---YNRNLYIQSMKFKGNGIKTN-------DFDFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --- VYQSKKVPLYVFVASDKPRDGQI--GLGWGSDTGTRLVTKF-EHNLI------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          {\tt KAQITKTDVQLNDEKTKVNVTIDVNEGLQYDLRSARIIGNLGGMSAELEPLLSALHLNDT}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TNQLTTDPDKLPVKRELLEQLLTVNMGEAY-----NLQAVRALSNDLIATRYFNMVNT 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LNEFAKSVKEHYASVGRY-NATVEPIVNTLPNNRAEILIQINEDDKAKLASLTF-----K 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KNLIENASAEHGYFDGRWLDRSVDVI---LPDNTADVSLIYDTGTQYRFDEVVFFTIDPK 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DVKAHQEGDVLVVSVVAKSIISDVKIKGNSVIPTEALKQNLDANGFKVGDVL----IREK 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DVIIHDLGEPVYIDYRA-----VEVRGEGA-DDKAFTTVADEVPLLIGDVFHHGKYETK 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         I-LMDISPIEFSASNLIQDKLNLVAAKARHLYDMPD----DRVLAINHDDGVNRSIL---
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                                 83334;
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                                                               gamma
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                                                               subdivision;
                                                               Enterobacteriaceae,
                                                                                                                                precursor
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Query Match
Best Local Similarity
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STRAIN-0157:H7 / RIMD 0509952;

MEDLINE-21156231; PubMed=11258796;

MEDLINE-21156231; PubMed=11258796;

Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunag Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";

DNA Res. 8:11-22 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schramm S., Duncan M. Davis K., Federspiel Lashkari D., Lew H.,
                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                         STRAIN-K12 / MC1655;
MEDLINE-97426617; PubMed-9278503;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F. Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                           SEQUENCE
                                                                                                   Outer membrane;
                                                                                                                             EcoGene; EG12676; yaeT.
InterPro; IPR000184; Bac_surfAg_D15
                                                                                                                                                                                                   EMBL; AE000127; AAC73288.1; -. EMBL; U70214; AAB08606.1; -.
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MEDLINE-97443975; PubMed-9298646;
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                                                                                                                                                           SWISS-2DPAGE;
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                                                                                                                                                                     U70214; AAB08606.1; -. AE005193; AAG54479.1; -. AP002550; BAB33602.1; -.
                                                                                                                 PF01103; Bac_surface_Ag;
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., Kalman S., Komp C., Kuro
ath A., Oefner P., Roberts
 NO.
3; DB 1;
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Tanaka M., Tobe T.,
awara N., Yasunaga T
             Length
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                           VDVATGVKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QSKKVPLYVFVASDKPRDGQIGLGWGSDTGTRLVTKFEHNLINRDGYQAGAELRLSEDKK 626
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                                                          ISDKYANSVRTSFFWDMGTVWDTNWDSSQYSGYPDYSDPSNIRMSAGIALQWMSPLGPLV
                                                                                         -NYEFMKDLRLAVFGDIGNAYDKGF------
                                                                                                                        SNTIGPKAVYFPHQASNYDPDYDYECATQDGAKDLCKSDDAVGGNAMAVASLEFITPTPF
                                                                                                                                                                                   DNEYYKVTLDTATYVPIDDDHKWVVLGRTRWGYGDGLGGKEMPFYENFYAGGSSTVRGFQ
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                                                                                         -TNDTKIGAGVGVRWASPVGQVR
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RESULT 5 D151_HAEIN ID D151_HAEIN AC P46024; DT 01_NOV-1995 DT 01-NOV-1995

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EMBL; U60833; A
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"The sequencing of the 80-kDa D15 protective surface antigen
Haemophilus influenzae.";
              349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene 156:97-99(1995).
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MEDLINE=95255676; PubMed=7737523;
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species and may represent a universal protective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Klein M.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
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European Bioinformatics Institute. There are no rest
by non-profit institutions as long as its content
ified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Outer membrane.
SIMILARITY: BELONGS TO THE SURFACE ANTIGEN D15 FAMILY.
LRFEGNTVSADSTLRQEMRQQEGTWYNSQLVELGKIRLDRTGFFETVENRIDPINGSNDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DVIIHDLGEPVYIDYRA-----VEVRGEGA-DDKAFTTVADEVPLLIGDVFHHGKYETK 315
                                                                                          FRRSDIADVE----NAIKAKLGERGYGSATVNSVPDFDDANKTLAITLVVDAGRRLTVRQ
                                                                                                                                      I-LMDISPIEFSASNLIQDKLNLVAAKARHLYDMPD----DRVLAINHDDGVNRSIL---
                                                                                                                                                                                       KAQITKTOVQLNDEKTKVNVTIDVNEGLQYDLRSARIIGNLGGMSAELEPLLSALHLNDT
                                                                                                                                                                                                                                   EIVFPEREQIONDOVSFEQSSSSRTEPAOVD-----ESTLEPVIETVELTDG
                                                                                                                                                                                                                                                                                    GNE-SVSSSTLQEQMELQPDSWWKLWGNKFEGAQFEKDLQSIR--
                                                                                                                                                                                                                                                                                                                                TNQLTTDPDKLPVKRELLEQLLTVNMGEAY-----NLQAVRALSNDLIATRYFNMVNT
                                                                                                                                                                                                                                                                                                                                                                               LNEFAKSVKEHYASVGRY-NATVEPIVNTLPNNRAEILIQINEDDKAKLASLTF----K
                                                                                                                                                                                                                                                                                                                                                                                                          KNLIENASAEHGYFDGRWLDRSVDVI---LPDNTADVSLIYDTGTQYRFDEVVFFTIDPK 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DVKAHQEGDVLVVSVVAKSIISDVKIKGNSVIPTEALKQNLDANGFKVGDVL~---IREK 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 19.8
58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immun.
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(Outer membrane proving influenzae.

Proteobar*
                                              ·GRISDAVSAVARAILPDES---ENEVIDLP----ERT----ALANRKTPAD-----
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AAB61974.1; -.
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87675 MW;
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D15 precursor (80 kDa
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Pred. No. 0.0
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PROTECTIVE SURFACE ANTIGEN D15

2 2F93DE538698AF1B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         215;
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RESULT 6
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                                                                                                                                                                                      Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O..
                     use by modified
                                                                                                          Science 269:496-512(1995).
-!- SUBCELLULAR LOCATION: Outer membrane.
-!- SIMILARITY: BELONGS TO THE SURFACE AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D152_HAEIN
P44935;
                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                 STRAIN=Rd / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
Fleischmann R.D., Adams M.D., White O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Protective surface antigen D15 precursor (80
                                                                                                                                                                                                                                                                                                                                                                                                                     Haemophilus
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                          Whole-genome random sequencing and
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pean Bioinformatics Institute. The
non-profit institutions as long
and this statement is not removed.
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                                                                                                                                                                          assembly of Haemophilus influenzae
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                           There are no restrictions ong as its content is in
                                                                                                             ANTIGEN D15 FAMILY.
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http://www.isb-sib.ch/announce/
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Antigen; Outer membrane; Signal; Complete proteome SIGNAL 1 19 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U32773; AAC22575.1; -. TIGR; HI0917; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000184; Bac_surfAg_D15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
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                                                                                                                                                 GPNATYAEHGNGNGTFKKISSDVIGGNAITTASAELIVPTPFVSDKSQNTVRTSLFVDAA
                                   EGNPIKLHFFIGTPF 919
                                                                                                           NAY-------DKGFTNDTKIGAGVGVRWASPVGQVRVDVATGVK--E 904
                                                                                                                                                                                                                       QGFYPL-----DRDHLWVVSAKASAGYANGFGNKRLPFYQTYTAGGIGSLRGFAYGSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NRDGYQAGAELRLSE----DKKGVKLYATKPLSHPLNDQLRATLGYQQEVFGHS-TNGFDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KNLIENASAEHGYFDGRWLDRSVDVI---LPDNTADVSLIYDTGTQYRFDEVVFFTIDPK 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DVKAHQEGDVLVVSVVAKSIISDVKIKGNSIIPTEALKQNLDANGFKVGDVL----IREK 127
                                                                                                                                                                                                                                                                                                                                                                                                          STRT----LEH---EISRSIIQNGGWNRT---YSLRYRLDKLKTQAPPETWQDLPVDFV 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRRSDIADVE - - - - NAIKAKLGERGYGSATVNSVPDFDDANKTLAITLVVDAGRRLTVRQ
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NDDVEQFQFSIGGSF
                                                                         SVWNTKWKSDKSGLDNNVLKSLPDYGKSSRIRASTGVGFQWQSPIGPLVFSYAKPIKKYE
                                                                                                                                                                                      SP---ISDKCY---
                                                                                                                                                                                                                                                            SGVYSFGDNAYGSNRAH--QMTGGIQAGYIWSDNFNHVPYRLRFFAGGDQSIRGYAHDSL
                                                                                                                                                                                                                                                                                                                                    NGKPSQEALLAGVAVHKTVADNLVNPMRGYRQRYSLEVGSSGLV----SDANMAIARAGI 769
                                                                                                                                                                                                                                                                                                                                                                       NENNSYYVGLGHTYNKISNFALE---YNRNLYIQSMKFKGNGIKTN-----DFDFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VDVVYKVK-----ERNTGSINFGIGYGTESGISYQASVKQDNFLGTGAAVSIAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----GRISDAVSAVARAILPDES---ENEVIDLP----ERT----ALANRKTPAD-----
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87478 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.5%; Score 167.5;
19.6%; Pred. No. 0.
                                                                                                                                                                                                                                                                                                 -NYNSLNRGYFPTKGVKASLGGRVTIPGSDNKYYKLSADV
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                                                                                                                                                                                      -LTGGQVLAVGTAE--YNYEFMKD----LRLAVFGDIG
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
Cellulose synthase 1 operon protein C precu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9WX63;
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- FUNCTION: Required for maximal bacterial cellulose synthesis.
may be involved in the formation of a membrane complex for
extrusion of the cellulose product (By similarity).
-!- PATHWAY: Bacterial cellulose biosynthesis.
-!- SUBCELLULAR LOCATION: Outer membrane (Potential).
-!- SIMILARITY: BELONGS TO THE ACSC/BGSC FAMILY.
-!- SIMILARITY: CONTAINS 8 TPR REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Cellulose
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InterPro; IPR001440; TPR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA Res. 6:109-115(1999-1-1-FUNCTION: Required
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Cloning of cellulose synthase genes from Acetobacter xylinum 7664: implication of a novel set of cellulose synthase genes." DNA Res. 6:109-115(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Umeda Y., Hirano A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=10382968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=JCM 7664 / IFO 13693;
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 192
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                                                                                                                                                                        43 PAHDTAIN--QAKAGNPPVLLTPEQIQARLNAAGL-NAKPQ------SQAL-----
                                                         PNDYIPEYQGEQPNSEVVVPPTLEPEKPGLIKRLYARLFNDGVNKVPRLKA--KFYQSS- 191
                                                                                     MEGLARLKDLQGFRTQAPVEAAAAAQSYRQTLSWLPVTAETQPLMQQWLTA------H
                                                                                                                                           PPHSLAIEYYQTMAGVP-----ADWDQARAGLAGLVAANPQDYRAQLAFAQTLTYNTSTR 219
 --QSGETSAIG----
                            PDD-----TALKEHMLHPPGGPPDKAGLARQAGFQQLNSG-----RLSAAEQSFQSAL
                                                                                                                ------DVVNFDDQSPI-SRIGEQSPPLGLD-MSVIEETTPLSLEELFAQESTEMGIN 134
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                                                                                                                                                                                                                   Similarity
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CELLULOSE SYNTHASE 1
TPR 1.
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precursor.
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                                                                                                                                                                                                      Indels 284;
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                                                                                                                       01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last seq
15-JUN-2002 (Rel. 41, Last ann
Cellulose synthase operon prot
                                                      Gluconacetobacter.
NCBI_TaxID=28448;
                                                                                                                                                                                                                                                                1013
 MEDLINE-91045951; PubMed-2146681;
                 STRAIN=1306-3
                            SEQUENCE FROM N.A.
                                                                                  Bacteria;
                                                                                             Acetobacter xylinus
                                                                                                                                                                               BCC1_ACEXY P19450;
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                                                                                                                                                                                                                                                                                     YNYEFMKDLRLAVFGDIGNAYDKGFTNDTKIGAGVGVRWASPVGQVRVDVATGVK
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                                                                                                                                                                                                                                                                                                                                           NFN-----HVPYRLRFFAGGDQSIRGYAH--DSLSPISDKGYL-----TGGQVLAVGTAE
                                                                                                                                                                                                                                                                                                                    DLNAGSVYDVP-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RQ--LIAAHQYTEAKQRLTSLARQPGQFTGATLMLADLQRTTGQIDASEQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RQTALVA-----ARAVGYY---DIDLSIIRNSIGEVDVIIHDLGEPVYIDY 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----WQDLPVDFVNGKPSQEA-----LLAGVAVH-KTVADNL---VNPMRGYRQ
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                                                                               Proteobacteria; alpha subdivision; Acetobacteraceae;
                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                           -GEAGFAPDVQFSN-SWVRADVG---ASPIGFPITNVLGGVE
                                                                                                                                                                                                                                                                                                                --- GTNMATEAYNQYVNSLSQNNSSSSLRTQQIQGGQ---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wong H.C.,
Amikam D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bruner R., Ben-Bassat A., Tal R., Genetic organization of the cellulose synthase operon in
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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Pfam; PF00515; TPR; 
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SIMILARITY: CONTAINS 9 TPR REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         extrusion of the cellulose product. PATHWAY: Bacterial cellulose biosynthesis. SUBCELLULAR LOCATION: Outer membrane (Pote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             c. Natl. Acad. Sci. U.S.A. 87:8130-8134(1990).
FUNCTION: Required for maximal bacterial cellulose
may be involved in the formation of a membrane comp
                                                                                                     GEVDVIIHDLGEPVYIDYRAVEVRGEGADDKAFTTVADEVPLLIGDVFHHGKYETKKNLI
                                                                                                                                    EQSFQ
                                                                                                                                                          GSSHQKTEPYANIKAALEDITQESAMDLNGSIPRLRQTALVAARAVGYYDIDLSIIRNSI
                                                                                                                                                                                                                                                                                   PPHSLAVEYYQTMAGVPAQWDQARAGLAGVVASNPQDYRAQLAFAQALTYNTSTRMEGLT
                                                                                                                                                                                                                                                                                                          PAHDTAI------NQAKAGNPPVLLT-PEQIQARL---NAAGLNAKPQSQAL-
                                  ----AAHQYTEAKQQLATLARQPGQYTGATLMLADLQRSTGQIAAAEQEYRGILSREPNN
                                                            ENASAEHGYFDGRW
                                                                                   GGMGLVSMRQGDTA--EARRYFEEAMAADPK----TADRWRPALAGMAVSGEYASVRQLI
                                                                                                                                                                                  PEYQGEQPNSEVVVPPTLEPEKPGLIKRLYARLFNDGVNKVPRLKAKFYQSSQSGETSAI 199
                                                                                                                                                                                                                                     RLKDLQSFRSQAPVEAAAAAQSYRQTLSWLPVNPETQPLMEQWLSA---
                                                                                                                                                                                                                                                          ---DVVNFDDQSPI-SRIGEQSPPLGLD-MSVIEETTPLSLEELFAQESTEMGINPNDYI 139
                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                    Conservative 131;
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Pred. No. 0.45;
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Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A. Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Browks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Eraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Horsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., James K., Jones M., Leather S., McDonald S., McLean J., Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                    Schizosaccharomyces pombe (Fission yeast)
Eukaryota; Fungl; Ascomycota; Schizosacch
Schizosaccharomycetales; Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TDF6_SCHPO STANDARD: PRT; 475 AA. Q10478; Q10478; Q1-0CT-1996 (Rel. 34, Created) Q1-0CT-1996 (Rel. 34, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Hypothetical protein C17C9.06 in chromosome I SPAC17C9.06.
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                                                                                                                                                                                                                                                                                                               STRAIN-972
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                          MEDLINE-21848401; PubMed-11859360;
                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4896
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RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller Auer S.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Borzym K., Cadieu E., Dreano S., Gloux S., Lehaure V., Mottier S.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lehaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RI Nature 415:871-880(2002).
RI Nature 415:871-880(2002).
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                                                                                              GFSEDRIGPKDGRDSLGGTAYMAFSMSLLFPLPKVDASKPFRLQLFANAG-----GLSNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  *Sekeyova Z., Roux V., Raoult D.;

*Phylogenetic analysis of Rickettsia spp. by comparing s 'gene D' coding for an intracytoplasmic protein.";

*Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

-!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Antigenic heat-stable 120 kDa protein (PS120)
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19.0%; Pred. No. 0.9
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O9ZD49; O9ZD48; O9AJ36;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Antigenic heat-stable 120 kba protein (PS120)
               SEQUENCE OF 11-1016 FROM N.A. Sekeyova Z., Roux V., Raoult D.; Supplied D.; Coding for an intracytoplasmic protein."; 'gene D' coding for an intracytoplasmic protein."; Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                MEDLINE=99039499; PubMed=9823893;
Andersson S.G.E., Zomorodipour A., Andersson J.O.,
Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M.,
Eriksson A.-S., Winkler H.H., Kurland C.G.;
"The genome sequence of Rickettsia prowazekii and the mitochondria.";
                                                                                                                                                                           Nature 396:133-140(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rickettsiaceae;
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LOCATION: Cytoplasmic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAUTION: REF.1 SEQUENCE DIF FRAMESHIFT IN POSITION 234.
                                  YATKPLSHPLND-----QLRATLGYQ-----QEVFGHST-----NGFDLSTR
EAPKKVSSLLNDISKRTIEKINNLRAMLSQDGNLKTFEEKKDEATKKVDELVKAFDNKSS
                                                                                                                                             V--ESKNDLLDRELITAGLVDGIYEAKGDNAVVHAISSMIANSNINQSEKEALKRSQDVV
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                                                                       SEKVLDKEIQNLDRELKAQNINESKLHDDIYNKTQDVANALKNVITTVLDDNSGQRGVSE
                                                                                                         SDKPRDGQI-GLGWGSDTGTRLVTKFEHNLINRDGYQAGA-----
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G -> R (IN REF. 2).
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Nakajima D., Nomura N., Ohara O.;

"Characterization of cDNA clones in size-fractionated cDN/
from human brain.";

DNA Res. 4:345-349(1997).

-!- FUNCTION: F-ACTIN-BINDING PROTEIN WHICH MAY PLAY A ROI
LINKING ACTIN TO OTHER CYTOSKELETAL PROTEINS. ALSO BIN
MICROTUBULES (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: CYTOPLASMIC.

-!- SUBCELLULAR LOCATION: CYTOPLASMIC.

-!- SIMILARITY: CONTAINS 1 ACTIN-BINDING DOMAIN.

-!- SIMILARITY: CONTAINS 2 CALPONIN-HOMOLOGY (CH) DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-2001)59; PubMed=10529403;
MEDLINE-2001)59; PubMed=10529403;
Okuda T., Matsuda S., Nakatsugawa S., Ichigotani Y.,
Takahashi M., Ishigaki T., Hamaguchi M.;
Takahashi m., Ishigaki T., Hamaguchi M.;
"Molecular cloning of macrophin, a human homologue of kakapo with a close structural similarity to plectin Blochem. Biophys. Res. Commun. 264:568-574(1999).
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Nagase T., Ishikawa K.-I., Kikuno
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MEDLINE=20026884; PubMed=10559237;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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                                                                                                                                                                                                                                                                                                                         "Prediction of the coding sequence complete sequences of 100 for large proteins in vitro.";
DNA Res. 6:337-345(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Brain;
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D., Nomura N., Ohara O.;
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AL137853;
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Q01082; IBI
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IPR001452; SH3.
IPR002017; Spectrin.
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IPR001715; Calponin-like.
IPR002048; EF-hand.
       :13664; MACF1
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37 SPECTRIN REPEATS
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             ---QLLTVNMGEAYNLQAVRALS----
                                     QEQKLLQRLLDDRKATVDMLQAEGGRI - -
                                                                                   WNTLNKKVAQRIAQLQEALLHCGKFQDALEPLLSWLADTEELIANQKPPSAEYKVVKAQI 3317
                                                                                                                                  EVEIINQQLADFKMFQKEQVDPLQMKLQQVNGLGQGLIQSAGKDCDVQGLEHDMEEINAR
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                                                                                                         FTT----VADEVPLLIGDVFHHGKYE-----TKKNLIEN---ASAEHGYFDGRW
                                                                                                                                                                                                                                                      KAKFYQSSQSGETSAIGSSHQKTEPYAN----IKAALED-----ITQESAMDLNG--
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                                                                                                                                                                                                                                                                                                     -----EQPNSEVVVPPTLEPEKPGL-----IKRLYARLEN----
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                                                           LDRS-VDVILPDNTADVSLIYDTGTQYRFDEVVFFTIDPKTNQLTTDPDKLPVKRELLE-
                                                                                                                                                                                                                                                                                                                              -----CSNKNLEKLRAQQEVLQALEPQVDYLRNFTQGLVEDAPDGSDASQLLHQAE 3032
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EF-HAND 1 (POTENTIAL).

EF-HAND 2 (POTENTIAL).

EF-HAND 2 (POTENTIAL).

POLY-SER.

4 X 4 AA TANDEM REPEATS OF [GS]-S-R-{AR}.

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MSSSDEETLSERSCRSERSCRSERSVRSVRVIV
-> MFPVLW

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V -> A (IN REF. 1).

E -> D (IN REF. 1).

E -> K (IN REF. 2).

M -> V (IN REF. 2).

C -> Y (IN REF. 1).

MISSING (IN REF. 2).

SILPSVG -> EYRLFKI (IN REF. 3).

Q -> R (IN REF. 2).

S -> T (IN REF. 2).

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O54537;
15-DEC-1998
SEQUENCE OF 281-433 FROM N.A.
MEDLINE-98192409; PubMed-9533725;
Coffey T.J., Enright M.C., Daniels M.,
Fenoll A., Spratt B.G.;
"Serotype 19A variants of the Spanish ;
clone of Streptococcus pneumoniae.";
Microb. Drug Resist. 4:51-55(1998).
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                                                                                                                                                                                                                    Streptococcus pneumoniae."; Mol. Microbiol. 27:73-83(1998).
                                                                                                                                                                                                                                                         Hryniewicz W., Paton J.C., Daniels M., Morona J.K., Morona R., Recombinational exchanges at the capsular polysaccharide biosynthetic locus lead to frequent serotype changes among natural isolates of Streptococcus neamon
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                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-ATCC 6323;
MEDLINE-98125733; PubMed-9466257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pneumoniae.
Science 293
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EMBL; 299802; CAB16927.1; -.
EMBL; 299865; CAB16990.1; -.
HSSP; P11411; IDPG.
TIGR; SP1243; -.
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Pfam; PF02781; G6PD_C; 1.
PRINTS; PR00079; G6PDHDRGNASE.
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1,5-lactone 6-phosphate + NADH.
-i- PATHMAY: Pentose phosphate pathway: first step-
-i- SIMILARITY: BELONGS TO THE GLUCOSE-6-PHOSPHATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-99065153; PubMed-9849901;
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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Eukaryota; Viridiplantae; Streptophyta; Embry,
Spermatophyta; Magnoliophyta; eudicotyledons;
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SUBUNIT: EIF-3 IS COMPOSED OF AT LEAST 10 DIFFERENT SUBUNITS
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 ISTQILFNRTMAQLGLCAF----
                           TGTQYRFDEVV-----FFTIDPKTNQLTTDPDKLPVKRELLEQLLTVNMGEAYNLQAV
                                                                                                                                     DIDLSIIRNSIGEVDVIIHDLGEPVYIDYRAVEVRGEGADDKAFTTVADEVP-----
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                                                                                                                                                                                                                                                                                                     SRAMMDILVSLIYRNGDERTKARAMLCDINHHALMDNFVTAR--DLLLMSHLQDNIQHMD
                                                                                                                                                                 -----IDPHT--REYVERLRDEPMFLALAQNIQDYFERMGDFKAAAKVALRRVEAIYY
                                                                                                                                                                                           IGSSHQKTEPYANIKAALEDITQES----AMDLNGSIPRL---RQTALVAARAVG--YY
                                                                                                                                                                                                                      -SNIVVDDTVEPDENETSKPTDYDGKI-----RVWGNLVAFLERVDTEFFKSLQC-----
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                                                                                                                                                                                                                                                                                                                                    il Similarity
156; Conserv
                                                                                -LLIGDVFHHGKYETKKNLIENASAEHGYFDGRWLDRSVDVILPDNTADVSLIYD
                                                                                                                                                                                                                                                                                                                                                                                        factor; Protein
900 AA; 102989
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(Rel. 39, Last sequence up
(Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                           EVYDAMRKLAELVEEEEETEEAKEESGPPTSFIVVPEVVPRKPTFPES
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20.1%;
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mw; 3C03FEDBF59AB5D1
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Pred. No. '
 -RAGMITESHSCL---
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tation update)
initiation factor 3 subunit
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                                                                                                                                                                                                                                                                                                                                                           Length 900;
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SELYFGQRV
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                                                                                                                                                                                                                                               internal adenylation domains.";
J. Bacteriol. 179:6843-6850(1997).
-i- FUNCTION: INCORPORATES SIX AMINO ACIDS (FOR TYROCIDINE A, ASN, GLN, TYR, VAL, ORN, AND LEU) IN THEIR L-CONFIGURATION INTO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      adenylase (AsnA)
adenylase (GlnA)
adenylase (TyrA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-2002 (Rel. 41, Last annotation update)
Tyrocidine synthetase II [Includes: ATP-dependent asparagine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BACBR
                    -
                                                                                                                                                                                                              PEPTIDE PRODUCT.
-!- COFACTOR: CONTAINS 6 COVALENTLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus brevis.
Racteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               adenylase (AsnA) (Asparagine activase); ATP-dependent glutamine adenylase (GlnA) (Glutamine activase); ATP-dependent tyrosine adenylase (TyrA) (Tyrosine activase); ATP-dependent valine adenylase (ValA) (Valine activase); ATP-dependent ornithine adenylase (OrnA) (Ornithine activase); ATP-dependent leucine adenylase (LeuA) (Leucine
                                                                                                                                                                                                                                                                                                                   "The tyrocidine biosynthesis operon of Bacillus brevis: Complete nucleotide sequence and biochemical characterization of functional
                                                                                                                                                                                                                                                                                                                                                                        STRAIN=ATCC 8185;
MEDLINE=98012987; PubMed=9352938;
                                                                                                                                                                                                                                                                                                                                                           Mootz
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                                               PATHWAY: Cyclic peptide antibiotic tyrocidine biosynthesis. SGBUNIT: LARGE MULTIENZYME COMPLEX OF TYCA, TYCB AND TYCC. DOMAIN: CONSISTS OF SIX MODULES, AND HARBORS A PUTATIVE THIOESTERASE DOMAIN AT ITS C-TERMINAL END. EACH MODULE INCORPORATES ONE AMINO ACID INTO THE PEPTIDE PRODUCT AND CAN FURTHER SUBDIVIDED INTO DOMAINS RESPONSIBLE FOR SUBSTRATE ADENYLATION, THIOLATION, CONDENSATION (NOT FOR THE INITIATION MODULE), AND EPIMERIZATION (OPTIONAL), AND N METHYLATION
                                                                                                                                                                                               SIMILARITY).
                MISCELLANEOUS: TYROCIDINE IS A MIXTURE OF
   DECAPEPTIDES,
                                    (OPTIONAL)
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InterPro; IPR001031;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       European Bioinformatics Institute. The by non-profit institutions as long
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QESAMDLNGS [PR-LRQTALVAARAVGY---YDIDL----SIIRNSIGEVDVIIHDLGE
                         ITEEEKQQLLVAYNDTAAEYPRDKTIF-----ELIAEQASRTPAKAAVVCGEDTLT
                                                I - - - - KRLYARLFNDGVNKVPRLKAKFYQSSQSGETSAIGSSHQKTEPYANIKAALEDIT
                                                                          YDLNVVVALAPSN--ELYVKLSYNAAVYESSFVNRIEGHLRTVIDQVIGNPHVHLHEIGI
                                                                                                    - DMSVIEETTPLSLEELFAQESTEMGINPNDYIPEYQGEQPN--SEVVVPPTLEPEKPGL
                                                                                                                            LASATYDFAPLYEIQSTTVLKQELIDHLVTFENYPDHSMKHLEESLGFQFTVESGDEQTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PR00154; AMPBINDING.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Repeat.
                                                                                                                                                                                                                                   102;
                                                                                                                                                                                                                                                                                            DOMAIN 6 (LEUCINE-ACTIVATING).

ACYL CARRIER (ACP) 1.

ACYL CARRIER (ACP) 2.

ACYL CARRIER (ACP) 3.

ACYL CARRIER (ACP) 4.

ACYL CARRIER (ACP) 5.

ACYL CARRIER (ACP) 5.

ACYL CARRIER (ACP) 6.

PHOSPHOPANTETHEINE (BY SIMILARITY).

                                                                                                                                                                                                                                                                                   MW;
                                                                                                                                                                                                                                          Score 136; UD 1
NO. 1e+02;
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      IN 1 (ASPARAGINE-ACTIVATING).

(1) 2 (GLUTAMINE-ACTIVATING).

(IN 3 (TYROSINE-ACTIVATING).

(IN 4 (VALINE-ACTIVATING).

(IN 5 (ORNITHINE-ACTIVATING).

(IN 6 (LEUCINE-ACTIVATING).
                                                                                                                                                      --DQSPISRIGEQSPPLGL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ASPARAGINE-ACTIVATING).
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                                                                                                                                                                                                                                                          DB 1;
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                                                                                                                                                                                                                                                         Length 6486;
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                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                    CRC64;
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RESULT 16
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                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collab
between the Swiss Institute of Bioinformatics and the EMBL outst
the European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                             MEDLINE=22013850; PubMed=12019221;
Spiers A.J., Kahn S.G., Bohannon J., Travisano M.,
"Adaptive divergence in experimental populations o:
fluorescens. I. Genetic and phenotypic bases of wr
              EMBL; AY074776; AAL71845.
                                                                         use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                  Genetics 161:33-46(2002)
                                                                                                                                                                                                                                                                                                                             STRAIN-SBW25
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                     Pseudomonas fluorescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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Matches 199; Conserv
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KADV-GVSPLGFLYNTLVGGVSVSRPFEANSNFRYGANISRRPVTDSVTSFAGSEDGAGN
                       QQEVFGHSTNGFDLSTRTLEHEISRSIIQNGG--WNRTYSLRYRLDKLKTQAPPE----
                                            RMPVGDNTVALRVTPVHLSAGSVKAESLSRFGKGGTEPAGSQSDSGVGLAVAFENPDQGL 1005
                                                                        SHPLNDQ - - - LRAT - -
                                                                                                               F-----GHNLINRDGYQA-GAELRLSEDKKGVK----LYATKPL
                                                                                                                                                            SENEVIDLPERTALANRKTPADVYQSKKVPLYVFVASDKPRDGQIGLGWGSDTGTRLVTK
                                                                                                                                                                                   KALAL---EPGNPEILTSAARIYQGLGKNSEAAELLRKALAIENAMKAKTQVAQASAPGT
                                                                                                                                                                                                                                                                                                                                                                      RVAVLAAAYVEVGAAQYG-----LDMMQKVVENNPNPTVDQKLLYANVLLKANKYSEAG
                                                                                                                                                                                                                                                                                                                                                                                             TKKNL----IENASAEHGYFDGRWLDRSVDVI--LPDNTADVSLIY------
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                                                                                            FVPPSSIASIDSPELSPARRALDTILRDRTGYVVQGLSVRSNNGEKGLSKITDVEAPFEA
                                                                                                                                        SYNPFVGLP-----GQRRQVTDLTVAGAVPPPI----DAPTKSVTSNAFASATSNDLSDP
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                                                                                                                                                                                                                                                      AQVDESTLEPVIETVELTDGILMDISPIEFSASNLIQDKLNL--VAAKA--RHLYDMPDD
                                                                                                                                                                                                                                                                              YRVKQADALREKNDLVAA--YDMLS----PALAQRPNDALGVGALARMYAASGNGK---
                                                                                                                                                                                                                                                                                                    YNLQAVRAL -- SNDLIATRYFNMVNTEIVFPEREQIQNDQVS-----FEQSSSSRTEP 452
                                                                                                                                                                                                                                                                                                                              EILREVQGQPLTETGRQ-RYDDLIYL-
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CCELLULOSE SYNTHASE OPERON PROTEIN C.
TPR 1.
TPR 2.
TPR 3.
TPR 4.
TPR 5.
TPR 5.
TPR 6.
TPR 7.
TPR 8.
TPR 9.
TPR 10.
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Pred. No. 10;
10; Mismatches
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EA7E42BE7810D201 CRC64;
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RESULT 17
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P75211; Q50346;
01-NOV-1997 (Re:
                                                           EMBL;
EMBL;
                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 641-678 FROM N.A. STRAIN=ATCC 29342 / M129; MEDLINE=95075318; PubMed=7984111;
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-ATCC 29342 / M129;
MEDLINE-97105885; PubMed-8948633;
Himmelreich R., Hilbert H., Plagens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-ATCC 29342 / M129;
MEDLINE-96257197; PubMed-8675035;
Proft T., Hilbert H., Plagens H., Herrmann R.;
"The P200 protein of Mycoplasma pneumoniae shows common the cytadherence-associated proteins HMW1 and HMW3.";
                                                                                                                                                                                                                                            "Identification and characterization of hitherto unknown Mycoplasma pneumoniae proteins.";
Mol. Microbiol. 13:337-348(1994).
-i- FUNCTION: PROTEIN CYTOSKELETON-ASSOCIATED WHICH COULD BE AN
               DOMAIN
                               DOMAIN
                                             Cytadherence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene 171:79-82(1996).
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AE000027; AAB95923.1; -.
Z32646; CAAB3569.1; -.
herence; Structural prote
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             MEDLINE-91014689; PubMed-2120541; Galli D., Lottspeich F., Wirth R.; "Sequence analysis of Enterococcus
                                                                                                                                                           01-NOV-1990
15-JUN-2002
                                                   STRAIN-DS16
                                                             SEQUENCE FROM N.A.,
                                                                                                Bacteria; Firmicutes;
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faecalis aggregation id pAD1.";
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Cell wall; Peptidoglycan-anchor; Signal;
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pfam; pF00746; Gram_pos_anchor; 1.
TIGRRAMS; TIGR01167; LPXTG_anchor; 1.
pROSITE; pS50847; GRAM_POS_ANCHORING;
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FUNCTION: AGGREGATION SUBSTANCE ALLOWS DONOR AND RECIPIENT STITUTED FORM TIGHT AGGREGATES WHICH ALLOW THE NON-MOTILE BACTERIA MAINTAIN PHYSICAL CONTACT OVER A PERIOD OF TIME SUFFICIENT TO PERMIT CONJUGATIVE TRANSFER OF THE SEX PHEROMONE PLASMID FROM DONOR TO RECIPIENT STRAINS.
SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan an amide bond (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way field and this statement is not removed. Usage by and for commercial
                  -EPVIETVELTDGILMDISPIE-FSASNLIQDK-LNLVAA---
                                                                                                                                                -----FFTIDPKTNQLTTDPDK-LPVKRELLEQLLTVNMGEAYNLQAVRALSNDLIA 416
                                                                                                                                                                                H----GNKVYSKTDIDVGTNGISISDWEAVQGKEYIGATVISTPNRIKFTFGNEIVNNPG
                                                                                                                                                                                                                                                                                                                 QYTVKATPDSKGRLNAFLHDDPVATIV---YGINIDPRTKKAGAEIEMLVRFFGEDGKEI 427
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                                                 TIEFNRYKANVVPVLVPNKE-VTDGQKNINDLNVKRGDSLQYIVTGDTTELAKVDPKTVT
                                                                              TRYFNMVNTEIV --- FPEREQIQNDQVSFEQSSSSR--
                                                                                                                 YDGNSMWFAFNTDLKAKSITPYQEKGRPKQPEK------
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LPXTG SORTING SIGNAL (POTENTIAL).

AMIDE-LINKED TO CELL WALL (POTENTIAL).

WW; 52123A133AD23E5B CRC64;
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RESULT 19
FAT2_HUMAI
 Poustka A., Wellenreuther R., Mewes H.-W., Weil B., Wiersubmitted (FEB-2000) to the EMBL/GenBank/DDBJ databases
                                                                            Nakayama M., Nakajima D., Nagase T., Nomura N., Seki N., Ohara ("Identification of high-molecular-weight proteins with multiple EGF-like motifs by motif-trap screening."; Genomics 51:27-34(1998).
                                                                                                                                                                                                                                                                                                                                                                             Q9NYQ8: O75091; Q9NSR7;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Protocadherin Fat 2 precursor (hFat2)
factor-like domains 1).
FAT2 OR MEGF1 OR CDHF8.
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                                    TISSUE-Testis;
                                                    SEQUENCE OF 4142-4349 FROM N.A.
                                                                                                                                              MEDLINE=98360089;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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SMART; SM00181; EGF; 2.
SMART; SM00282; LamG; 1
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IPR000561; EGF-like.
IPR001791; Laminin_G
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                                                                               Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;.
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                        TRX_DROME PRT; 3:
P20659; Q27255; Q27337;
01-FEB-1991 (Rel. 17, Created)
16-OCT-2001 (Rel. 40, Last sequence upon the control of the control 
SEQUENCE FROM N.A MEDLINE-90192757;
                                                                                                                                                                                                                                                                                            Trithorax protein.
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PubMed=2107543;
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Pfam; PF00628; PHD; 3.
Pfam; PF00856; SET; 1.
SMART; SM00542; FYRC; 1.
SMART; SM00541; FYRN; 1.
SMART; SM00249; PHD; 4.
SMART; SM00108; POSTSET; 1.
SMART; SM00117; SET; 1.
PROSITE; PS50280; SET; 1.
                                                                                                                                                                                                                                                             EMBL; M31617; AAA29025.1; --
EMBL; Z50152; CAA90514.1; --
EMBL; Z50152; CAA90513.1; --
EMBL; Z31725; CAA83516.1; --
EMBL; Z31725; CAA83515.1; --
EMBL; Z31725; CAA83515.1; --
PIR; A35085; A35085.
HSSP; P20393; 1A6Y.
                                                                                                                                                                                                                                   TRANSFAC;
FlyBase; F
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"The trithorax gene, a trans-acting regulator of the bithorax in Drosophila, encodes a protein with zinc-binding domains.";
Proc. Natl. Acad. Sci. U.S.A. 87:2112-2116(1990).
[2]
 PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-Oregon-R;
MEDIJINE-96100387; PubMed-8555104;
Tillib S., Sedkov Y., Mizrokhi L., Mazo A.;
"Conservation of structure and expression of the tritho between Drosophila virilis and Drosophila melanogaster.
Mech. Dev. 53:113-122(1995).
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"The bithorax complex is regulated by trithorax earlier during
Drosophila embryogenesis than is the Antennapedia complex, correlat-
with a bithorax-like expression pattern of distinct early trithorax
                                                                                                                                            InterPro; IPR001214; InterPro; IPR001965; InterPro; IPR001841;
                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (S or send an email to license@isb-sib.ch).
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[3]
                                                                                                                                                                                      InterPro; IPR003616;
                                                                                                                                                                                                      InterPro; IPR003889; FYrich_C.
InterPro; IPR003888; FYrich_N.
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SIMILARITY: CONTAINS 5 PHD-TYPE ZINC FINGERS
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SIMILARITY: CONTAINS
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ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
MISCELLANEOUS: THIS PROTEIN HAS BEEN EXPERIMENTALLY SHOWN TO BI
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
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ZF_PHD_1;
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Transcription regulation; Zinc-finger; Metal-binding; DNA-binding;
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                                                                                                                                                                          A--SAGYQQMVEDVL
                                                                                                                                                                                                                      MRTSACND
                                                                                                                                                                                                                                                                                     QTALVAARAVGYYDIDLSIIRNSIGEVDVIIHDLGEPVYIDYRAVEVRGEGADDKAF---
                                                                                                                                                                                                                                                                                                                              GVNKVPRLKAKFYQSSQSGETSAIGSSHQKTEPYANIKAALEDITQESAMDLNGSIPRLR 235
                                                                                                                                                                                                                                                                                                                                                      CYAQKST----LPS---PVYEAELKVSSVLESIVPDVTMDAILEEQP-----VTQSIYTE
                                                                                                                                                                                                                                                                                                                                                                          LFAQESTEMGINPNDYIPEYQGEQPNSEV---VVP----PTLEPEKPGLIKRLYARLFND
                                                                                                                                                                                                                                                                                                                                                                                                                     QARLNAAGLNAKPQSQALDVVNFDDQSPISR----IGEQSPPLGLDMSVIEETTPLSLEE 122
KCSKYTPKYHKRNGNVSTAANGAHGGNLGGSSASAALSVSGGDSHGLLDYGSDQ--
                                           IWEKVFEAVQVARRA-----
                                                               ILGRISDAVSAVARAILPDESENEVIDLPE---
                                                                                      APEPPQPIQEPKKMTGPHL---
                                                                                                         LTDGILMDISPIEFSASNLTQDKLNLVAAKARHLYDMPDDRVLAINHDDGVN-----RS
                                                                                                                                                    SNDLIATRYFN-MVNTEIVFPEREQIOND-OVSFEQSSSSRTEPAOVDESTLEPVIETVE
                                                                                                                                                                                               LIYDTGTQYRFDEVVFFTIDPKTNQLTTDPDKLPVKRELLEQLLTVNMGEAYNLQAVRAL
                                                                                                                                                                                                                                           --TTVADEVPLLIGDVFHHGKYETKKNLIENASAEHGYFDGRWLDRSVDVILPDNTADVS
                                                                                                                                                                                                                                                                                                                                                                                               {\tt QAPSTTSSSTTRPTNRVLPMQQRQEPAPLSNECPVVSSPTPPKPVEQPIIHQMTSASVSK}
                                                                                                                                                                                                                                                                                                                                                                                                                                           MPIITLAEAPVVQSQFVMEPQALEQQ-ELANRVQHFSTSSSS-SSSNCSLPTNVVNPMQQ 3054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156;
                      SKKVPLY----VFVASDKPRDGQIG-----
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                                                                                                                              AATYINEMADAHVL--DLKQLQNGVELELRRKEEQRTVSQEQEQSKAAIVPTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122;
                                           HGLTPLPEGPLADMGGIQMIGLKTNALKYLIEQLPGVE
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Pred. No. 63;
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-> S (IN REF. 1).
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                                                                                                                                                                                                                                                                                                           -KTEQLLLQQQQREQLNQQ--LVNNG-----
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                                                                 ----RTALANRKTPADVYQ-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       281;
                                                                                                                                                                                                                                                                 -YREEDLEEEEDEDDDFSLK
                      ----LGWGSDTGTRLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 3726;
                                                                                     IQSEDGFTYKSSSITE
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                                             Pfam; PF00004; AAA; 2.
Pfam; PF02861; C1p_N; 2.
PRINTS; PR00300; CLPPROTEASEA
ProDom; PD000739; GSPII_E; 1.
SMART; SM00382; AAA; 2.
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Science 269:496-512(1995).
Science 769:496-512(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAEIN
PROSITE; PS00870; CLPAB_1; 1.
PROSITE; PS00871; CLPAB_2; 1.
Chaperone; ATP-binding; Repea
                                                                                                                                                                                     EMBL: U32767; AAC22518.1; -. TIGR; HI0859; -.
                                                                                                                                                                                                                       modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ClpB protein.
CLPB OR HI0859
                                                                                                                                                        InterPro;
                                                                                                                                          InterPro;
                                                                                                                                                                        InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                        "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1995
15-JUN-2002
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01-NOV-1995
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SIMILARITY: BELONGS TO THE CLPA/CLPB FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---VNGK-----PSQEALL--AGVAVHKTVADNLVNPMRGYRQRY--SLEVG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RSHIHGRGLYCTKDIEAGEMVIEYAGELIRSTLTDK-----RERYYDSRGIGCYMFK 3645
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                                                                                                                 IPR003959; AAA_ATPase_centr
IPR001270; Chaprnin_clpA/B.
IPR004176; Clp_N.
                                                                                                                                                                   IPR003593; AAA_ATPase
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(Rel.
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Repeat; Complete proteome
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annotation updat
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                                                                                                                                                                              Q10411;
01-OCT-1996
01-OCT-1996
15-JUN-2002
                                                                                                                                                     15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein CIF3.06c in chromosome I.
SPACIF3.06C.
                                                                                            Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                                                                   Schizosaccharomycetales;
                                                                                                                            Schizosaccharomyces pombe (Fission yeast). Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           TNQLTTDPDKLPVKRELLEQLLTVNMGEAYNLQAVRALSNDLIATRYFNMVNTEIVFPER 432
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856
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(Rel. 34, Last sequence up
(Rel. 41, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                              STANDARD;
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                                                                                                                   Schizosaccharomycetaceae;
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Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Ste Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman Brooks K., Brown D., Brown S., Chillingworth T., Churcher C. Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fra

Stewart

MEDLINE=21848401; PubMed=11859360;

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RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quall M.A., Rabbinowitsch E.,
RA Oliver K., O'Neil S., Pearson D., Quall M.A., Rabbinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller Auer S.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Gorzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Gailbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Gailbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Shakovski G.V., Ussery D., Barrell B.G., Nurse P.;
"The genome sequence of Schizosaccharomyces pombe.";
RI Nature 415:871-880(2002).
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Holroyd S., Hornsby
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QNDQVSFEQSSSRTEPAQVDESTLEPVIETVELTDGILMDISPIEFSASNLIQDK----
                                                              CANFVDDLKEKSDALEQLTNE------KNELIVSLEQSNSNNEALVEERSDL
                                                                                          TTD-PDKLPVKRELLEQLLTVNMGEAYNLQAVRALSNDLIATRYFNMVNTEIVFPEREQI 435
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Hornsby T., Howarth S., Huckle E.J., Hunt S.,
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01-NOV-1995 (Rel. 3
01-NOV-1995 (Rel. 3
                                                                                                                                                                                                                                                                                           Submitted (MAY-1991) to the EMBL/GenBank/DDBJ databases.

-i-FUNCTION: MAY AID IN THE PASSAGE OF THE NASCENT POLYPEPTIDE CHAIN THROUGH THE RIBOSOME CHANNEL INTO THE CYTOSOL. SUCH AN INTERACTION COULD BE CRUCIAL FOR CONTINUOUS TRANSPORT OF THE POLYPEPTIDE;

COULD SERVE TO PREVENT THE NASCENT POLYPEPTIDE FROM INTERFERING WITH TRANSLATION BY CLOGGING THE RIBOSOME CHANNEL (BY SIMILARITY).

-i-SUBCELLULAR LOCATION: CYTOPLASMIC. ASSOCIATED WITH TRANSLATING RIBOSOMES; MAY BIND DIRECTLY TO THE NASCENT POLYPEPTIDE.

-i-SUBLIBLIULAR LOCATION: CYTOPLASMIC. ASSOCIATED WITH TRANSLATING RIBOSOMES; MAY BIND DIRECTLY TO THE NASCENT POLYPEPTIDE.
                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                 PRINTS; PR00301; HEATSHOCK70.
ProDom; PD000089; Hsp70; 1.
                                                   Pfam; PF00012; HSP70;
                                                                                         EMBL; X59963; CAA42589.1; -. HSSP; P08107; 1HJO.
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an email to license@isb-sib.ch).
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Best Local
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                                                                              DNA double-strand break repair RAD50 OR TA0157
Archaea; Euryarchaeota; Thermopl
Thermoplasmataceae; Thermoplasma
                                                        Thermoplasma acidophilum
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                      Thermoplasmata;
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Pred. No. 4.5;
94; Mismatches
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571B8B1571A78410 CRC64;
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ATPase.
                                                                                                                                                          update)
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                      Thermoplasmatales;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=DSM 1728; pubMed=11029001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA repair; Hydrolase; ATP-binding; Coiled coil; Complete NP_BIND 37 ATP (BY SIMILARITY).

DOMAIN 151 744 COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (Son send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 407:508-513(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF02463; SMC_N; 1.
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                                                                                                                                                                                                                                                                                                                                            261 YEEEIRKIDGKLQEISGSTERYNEITSSKVYASRERIRGYWTDKGQ--IIDYRKMLKNID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity).
SUBUNIT: Forms a complex with mrell (By similarity).
SIMILARITY: BELONGS TO THE SMC FAMILY. RAD50 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: Involved in DNA double-strand break repair (DSBR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rad50/mrell complex possesses single-strand endonuclease activity. And ATP-dependent double-strand-specific exonuclease activity. Rad50 provides an ATP-dependent control of mrell by unwinding and/or repositioning DNA ends into the mrell active site (By
                                                                                                                                                  DKLPVKRELLEQ-----LLTVNMGEAYNLQAVRALSNDL-----IATRY---FNMVNT
   SRTEPAQVDESTLEPVIETV -- ELTD ----
                                                                                                                GNLQVKIGALRQKEEEIRRNMNMLEGHNKCPV--CGTDLGDEGSRRIREHYSEDLNRLNE
                                                                                                                                                                                                                           HGYFDGRWLDRSVDVILP-----DNTADVSLIYDTGTQYRFDEVVFFTIDPKTNQLTTDP
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                                       EIDHLEREASAIDEKKRQLISMESYLAKGKIREYETYDRQMKDLEAQITDDENSLSTIAY
                                                                         EIVFPERE----
                                                                                                                                                                                         REEYRKKQKDLGDEISRTLGRAFANASELVAIYE---EIRRD-----IDEINTDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PESNAMIMV---DGSALSQSVKDANDY-IEKNIITKSKDVFLNSVFSKQG-EM----DDL 143
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896 AA;
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                                                                                                                                                                                                                                                                                                    ----AVEVRGEGADDKAFTTVADEVPLLIGDV-FHHGKYETKKNLIENASAE 325
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103435 MW;
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Pred. No. 8.7;
22; Mismatches
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   -GILMDISPIEFSASNLIQDKLNLVAAKAR
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16-UCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DNA-directed RNA polymerase beta chain (EC 2.7.7.6) (Transcriptase beta chain) (RNA polymerase beta subunit).
         SEQUENCE
                                     Complete
                                                          InterPro, IPR001572; RNA_POl_B.
Pfam; PF00562; RNA_POL_BETA;
PROSITE; PS01166; RNA_POL_BETA;
Transferase; Transcription; DNA-
                                                                                                                                                                                EMBL; AE002118; AAF30594.1; -. HSSP; Q9KWU7; 1HQM.
                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 407:757-762(2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glass J.I., Lefkowitz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Serovar 3;
MEDLINE=20500219; PubMed=11048724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ureaplasma parvum (Ureaplasma urealyticum biotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cassell G.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=134821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes;
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SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
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SUBUNIT: THE ENZYME CONSISTS OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE SUBSTRATES (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complete sequence of the mucosal pathogen Ureaplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TVADNLVNPMRGYRQRYSLEVGSSGLVSDANMAIARAGI
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                                  proteome
      1434 AA;
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      162022 MW;
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                                                    ETA; 1.
DNA-directed RNA polymerase;
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   2841BFA50C19BA7A CRC64;
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SCA4_RICFE STANDARD; PRT; 981 AA. 09AJ37; 09AJ37; 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) 17-OCT-2001 (Rel. 40, Last annotation update) 17-OCT-2001 (Rel. 40, Last annotation update) 18-OCT-2001 (Rel. 40

Rickettsia felis (Rickettsia azadi) Bacteria; Proteobacteria; alpha sub

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SCA4 OR D

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                                                                                                                              MVDDKIHSRSVGPYSKITQQPLGGKSQNG---GQRFGEMEV---
                                                                                                                                                                                            KISTPVFDGANHDDIVSIMNEANIDIENNKGKQVLYDGRTGEPFDGLISVGLTYMLKLDH
                                                                                                                                                                                                                                                               KQAKQAKD--IDLIDVTIILK--
                                                                                            RLDKLKTQAPPETWQDLPVDFVNGKPSQEALLAGVAVHKTVADNL
                                                                                                                                                             PLNDQLRA-TLG-----YQQEVFGHSTNGFDLSTRTLEHEISRSIIQNGGWN-RTYSLRY
                                                                                                                                                                                                                             RLVTKF----EHNLI------NRDGYQAGAELRLSEDKKG---VKLYATKPLSH 638
                                                                                                                                                                                                                                                                                                                              GQILELHLGYAAAEIGKKQLIQIAIDQ----LGYEKYISLFGINEIIAKKLYENISNLIKH 1183
                                                                                                                                                                                                                                                                                                                                                               SNLIQDKLNLVAAK--ARHLYDMPDDRVLAINHDD-----GVNRSILGRISDAVSAVARA
                                                                                                                                                                                                                                                                                              ILPDESENEVIDLPERTALANRKTPADVYQSKKVPLYVFVASDKPRDGQIGLGWGSDTGT 597
                                                                                                                                                                                                                                                                                                                                                                                              KRKIQVGDKMAGRHGNKGIV-----SKVVPIQDMPFLKDGTPLDIMLNPLGVPSRMNI 1126
                                                                                                                                                                                                                                                                                                                                                                                                                                REQIQ-NDQVSFEQSSSSRTEPAQVDESTLEPVIETVELTDGILMDIS-----PIEFSA 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FGDKSKTVKDSSLKVKHGQEGIVAAVKRIKSSDENGSELPDDVI-----EIIKVYIV--Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GDEEITRDMPNVSDTAKRFLDNQGIVLVGAEVHEGDVLVGKTTPRGNVETAPEDRLLQTI 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --PDNTADVSLIYDT-------GTQYRFDEVVFFTIDPKTNQLTTDPDKL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GPAMQNGELALGRNILVGYTTWRGYNFEDAIIISERLVDQDVFTSIHIDEHTIQCMKTKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NDNDKLD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QATPLIKPYAPIVGTGTEFKIAHDSGM---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RILDEQVVARYRGSTGLFSPNEVDFIDIVPKQVVSIAASAIPFIENDDGARALMGSNMQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PGLIKRLYAR-----LFN----DGVNKVPRLKAKFYQS-----SQSGETSAIGSSHQK 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---MSLASLAKVDENGFIVAPYYVVEDGVVKEDY--KYLTAHEDDNYIIAESSVQLDENK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTPLSLEELFAQES-----TEMGINPNDYIPEYQGEQPNSEVVVPPT---LEPEK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NPLAELTNKRRISAMGPGGISREDPNLDIRDV----HHSHSSRICPIETPEGMNIGLI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NPPVLLTPEQIQARLNAAGLNAK-PQSQALDVVNFDDQSPISRIGEQSPPLGLDMSVIEE 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --PVKRELLEQLLTVNMGEAYNLQAVR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --VFHHGKYETKKNLIENASAEHGY-----FDGRWLDRSVDVIL-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NSIGEVDVIIHDLGEPVYIDYRAVEVRGEGADDKAFTTVADEVPLL------IGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----TEPYANIKAALED--ITQESAMDLNGSIPRLRQTALVAAR--AVGYYDIDLSIIR 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                               ----IKSDDVQGR--NQAYNAIIKGHDVVADGM 1355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----DYKLIKYRKSNQD-----TCNNQIPIVKVGQRVHKSETIGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 131; D
Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----ALSNDLIATRYFNMVNTEIVFPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1:
                                                                                                                                                                                                                                                               -----ELGLSY-DDIGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                              736
                                                                                                                                WALEAYGAAY
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                                                                                                                                                             691
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF196973;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=42862;
                                519
                                                                                              459
                                                                                                                                                             414
650 YQQEVFGHSTNGFDLSTRTLEHEISRSIIQNGGWNRTYS-----LRYRLDKLKTQAPPE 703
                                                                                                                             556 LANRKTP-----
                                                                                                                                                                                             502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 TTPLSLEELFAQESTEMGINPNDYIPEYQGEQPNSEVVVPPTLEPEKPGLIKRLYA---- 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 TPEQIQARLNAAGLNAKPQSQALDVVNFDDQS-PISRIGEQSPPL--GLDMSVI----EE 114
                                                            GSDTGTRLVTKFEHNLINR-DGY-QAGAELRLSEDKKGVKLYATKPLSHPLNDQLRATLG
                                                                                                                                                                                           LYDMPDDRVLAINHDDGVNRSILGRISDAVSAVARAILPDESEN-----EVIDLPERTA 555
                              AVDVGLSL--KDDASRVTAIDGITDAVIKSNLSTEDKGTMLIAV-----
                                                                                            NNNDLTPDTKVAGVNAVLETIKNDQNTPDLEKSKMLEATVAIALNSENQEPKQKQQMLEK 518
                                                                                                                                                                                                                                                        FEOSSSSRTEPAOVDESTLEPVIETVELTDGILMDISPIEFSASNLIQDKLNLVAAKARH
                                                                                                                                                                                                                                                                                          VTRGKYKEMMREVELNQGQSVDLS--QTIAEDLTKVQGRSQETPQPIITPNQELKS---S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VVRNDAGDELCTLNETTVKTKPFTVAKQDG-----TQVQINSYREIDF-----PIKLD 228
                                                                                                                                                                                                                          TETPTTTQVPPITPANQPLQPETSQMPQPQQVNPNLLYATSALSTSMQDLLNYVNA----
                                                                                                                                                                                                                                                                                                                        VKRELLEQLL---TVNMGEAYNLQAVRALSNDLIATRYFNMVNTEIVFPEREQIQNDQVS 441
                                                                                                                                                                                                                                                                                                                                                        EHGYFDGRWLDRSVDVILPDNTADVSLIYDTGTQYRFDEVVFFTIDPKTNQLTTDPDKLP 384
                                                                                                                                                                                                                                                                                                                                                                                                                       KADGSMHLSMVALKADGTKPSKDKAVYFTAHYEEGP----NGKPQLK----EISSP 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----YRAVEVRGEG---ADDKA--FTTVADEVPLLIGDVFHHGKYETKKNLIENASA 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFIDKALENPELKKKLESIEIAGYKNVL-STYSAANGYQGGFKPVQWENQISASDLRAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RLFNDGVNKVPRLKAKFYQSSQSGETSAIGSSHQKTEPYANIKAALEDITQESAMDLNGS 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IAEQILKDLAALADRDL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TPQELEA---DDGFSFTPASSTQSTPSISSLSGGISSDSQTSDPITKAVRETIIQPQKDE 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           981
981 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative 136; Mismatches 348; Indels 252;
                                                                                                                                                           --GLTKEKDGNKQI-----DLINEAATAILNNEKSDIAEKQANIIALTENTV 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---LRQTAL----VAARAVGYYDIDLSIIRNSIGEVDVIIHDLGEPVYID 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAK31304.1;
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981
; 107514 MW;
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                                                                                                                         ------ADVYQSKKVPLYVFVA----SDKPRDGQIGLGW
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Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----AEQKRKEI-----EEEKDKTLSAFFGNPAN 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7F18F421E2C262E1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 981;
                                                                                                                                                                                                                                                                                                                                                     ----TLA 302
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                                                            649
                                                                                                                                                                                                                                                                                          357
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				RESULT PGCV_R ID AC OT DT DT DT DT T DT C OC O	Qy Db	Qy Db	Оу	Qy Db	Db
SEQUENCE OF 2535-2738 FROM N.A. STRAIN-Sprague-Dawley; TISSUE-Lung; Blomberg L.A., Chan WY., Clerch L., Massaro D.; Blomberg L.A., Chan WY., Clerch L., Massaro D.; "Molecular cloning and characterization of two developmentally regulated genes in rat lung."; submitted (SEP-2000) to the EMBL/GenBank/DDBJ databasesi- FUNCTION: May play a role in intercellular matrix. May take part in connecting cells with the extracellular matrix. May take part in the regulation of cell motility, growth and differentiation. Binds hyaluronic acidi- SUBCELLULAR LOCATION: Secreted; extracellular matrix.	Res -2463 ; Pubh sen P pressi 70(199	9-2738 FROM N.A. (ISOFORM VO).  Kyoto; 94; PubMed=9642104; el P. Chiba A., Mevissen M., Popp S. Margolis R.U.; Margolis R.U.; regulation of expression of hyalurona in developing brain: aggrecan, versic	A. ( )F 26 19768  rel  rel	PGCV_RAT  PGCV_RAT  STANDARD;  PRT; 2738 AA.  99RB4; 008592; 088564; 09R1K4;  16-OCT-2001 (Rel. 40, Created)  16-OCT-2001 (Rel. 40, Last sequence update)  15-JUN-2002 (Rel. 41, Last annotation update)  15-JUN-2002 (Rel. 41, Last annotation update)  Versican core protein precursor (Large fibroblast proteoglycan)  (Chondroitin sulfate proteoglycan core protein 2) (PG-M) (Glial hyaluronate-binding protein) (GHAP) (Fragments).  CPGG2.  Rattus norvegicus (Rat).  Rattus norvegicus (Rat).  Rakaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  NCBI_TaxID=10116;	878 KI 879     755 AI 756	18 SIRGYAHDSLSPISDKGYLTGGQVLAVGTAEYNYEFMKDLRLAVFGDIGNAYDKGFTNDT 8	764 IARAGISGVYSEGDNAYGSNRAHOMTGGIQAGYIWSDNENHVPYRLREFAGGDQ 817	704 TWQDLPVDFVNGKPSQEALLAGVAVHKTVADNLVNPMRGYRQRVSLEVGSSGLVSDANMA 763	561GDKVNASELSNAE-KOKLLGSVLKKGVEAQVLSPEQQQLMQQNLDKI-TAEQTK 612

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InterPro; IPR000436; SUShi_SI
PRINTS; PR01265; LINKMODULE.
SMART; SM00032; CCP; 1.
SMART; SM00034; CLECT; 1.
SMART; SM00181; EGF; 2.
SMART; SM00179; EGF CA; 2.
SMART; SM00405; IG; 1.
SMART; SM00405; LINK; 2.
SMART; SM00445; LINK; 2.
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SIGNAL
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or send a
                                                                                                                                                                                                            DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycoprotein; Proteoglycan; Lectin;
Signal; Repeat; EGF-like domain; Ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                   PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALTERNATIVE PRODUCTS: At least 3 isoforms; v0 Vint; are produced by alternative splicing. TISSUE SPECIFICITY: In kidney is expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             but not in glomeruli.
DEVELOPMENTAL STAGE: Disappears after the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; AF072892; AAC
; AY007691; AAG
; P01132; 1EPG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF062402; AAC40166.1; -. U75306; AAB51125.1; -. AF084544; AAD48544.1; -. AF072892; AAC26116.1; -.
                                                                                                                                                                                                                                                                                                                                                                            E; PS00010; ASX_HYDROXYL; 1.
E; PS00615; C_TYPE_LECTIN_1; 1
E; PS00641; C_TYPE_LECTIN_2; 1
E; PS00022; EGF_1; 2.
E; PS01186; EGF_2; 1.
E; PS01187; EGF_CA; 1.
E; PS01241; LINK; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    o; IPR000152; Asx_hydroxyl.
o; IPR000561; EGF_1ke.
o; IPR000742; EGF_2.
o; IPR001881; EGF_Ca.
o; IPR003599; Ig_like.
o; IPR001304; Lectin_C.
o; IPR000538; Link.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
       696
2431
2469
2518
2637
44
172
196
270
294
                                                                                                                                                                                                                                                                                                                              acid;
                                                                                                                                                                                                                            21
348
37
167
265
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                                                                                                                                                                                                                                                                                                                             Alternative
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       2431
2467
2505
2632
2695
130
130
243
217
345
2446
                                                                                                                                                                                                                          20
2738
349
137
244
346
                                                                                                                                                                                                           695
GAG-BETA.

EGF-LIKE 1.

EGF-LIKE 2. CALCIUM-BINDING.

C-TYPE LECTIN.

SUSHI.

BY SIMILARITY.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCR_CCP.
                                                                                                                                                                                                                                                                                                                           splicing
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STRAIN-WARL B3312;
MEDLINE-94374689; PubMed-7522196;
ANDERTH-91vert E., Davies J.;
ANDERTH-P1vert E., Davies J.;
Plosynthesis of butirosin in Bacillus circulans NRRL B3312:
Identification by sequence analysis and insertional mutagenesis of the butB gene involved in antibiotic production.";
Gene 147:1-11(1994).

-I- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA. MAY PLAY A ROLE IN THE EXPORT OF BUTIROSIN FROM THE ORGANISM.

-I- SUBGELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-LAYER WITH HEXAGONAL SYMMETRY.
                                Pfam; PF00395; SLH; 1.
Pfam; PF02368; Big_2; 1.
Signal; Cell wall; S-layer.
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                                                                                                  InterPro; IPR003343; Big_2. InterPro; IPR0011119; SLH.
                                                                                                                                   EMBL; L20421; AAA62588.1; -.
                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                       -
                                                                                                                                                                                                                                                                                                                                                                           Thompson S.A., Wang L.L., West A., Sparling P.F. "Neisseria meningitidis produces iron-regulated the RTX family of exoproteins.";
J. Bacteriol. 175:811-818(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=FAM20 / Serogroup C;
MEDLINE=93139051; PubMed=8423153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neisseria meningitidis (serogroup
Bacteria; Proteobacteria; beta sub
NCBI_TaxID=135720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P55126;
01-OCT-1996
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   hes 205;
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STRAIN-FAM20 / Sej
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         894
                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: OUTER-MEMBRANE ASSOCIATED AND SECRETED. DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYT
                                                                                                                                                                                                                                                                        European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                              DISEASE
                                                                                                                                                                                                                                                                                                                                                                FUNCTION: MAY PARTICIPATE IN THE PATHOGENESIS OF MENINGOCOCCAL
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            Similarity
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907
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2.7%; Score 129; DI
19.9%; Pred. No. 17;
Live 102; Mismatches
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subdivision; Neisseriaceae; Neisseria
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        DTYVFGEGFG
                         DTKI-GAGVG
                                          TLDGGEGNDALYGYNGNDALNGGE----
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QSIRGYAHDSLSPISDKGYLTGGQVLAVGTAEYNYEFMKDLRLAVFGDIGNAY-DKGFTN 875
                                                                                                                                                                                                                             QAPPETWQDLPVDFVNGKPSQEALLAGVAVHKTVADNLVNPMRGYRQRYSLEVGS--SGL
                                                                                                                                     VSDANMATARAGISGVYSFGDNAYGSNRAHQMTGGIQAGYIWSDNFNHVPYRLRFFAGGD
                                                                                                                                                                                                                                                                                   DIIRFTDGITADMLTFTREGNHLLIKAKDDSGQVTVQSYFQNDG----
                                                                                                                                                                                                                                                                                                                          -----TNGF--DLSTRTLE--HEISR------SIIQNGGWNRTYSLRYRLDKLKT
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                                                                                                                                                                                    -----THFDNGKVLDVA-----TVKELVQQSTDGSDRLYAYQSGSTLNGG
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                                                                                          -DYLYGADGNDLLNGDAGNDSIYSGN--
-GNDHLNGEDGND---TLIGGAGNDYLEGGSGS
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RESULT 30
RA Ballew R.M., Basu A., Baxendale J., Budrews Flaminoch C., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew II., Dietz S.M.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew II., Dietz S.M.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew II., Dietz S.M.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew II., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mentulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mentulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Melson D.R., Pacleb J.M., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Palazzolo M., Stiden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Syler B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Syler B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Finder M., Weissenbach J.,

RA Wang Z.-Y., Wassarman D.A., Weinsenbach J.,

RA Kimmel B.C
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Drosophila melanogaster (Fruit fly)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM B3).
                                                                                                                          FUNCTION: MAY PLAY AN IMPORTANT ROLE IN THE REGULATION MICROTUBULE ASSEMBLY AND INTERACTION.
SUBCELLULAR LOCATION: ASSOCIATED WITH CYTOPLASMIC MICROWITH THE MITOTIC SPINDLE.
ALTERNATIVE PRODUCTS: 3 ISOFORMS; C2, B3 AND J5 (SHOWN
                                                              PRODUCED BY ALTERNATIVE SPLICING.
MISCELLANEOUS: PHOSPHORYLATION OF VARIOUS SERINE RESIDUES MAY PLAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biol. 111:2563-2572(1990).
CONSENSUS SEQUENCES OF
                                    THE BASIC
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                                    DOMAIN CONTAINS
SEVERAL
                                    NUMEROUS
DIFFERENT
                                                                                                                                        (SHOWN HERE); ARE
                                                                                                                                                                                                               MICROTUBULES
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Best Local S
Matches 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. The use by non-profit institutions as long
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                                                         707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TSAIGSSHQKTEPYANI----KAALEDITQ---ESAMDLNGSIPRLRQTALVAARAVGYY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEQLQQQQQIESQGVHEDPRQE-----DEDEHSSVATTYGTSSLSENNSSPLDQEEVVMV 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEQI--QARLNAAGLNAKPQSQALDVVNFDDQSPI-----SRIGE-QSPPLGLDMSVIE 113
                                                      PLSSASKEKLLPDTTDEQLLTSALEEKLRSVAPEESV----STAADGQSISQFDEYV-IA
                                                                                                            ---SAVARAILPDESENEVID
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                                                                                                                                                                                                                                                                         YETQNFDEISSPPEGINPFAQPFTPAHLVIEQANTMMEDVGGMPIPASEDFAICDK----V
                                                                                                                                                                                                                                                                                                                                                                                     ELVEEYTLDPESHFFGVVSSQAPLQLFGKHTLPSIIHSCKHRVASEQNDEENAVFESVSG
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                                                                                                                                                               ASKSSN--EVEDHRSEQQAFVKEELLHPVGDVVAQVENLGTEKNFVVEEERLPISVSDEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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RDGQIGLGWGSDTGTRLVTKFEHNLINRDGYQAGAELRLSEDKKGVKL
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18.1%;
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                                                                                                                                                                                                                                                                                                                               --STLEPVIETVELTDGILMDIS--PIEFSASNLIQDKLNLV 495
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ASP/GLU-RICH (BASIC).
ARG/LYS-RICH (BASIC).
ASP/GLU-RICH (ACIDIC).
ASP/GLU-RICH (ACIDIC).
TO MICROTUBULES (POTENTIAL).
MISSING (IN ISOFORM B3 AND IS
MISSING (IN ISOFORM C2).
D -> N (IN ISOFORM C2).
D -> N (IN ISOFORM C2).
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Pred. No.
                                                                                                                                                                                                                     ----VLAINHDDGVNRSILGR-----ISDAV 531
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                                                                                                         -LPERTALANRKTPADVYQSKKVPLYVFVA 578
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Azevedo V., Bertero M.G., Bessleres P., Bolotin A., Borchert S.,
AB Dorriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
AB Bourists R., Bourschi C.V., Caldwell B., Capuano V., Carter N.M.,
Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
A Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
A Denizot F., Errington J., Fabret C., Ferrari E., Foulger D.,
A Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
A Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
A Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
A Guiseppi G., Guy B.J., Haga K., Hariech J., Harwood C.R., Henaut A.,
A Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
A Hilbert H., Holsappel S., Kasahara Y., Klaerr-Blanchard M., Klein C.,
A Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
A Kurita K., Lardious A., Lardious S., Lauber I., Lazarevic V.,
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Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
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Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
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Soldo
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Vianta A., Marchar P., Wassarotti A.,
Vianta A., Wannter F., Vassarotti A.,
Vianta A., Wannter F., Wassarotti A.,
Vianta A., Wannter
                                                 Nature
-!- FUN
                                                                                                                                                Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.; "The complete genome sequence of the Gram-positive bacterium Bacill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lapidus A., Galleron N., Sorokin A., F
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Microbiology 143:3431-3441(1997).
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Transferase; DNA-directed DNA polymerase; DNA replication;

Transferase; Exonuclease; DNA-binding; Complete proteome.

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01-OCT-1993
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P32926;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HUMAN
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                                                                                                                                                                                                                    Amagai M., Klaus-Kovtun V., Stanley J.R.;
"Autoantibodies against a novel epithelial cadherin in pemphigus vulgaris, a disease of cell adhesion.";
                                                                                                                                                                                                                                                                   MEDLINE-92069753; PubMed=1720352;
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                  DSG3
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                             DISEASE: PEMPHIGUS VULGARIS (PV) IS A POTENTIALLY LETHAL SKIN DISEASE IN WHICH EPIDERMAL BLISTERS OCCUR AS THE RESULT OF THI LOSS OF CELL-CELL ADHESION CAUSED BY THE ACTION OF AUTOANTIBO
                                                                                                                         FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS FILAMENTS MEDIATING CELL-CELL ADHESION.
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: EPIDERMIS, TONGUE, TONSIL,
                                                                                             DOMAIN: CALCIUM MAY BE
                                                                                                              CARCINOMAS
                                                                              (POTENTIAL)
                                                                                                                                                                                                     67:869-877(1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DIHTKTAMDVFHVAKDEVTSAMRRQAKAVNFGIV-YGISDYGLSQNLGITRKEAGAFI--
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(Rel. 27, Last sequence update)
(Rel. 40, Last annotation update)
3 precursor (130 kDa pemphigus vulgaris antigen) (PVA).
                                                                                                                                                                                                                                                                                                                                                                (Human)
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 CONTAINS 5 CADHERIN DOMAINS
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                                                                                             BOUND BY
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
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                            VINVREGIAFRPASKT-----FTVQKGISSKKLVDYIL--
                                                                                                                                                              KNLIENASAEHGYFDGRWLDRSVDVILPDNTADVSLIYDTGTQYRFDEVVFFTIDPKTNQ 375
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NLVAAKARHL--
                                                    IQN--DQVSFEQSSSSRTEPAQVDESTLEPVIETVELTDGILMDISPIEFSASNLIQDKL
                                                                                                          LTTDPDKLPVKREL-LEQLLTVNMGEAYNLQAVRALSNDLIATRYFNMVNTEIVFPEREQ 434
                                                                                                                                                                                         SLDREQASSYRLV-VSGADKDGEGLSTQCECNIKVKDVNDNFPM-----FRDSQYSARIE
                                                                                                                                                                                                                  DLGEPVYIDYRAYEVRGEGADDKAFTT-----VADEVPLLIGDVFHHGKYETK--
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                                                                                                                                     ENILSSELL----RFQVTDLDEEYTDNWLAV-YFFTSGNEGNWFEI---QTDPRTNE
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DESMOGLEIN REPEAT 2.
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 128.5;
Pred. No. 15;
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CHAIN
                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                        merozoites.",
Cell 69:1213-1226(1992).
-I- FUNCTION: INVOLVED IN RETICULOCYTE
HUMAN RETICULOCYTE CELLS.
-I- SUBUNIT: HOMODIMER (POTENTIAL).
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MEDLINE=92315338; PubMed=1617731;
Galinski M.R., Medina C.C., Ingravallo P.,
"A reticulocyte-binding protein complex of
                                                                                                             EMBL; M88097; AAA29743.1;
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                                                                                                                                                                                      entities
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01-OCT-1996
                                                                                 Malaria;
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Eukaryota; Alveolata; Apicomple)
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                                                                                                                                                        requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                         Receptor; Signal;
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Pred. No. 75;
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F CRC64;
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(Rel. 40, Creat (Rel. 40, Last

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                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN-MC58 / Serogroup B;
MEDLINE-20175755; PubMed=1
                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                          TIGR; NMB0585
                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE002414; AAF41013.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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Science 287:1809-1815(2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nelsseria meningitidis (serogroup B).
Bacteria; Proteobacteria; beta subdivision; Nelsseriaceae; Neisseria
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                                                                                               163 GLIKRLYARLFN---DGVNKVPRLKAKFYQSSQSGETSAIGSSHQKTEPYA-----NIK 213
                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISEASE.
SUBCELLULAR LOCATION: OUTER-MEMBRANE ASSOCIATED AND SECRETED
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                        YHVYD---PLALDLDGD-----GIETVAAKGFSGSLFDHTNNGIRTATGWVSADDGLL
                                              AALEDITQESAMDLNGSIPRLRQTALVAARAVGY----YDIDLSIIRNSIGEVD----VI 265
                                                                        GIINDLYKSVVKREWTGIFEIVNNNIKQFRDLFPNPEGWIDDGHQCFAPWVKETKKRNGK 282
 IHDLGEPVYIDYRAVEVRGEGADDKAFTTVADEVPLLIGDVFHHGKYETKKNLIENASAE 325
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Similarity 19.6%;
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                                                                                                                                   Score 126.5;
Pred. No. 29
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X REPEATS, GLY-RICH.
                                                                                                                        Mismatches
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15-JUN-2002 (Rel. 41, Last and
15-JUN-2002 (Rel. 41, Last and
                                                              Bacteria; Proteobacteria; Gluconacetobacter.
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MEDLINE=98296257;
            STRAIN-BPR
                        SEQUENCE FROM N.A.
                                               NCBI_TaxID=28448;
                                                                                    Acetobacter xylinus
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 PubMed=9630539;
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                                                                        alpha subdivision; Acetobacteraceae;
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Best Local Similarity 19.0%; Pr
Matches 199; Conservative 134;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR01441; CELLSNTHASEC.
Cellulose biosynthesis; Repeat; TPR repeat; Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AB010645; BAA31465.1; -.
InterPro; IPR003921; Cellsynth_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001440;
Pfam; PF00515; TPR; ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY:
        488
                                                                                                                                                                                                                                                                                          337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 AATQSYRQTLSWLPVNPDTQPLMEQWLSA------HPND-----AALREHMLHPPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47 TAINQAKAGNPPVLLT-PEQIQARL---NAAGLNAKPQSQAL----DVVNFDDQSPI-SR 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: Required for maximal bacterial cellulose synthesis. may be involved in the formation of a membrane complex for extrusion of the cellulose product (By similarity). PATHWAY: Bacterial cellulose biosynthesis. SUBCELLULAR LOCATION: Outer membrane (Potential). SIMILARITY: BELONGS TO THE ACSC/BCSC FAMILY. SIMILARITY: CONTAINS 6 TPR REPEATS.
                                                                                                                                                                                                                                                                                                                                                                      YRAVEVRGEGADDKAFTTVADEVPLLIGDVFHHGKYETKKNLIENASAEHGYFDGRWLDR 336
:| | | | | | | | : : | | | | | | : :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GPPDKAGLARQ-------AGYQQLNAGRLSAAEQSFQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IGEQSPPLGLD-MSVIEETTPLSLEELFAQESTEMGINPNDYIPEYQGEQPNSEVVVPPT 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TQWDQARAGLAGIVASNPQNYRAQLAFAQALTYNTSTRMEGLTRLKDLQSFQSQAPVEAA 240
        TSDSARKVSILREA-----
                                                    TEPAQVDESTLEPVIETVELTDGILMDISP----IEFSASNLIQDKLNLVAAKARHLYDM 505
                                                                                                                                                                 LEQLLTVNMGEAYNLQAVRALSNDLIATRYFNMVNTEIVFPEREQIQNDQVSFEQSSSSR
                                                                                                            LMGLARVDMAQGNTAEARQLLSR--VSPQY-----ASQVGEIEVSGLMAAASQ
                                                                                                                                                                                                                                                                                 SVDVILPDNTADVSLIYDTGTQYRFDEVVFFTIDPKTNQLTTDPDKL-----PVKREL
                                                                                                                                                                                                                                                                                                                                         HRYFE-EAMAADPK----TADRWRPALAGMAVSGDYAAVRQLI----AAHQYTEAK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----SALQINS-------HDAD-----SLGGMGLVSMRQGDTAEA- 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EDITQESAMDLNGSIPRLRQTALVAARAVGYYDIDLSIIRNSIGEVDVIIHDLGEPVYID 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LEPEKPGLIKRLYARLFNDGVNKVPRLKAKFYQSSQSGETSAIGSSHQKTEPYANIKAAL 216
                                                                                                                                                                                                                         ------QKLATLARQPGQYTGATLMLADLQRSTGQVAAAEQEYRGILSREPNNQLA 441
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CELLULOSE SYNTHASE OPERON PROTEIN C.

TPR 1.

TPR 2.

TPR 3.

TPR 4.

TPR 5.

TPR 6.
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Pred. No. 30
MAQAPRDPWVRINLANALQQQGD-VAEAGRVMQPI 535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                            487
                                                                                                                                                                                                                                                                                                                                         391
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(Rel. 40, Last sequence update) (Rel. 40, Last annotation update) (Rels) (Re		Qy 767 AGISGVYSFGDNAYGSNRAHOMTGGIQAGYIWSDNFNHVPYRLRFFAGGDQSIRG	689 LRYRLDKL-         :   832 LRLQQVE   722LLAG   :   :   890 DTSDQMLSS	Qy 612 GYQAGAELRLSEDKKGVKLYATKPLSHPLNDQLRATL	Qy 585	Qy 555 ALANRKTPADVYQSKKVPLYVFVASDKPRD ::	Qy 506PDDRVLAINHDDGVNRSILGRISDAVSAVARAILPDESENEVIDLPERT
ipdate) ;ion; Neisseriaceae; Neisseria.	9 0	NENHVPYRLREFAGGDQSIRG 821	WQDLPVDFVNGKPSQEA ;	KP		<pre>(KPPLYVFVASDKPRD 584 : : :     :   RGDMVHARMALRIASTRTIDLSPDQRL 654</pre>	SDAVSAVARAILPDESENEVIDLPERT 554

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Best Local Similarity
                                                                                        Matches
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TIGR; NMB1415; -.
InterPro; IPR001343; Hemlysn_Ca_bind.
Pfam; PF00353; hemolysinCabind; 22.
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                                         170 ARLFNDGVNKVPRLKAKFYQSSQSGETSAIGSSHQKTEPYA----NIKAALEDITQES 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC ACTIVITY.
SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
AREFFKGLPSFKDLAEKFRDLFPNPE-GWIDDGHQCLAPWVKETKKRNGKYHVYD---PL 416
                                                                                          186;
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uter membrane; Repeat; Complete proteome.
1702 43 X REPEATS, GLY-RICH.
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                                                                                     ; Score 126.5;
; Pred. No. 48;
86; Mismatches
                                                                                                                                                                                    MW;
                                                                                                                                                                                  8F63506E1F6D9B40 CRC64;
                                                                                          306;
                                                                                                                                    DB 1;
                                                                                          Indels
                                                                                                                                    Length 1829;
                                                                                          345;
                                                                                     Gaps
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RESULT RP1_HU ID RP AC P OT 3 DT 3 DT 3 DT 1 DE ( GN R		Qy  Db 1  Qy  Db 1	Db Qy Db	Qy Db	Оу	Qy Db	ОУ	Оy	Qу	Qy Db	Qу	Qу	Qу
HIMAN  RP1_HUMAN  RP1_HUMAN  RP1_HUMAN  RP1_HUMAN  RP1_HUMAN  RP1	O NUALIGINGNDALMGGE - GRUHINGEDGND - ILIGGRONDI DEGGGGDI FEGA 110 2 GYGYRWASPYGOYRVDYATGYKE 904	764 IARAGISGVYSFGDNAYGSNRAHOMTGGIOAGYIWSDNFNHVPYRLRFFAGGDOSIRGYA 823	1   1   1   1   1   1   1   1   1   1	26 KGVKLYATKPLSHPLNDQLRATLGYQQEVFGHSTN 6	596GTRLVT	LYVFVASDKPRDGQIGLGWGSDT	513 INHDDGVNRSILGRISDAVSAVARAILPDESENEVIDLPERTALANRKTPADVYQSKKVP 572 ::	470 TDGILMDISPIEFSASNLIQDKLNLVAAKARHLYDMPDDRVLA 512	410 LSNDLIATRYFNMVNTEIVFPEREQIQNDQVSFEQSSSSRTEPAQVDESTLEPVIETVEL 469	371PKTNQLTTD	340 VILPDNTADVSL	280 VEVRGEGADDKAFTTVADEVPLLIGDVFHHGKYETKKNLIENASAEHGYFDGRWLDRSVD 339	224 AMDLNGSIPRLRQTALVAARAVGYYDIDLSIIRNSIGEVDVIIHDLGEPVYIDYRA 279

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EMBL; AF143226; AAD44197.1; JEMBL; AF143224; AAD44197.1; JEMBL; AF143225; AAD44197.1; JEMBL; AF143225; AAD44198.1; JEMBL; AF143221; AAD42072.1; LEMBL; AF152242; AAD46774.1; JEMBL; AF152241; AAD46774.1; JEMBL; AF152241; AAD46774.1; JEMBL; AF146592; AAD46769.1; JEMBL; AAD467692; 
       Vision;
DOMAIN
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or send a
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the Euro
                                                                            InterPro; IPR003533; DCX. Pfam; PF03607; DCX; 2. SMART; SM00537; DCX; 2. PROSITE; PS50309; DC; 2.
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MIM; 180100; -.
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Sullivan L.S., Heckenlively J.R., Bowne S.J., Zuo J., Hide W.A.,
Gal A., Denton M., Inglehearn C.F., Blanton S.H., Daiger S.P.;
"Mutations in a novel retina-specific gene cause autosomal dominant
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Nat. Genet. 22:255-259(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-99330563; PubMed-10401003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Ex-
European Bioinformatics Institute. There are no restr
by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: COULD HAVE A RÔLE IN THE DIFFERENTIATION PHOTORECEPTOR CELLS:
TISSUE SPECIFICITY: EXPRESSED IN RETINA. NOT EXPRES BRAIN, PLACENTA, LUNG, LIVER, SKELETAL MUSCLE, KIDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WWW-"http://www.sph.uth.tmc.edu/retnet/".
DATABASE: NAME=Mutations of the RP1 gene;
NOTE-Retina International's Scientific Newsletter;
WWW-"http://www.retina-international.com/sci-news/rplmut.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: CONTAINS 2 DOUBLECORTIN DOMAINS DATABASE: NAME=RetNet;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISEASE: DEFECTS IN RP1 CAUSE RETINITIS PIGMENTOSA FORM 1 (RP1); A DISEASE CHARACTERIZED BY CONSTRICTION OF THE VISUAL FIELDS, NIGHT BLINDNESS, AND FUNDUS CHANGES. THE DISEASE SEEMS TO BE ASSOCIATED WITH TRUNCATED (STOP OR FRAMESHIFT MUTATIONS) FORMS OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE=Retinal information network;
Retinitis pigmentosa; 36 118 [
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and this statement is not removed. requires a license agreement (See an email to license@isb-sib.ch).
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Primates; Catarrhini; Hominidae; Homo
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Polymorphism; Repeat.
DOUBLECORTIN 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kozak C.A.,
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photoreceptor
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Qy	DЬ	Qy	Db .	Qγ	da Vy	, 5	P 04	Db	Qy	DЪ	Qy	Дb	Qy	DЬ	Qy	DЬ	Qy	Оy	Db	Qy	Db 43	ΟV	Qy Db	Ma Ma	SQ	1 T T	F F	1 F F	1 F F	177	7 T T
664 LSTRTLEHEISRSIIQNGGWNRTYSLRYRLDKLKTQAP	751 STISKNFHRNKLNTTQNSKVQGLLTKRKSRSLNKIS	624DKKGVKLYATKPLSHPLND	691 ATKGILNKNERINTKGRITKEMIVQDSDS	588 GLGWGSDTGTRLVTKFEHNLINRDGYOA	528 SDAVSAVARAILPDESENEVIDLPERTALANRKTPAD      :  :: :: :   : :  :  635 SSTVTARIDRLINEFAQCGLTKLPKNEKKILSS	100 TABBUAABCAAFDNXTGIAN	487 LIQDKLNLVAAKARHLYDMPDDRVL	::  :	452 PAQVDESTLEPVIE	459 QKKSV-IGSVTLVSETEVQEKMIGQFSYSE	398 MGEAYNLQAVRALSNDLIATRYFNMVNTEI	Db 408 INIQMTDQVAETCSSASWENATVDTDIIQGTQDQAKHRF	338 VDVILPDNTADVSLIYDTGTQYRFDEVVFFTIDP	357 GPSNNDEKSEMSFPGRTESRSSGLKLAACSFSADV	297DEVPLLIGDVFHHGKYETKK	311 PIYPSEDDIEKSIIFNQDGTMTV	246 GYY	188 YOSSQSGETSAIGSSHQKTEPYANIKAALEDITQESAMDL         :   :   :   :   :   :   :   :	201 TDGRRVPSLQAVILSSGAVVAAGREPFK	136NDYIPEYQGEQPNSEVVVPPTLEPEKPGLIKRLY	156LYVERNGDPKTRRAVLLS	82 OALDVVNFDDOSPISRIGEOSPPLGIDMSVIFFTTDIS	Qy 22 PLMTSQALAQQNNPANIINHVPAHDTAINQAKAGNPPVLLTP   :: : ::          :   126 PWLSSRAISAHSPPHPVAV	Query Match 2.7%; Score 126.5; DB Best Local Similarity 17.5%; Pred. No. 62; Matches 181; Conservative 159; Mismatches 3	SEQUENCE 2156 AA; 240659 MW; 55AEDBEC43D	VARIANT 2033 2033 /FTId=VAR_00781	FT VARIANT 1691 1691 S -> P.	VARIANT 1670 1670 A -> T.	VARIANT 985 985 N -> Y.	DOMAIN 1687 1691 POLY-SER. VARIANT 872 872 R -> H.	FT DOMAIN 154 233 DOUBLECORTIN 2. FT DOMAIN 268 273 POLY-SER. FT DOMAIN 671 675 POLY-IVS
PETWQDLPVDFVNGKPSQEALL 723	LGAPKKREIGQRDKVFPHN 805	QLRATLGYQQEVFGHSTNGFD 663	DTVIESNTFCSKSNLN 7	IRISE 623	VYQSKKVPLYVFVASDKPRDGQI 587	C)	DGVNRSILGRI 52	:: HNNGLPSTISNNS 57	TVELTDGILMDISPIEFSASN 486	YHMETHSCSKMSSVSNK 51	DQVSFEQSSSSRTE 451		KTNOLTTDPDKLPVKRELLEQLLTVN 397	:  :     RSSNQEGSLAEE 4	NLIENASAEHGYFDGRWLDRS 337	::   :::    : EMKVRFRIKEEETIKWTTTVSKT 356	EGADDK	NGSIPRLRQTALVA ARAV 245 :   : : : : : : : : : : : : : : : : :	NYDIQKYLLPARLPGISQRV 250	ARLFNDGVNKVPRLKAKF 187	RRVTQSFEAFLQHLTEVMQRPVVKLYA 200	AORCHRACTND 13	TPEQIQARLNAAGLNAKPQS 81	1; Length 2156; 67; Indels 325; Gaps	A. 6A507 CRC64;				).		

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         Hypothetical protein; Calcium CA_BIND 2025
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Consell M., Copsey T., Coulson A
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen I
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
Materston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                  Pfam; PF00036; efhand; 2.
Pfam; PF00435; spectrin; 10.
Probom; PD000012; EF-hand; 1
SMART; SM00150; SPEC; 5.
PROSITE; PS00018; EF_HAND; 1
                                                                                                                                                                                                                                                                                                                                                                                                              "2.2 Mb of contiguous nucleotide sequence from elegans.";
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                                                                                                                                       EMBL; L14433; AAAAZ7973.1; -. WOORMPOP; C50C3.2; CE01861. InterPro; IPR002048; EF-hand. InterPro; IPR002017; Spectrin.
                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                         Nature 368:32-38(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-Bristol N2;
MEDLINE-94150718; PubMed-7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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P34367;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 28, C)
(Rel. 28, L,
(Rel. 41, L,
al 256.3 kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                     EF-hand; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , Last sequence update)
, Last annotation update)
Da protein C50C3.2 in chromosome
                                 Calcium-binding; Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TKIAGLTGDNLCKEGDKSF - -
                  EF-HAND (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
 CD1B2C1092C5EDC8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -SGVYSFGDNAYGSNRAHOMTGGIQAGYI 797
                                                                                                                                                                                                                                                                                                                                                                                                                                chromosome
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                                                                                                                                                  PGCV_HUMAN STANDARD; PRT; 3396 AA.
P13611; P20754; O3UNW5; Q13010; Q13189; Q15123;
O1-JAN-1990 (Rel. 13, Created)
O1-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Versican core protein precursor (Large fibroblast proteoglycan)
(Chondroitin sulfate proteoglycan core protein 2) (PG-M) (Glial
                                                                                                                                                                                                                                                                                                           HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1455
MEDLINE=95105188; PubMed=7528742; Naso M.F., Zimmermann D.R., Tozzo
                                                                                         Eukaryota; Metazoa; Mammalia; Eutheria;
                                     SEQUENCE FROM N.A.
                                                                      NCBI_TaxID=9606;
                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1702 CRKLQNSTDAEKKLSLVSERLNALKKQLDLLAEKIAVDDKFKLKVQNIQDEYSRTACELG 176:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  486
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nes 124; Conserv
                                                                                                                                                                                                                                                                                                                                                                      WN
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                                                                                                                                                                                                                                                                                                                                                                                                                 GW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --IDEKVAELT------ELLES-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NLINRDGYQAGAELRLSEDKKGVKLYATKPLSHPLNDQLRATL----GYQQEVF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KWLKMNEELKKMHQKIKESIEFTK---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EIVFPEREQIQNDQVSFEQSSSSRTEPAQVDESTLEPVIETVELTDGILMDISPIEFSAS 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FTIDPKTNQLTTDPDKLPVKRELLEQLLTVNMGEAYNLQAVRALSNDLIA-TRYFNMVNT 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STNVGNDVSSNDVLKRKHQRLQLETQRREQKVAKVVYLTTELVSSHRRPSLEYKFVE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HGKY--ETKKNLIENASAEHGYFDGRWLDRSVDVILPDNTADVSLIYDTGTQYRFDEVVF 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IVEKLRNGISQLQMLIKANNEDLDV-WKSMQ------KVVTAIDDEICWFKEINVIFS 1454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DLSIIRNSIGEVDVIIHDLGEPVYIDYRAVEVRGEGADDKAFTTVADEVPLL--IGDVFH 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GMSIWLIDAETDVHSTTNFIGLYNSVDAEKASRLLVSLGEQAGEKDDILIRIQCDESVDV 1403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPEYQGEQPNSEVVVPPTLEPEKPGLIKRLYARLFNDGVNKVPRLKAKFYQSSQ-----S 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---IREKEQLL-DQILDLKTGLPETVLADVERKL--QVLETV---
                                                                                                                                                                                                                                                                                                                                                                                                                 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -GDHMDTLTIKAE---QMSDDEVI-------RTKVAVTAI------DQLRK 1619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -REQEEKIGNLVRHQKPASNFENTAYHSTMTFVETYTKDTFEKLKVV 1701
                                       (ISOFORM VO)
                                                                                         Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -EEEKVQVIRHLWSSLIESSTTRQKSL-AQECQKSRLFELLD 1343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 126.5;
Pred. No. 64;
01; Mismatches
   Iozzo
                                                                                         Craniata; Vertebrata;
Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---FVST--
   R.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NRQIAEIRTNRLEKWTEYFVTMNE 1549
                                                                                           Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -FDLSTRTLEHEISRSIIQNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -CDTGIQCI----
                                                                                                           Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2198;
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versican J. Biol. [2]

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Paulus W., Baur I., Dours-Zimmermann M.T., Zimmer "Differential expression of versican isoforms in J. Neuropathol. Exp. Neurol. 55:528-533(196).
                                                                                                                                                                                                                                           TISSUE SPECIFICITY OF ISOFORMS. MEDLINE-96213482; PubMed-862734
                                                                                                                                                                                                                                                                                                   Perides G., Lane W.S., Andrews D., Dahl "Isolation and partial characterization hyaluronate-binding protein.";
J. Biol. Chem. 264:5981-5987(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF JULY
TISSUB-Aortic smooth muscle;
MEDLINE-99327053; PubMed-10397680;
MEDLINE-99327053; Araun K.R., Maurel P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arterioscler.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wight T.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 3333-3396 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Brain;
MEDLINE-95181355; PubMed-7876137;
                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-89174663;
                                                                                                                                                                                                                                                                                                                                                                                                                                    PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    without a chondroitin tissues.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "A fibroblast chondroitin sulfate proteoglycan core protein contains lectin-like and growth factor-like sequences.";
J. Biol. Chem. 262:13120-13125(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-95105187; PubMed-7806529;
Dours-Zimmermann M.T., Zimmermann D.R.;
"A novel glycosaminoglycan attachment domain ic alternative splice variants of human versican."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Versican/PG-M isoforms in vascular smooth muscle cells.",
Arterioscler. Thromb. Vasc. Biol. 19:1630-1639(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zako M., Shinomura T., Ujita M., Ito K., I
"Expression of PG-M(V3), an alternatively
without a chondroitin sulfate attachment :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM V3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Mapping of the versican proteoglycan human chromosome 5 (5q12-5q14)."; Genomics 14:845-851(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 251-347 FROM N.A. MEDLINE=93122792; PubMed=1478664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Lung fibroblast;
MEDLINE-88007514; PubMed=2820964;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zimmermann D.R., Ruoslahti E.;
"Multiple domains of the large fibroblast proteoglycan, versican.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IOzzo R.V., Naso M.F., Cannizzaro L.A.,
McPherson J.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 2711-3396 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Glial tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM V2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-90059882;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Characterization versican gene and
                                                                                                      Neuropathol. Exp. Neurol. 55:528-533(1996).

FUNCTION: May play a role in intercellular signaling and in connecting cells with the extracellular matrix. May take part the regulation of cell motility, growth and differentiation. B
      SÜBCELLULAR LOCATION: Secreted; extracellular matrix.
ALTERNATIVE PRODUCTS: At least 5 isoforms; V0 (shown here),
V2, V3 and Vint; are produced by alternative splicing.
TISSUE SPECIFICITY: Cerebral white matter. V0 and V1 is expl
                                                                                             hyaluronic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8:2975-2981(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chem. 270:3914-3918(1995).
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Chem.
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and functional analysis of its promoter.";
269:32999-33008(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        269:32992-32998(1994)
                                                                                                                                                                                                                                      PubMed=8627343;
                                                                                                                                                                                                                                                                                                                                                                   PubMed=2466833;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ISOFORM VINT)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene (CSPG2) to
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                                                                                                                                                                                                                                                                                                                                             D., 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kimata K.;
y spliced form of PG-M
in region in mouse and
                                                                                                                                                                                           Zimmermann I
rms in brain
                                                                                                                                                                                                                                                                                                                                             Bignami A.;
a glial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    region in mouse and human
      and V1 is expressed
                                                                                                                                                                                                                 D.
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                                                                                                                                                                                           tumors.";
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    THE TENT OF THE TE
                                                                                                                                                                                                 PROSITE; PS00010; ASX_HYDROXYL; 1.
PROSITE; PS00022; EGF_1; 2.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS01181; LINK; 2.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS00615; C_TYPE_LECTIN_2; 1.
                                                                                                          Hyaluronic acid: SIGNAL CHATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U16306; AAA65018.1; -. EMBL; X15998; CAA34128.1; -. EMBL; S52488; AAB24878.1; -. EMBL; U26555; AAA67565.1; -. EMBL; D32039; BAA06801.1; -. EMBL; J02814; AAA36437.1; -. EMBL; AF084545; AAD48545.1; -.
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PIR; A29348; A29348.
PIR; A30358; A30358.
HSSP; P01132; IEGF.
Genew; HGNC:2464; CSP
                   CHAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                            SMART;
SMART;
SMART;
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InterPro;
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Glycoprotein;
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ProDom; PD000918; Link; 2.
SMART; SM00032; CCP; 1.
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Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                         SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000436; Pfam; PF00008; EGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART;
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r; SM00034; CLECT; 1.
r; SM00179; EGF_CA; 1.
r; SM00001; EGF_1ke; 1.
r; SM00409; IG; 1.
r; SM00445; LINK; 2.
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: IPR001438; I
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sushi; 1.
xlink; 2.
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                                                                                                                                                                 EGF-like domain; Calcium;
                                                                                                                                               Alternative
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EGF_II.
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Ig_MHC.
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EGF-like.
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                                                        VERSICAN CORE PIG-LIKE V-TYPE LINK 1.
                                         LINK
                 GAG-ALPHA
DOMAIN)
                                                                                                                              POTENTIAL
                                                                                                                                                               Extracellular matrix; lcium; Immunoglobulin
                   (GLUCOSAMINOGLYCAN ATTACHMENT
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Biol.

Genomics

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PROTEIN.

Sushi;

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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                             DEVELOPMENTAL STAGE: Disappears after the cartilage SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE D SIMILARITY: CONTAINS 2 LINK DOMAINS. SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS. SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN. SIMILARITY: CONTAINS 1 SUSHI (SCR) DOMAIN. SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEO
                                                                        ween the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
ified and this statement is not removed. Usage by and for com
                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration -
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                                                                                 KRE--LLEQLLTV-----NMGEAYNLQAVRALSNDLIATRYFNMVNTEIV-FPEREQIQN
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                         DQVSFEQSSSSRTEPAQVDESTLEPVIETVELTDGILMDISPIEFSASNLIQDKLNLVAA 497
                                                     SGDKILVEGISTVIYPSLQTEMTHRRERTETLIPEMRTDTYTDEIQEEITKSPFMGKTEE
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EVFSGMKLSTSLSEPIHVTES
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18; Mismatches
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EGF-LIKE 1.
EGF-LIKE 2, CAL
C-TYPE LECTIN.
SUSHI.
BY SIMILARITY
BY SIMILARI
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RESULT 40
P200_MYCGE STANDARD;
ID P200_MYCGE STANDARD;
AC Q49429; Q49259; Q49298; Q4
AC Q49479; Q49259; Q49298 Q7
01-NOV-1997 (Rel. 35, Last
DT 01-NOV-1997 (Rel. 35, Last
DT 15-JUN-2002 (Rel. 41, Last
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P SEQUENCE FROM N.A.

C STRAIN-ATCC 33530 / G-37;

X MEDLINE-96026346; PubMed-7569993;

X MEDLINE-96026346; PubMed-7569993;

X Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,

RA Fitischmann R.D., Bult C.J., Kerlavrage A.R., Sutton G., Kelley J.M.,

RA Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,

RA Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,

RA Nguyen D.T., Dugherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,

Potterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;

RA Petterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;

"The minimal gene complement of Mycoplasma genitalium.";
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EMBL; U02245; AAA03400.1; -
EMBL; U02245; AAA03401.1; A
EMBL; U022175; AAD12458.1; -
EMBL; U02126; AAD12402.1; -
TIGR; MG386; -
                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 256-427; 432-543 AND 1083-1140 FRC STRAIN-ATCC 33530 / G-37; MEDLINE-94075230; PubMed-8253680; Peterson S. N., Hu p.-C., Bott K.F., Hutchison Pasurvey of the Mycoplasma genitalium genome
                                                                                                                                                                                                                                                                                   sequencing.";
J. Bacteriol. 175:7918-7930(1993).
-i- FUNCTION: COULD BE A ACCESSORY
CYTADHERENCE (BY SIMILARITY).
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Cytadherence; Structural DOMAIN 1205 1389

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Search completed: April 28, 2003, 16:22:31 Job time : 67 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76 NAKPOSQALDVVNFDDQSPISRIGEQSPPLGLDMSVIEETTPLSLEELFAQESTEMG--- 132
                                                                                                  TESAETPNEFSSEQKDTLEFISQTQE------VETSESNVPTVEQETKLFEHQDE 787
                                                  NNLFTPLPLDLTEIIESNALFDSKPDEK 815
                                                                                                                             EQSSSSRTEPAQVDESTLEPVIETVELTDGILMDISPIEFSASNL------IQDK 491
                                                                                                                                                       KSLETKTTSVELNHEEIGNEFINLDVSEKEVQEQPTTQLETDSEFVLPTYQIVED---SF 738
                                                                                                                                                                          EAYNLQAVRA-LSNDLIATRYFNM------------VNTEIVFPEREQIQNDQVSF 442
                                                                                                                                                                                                                                      EVVFFTIDPKTNQ------LTTDPDKL-----P-VKRELLEQLLTVN-MG
                                                                                                                                                                                                                                                                 EKIKETNSDESVNTDLTALFSEKLVNEVLLTNEYVDVNAPFSTETEVKVSSELPKSELVD
                                                                                                                                                                                                                                                                                                                                                                         DYSKEIKDS-----AKA-----DLSNISDDIDSVWKEFGSFTDETQKSVEEKS
                                                                                                                                                                                                                                                                                                                                                                                                   ESAMDLNGSIPRLRQTALVAARAVGYYDIDLSIIRNSIGEV-----DVIIHDLGEPV 273
                                                                                                                                                                                                             EITFINNDPKPQEGLEYKVDFLETEPKSLFDEKTTIVVESEPPFIQPDLSLELDSVNDVD 681
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256
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1616
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158 1399 1-2.
191 1389 2 X 26 AA REPEAT.
101 1186 2-1.
102 2-2.
1039 2-2.
104 304 S -> F (IN REF. 2).
105 AA; 185678 MW; 6AF76A13AC49E4FF CRC64;
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Result
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Maximum
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Maximum Match 10
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479
353-54
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532
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Match
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sp_rvirus:*
sp_bacteriap:*
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sp_virus:*
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9 Q9EX31
9 Q9EX14
9 Q9EX31
9 Q9EX14
9 Q9EX31
9 Q9EX14
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                        Q8XZI3
                                                         Q9ey32 xanthomonas
Q9pd7 xylella fas
Q8rht4 fusobatteri
P95359 neisseria g
Q9k1h0 neisseria m
Q9y31 neisseria m
Q8vq24 bartonella
Q30912 neisseria m
                                                                                                                                                                                                                              Q9i0ul pseudomonas
Q9ck26 pasteurella
Q8zb95 yersinia pe
Q8xel5 salmonella
Q9kp31 vibrio chol
                                                                                                                                                                                                                                                                                                                                                                Description
Q8xxi3 ralstonia s
Q8xwt6 ralstonia s
Q8uc83 agrobacteri
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Q910U1; Q910U1; 01-MAR-2001 01-MAR-2001 01-OCT-2001

PRELIMINARY;

579

(TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 18, Last annotation update)

Pseudomonas aeruginosa. Bacteria; Proteobacteria;

gamma subdivision; Pseudomonadaceae;

Hypothetical PA2543.

protein

PA2543

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Q9a711 caulobacter			769		•	ō
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Q9zlh9 helicobacte			906		194.5	7
			776		197	6
Q8yur6 anabaena	6 Q8YUR6		833	4.2	197.5	ű
Q9x3v8 zymomonas	O		738		198	4
Q92j67 rickettsia			768	4.3	202.5	ū
Q9ze03 rickettsia			768	4.3	205.5	2
025369 helicobacte			916	4.4	206.5	Ξ
Q8yei3 brucella			623		209	õ
Q8zh58 yersinia	6 Q8ZH58		795	4.5	211.5	9
Q9pei2 xylella fas			784	4.5	214	œ
Q9jxb7 neisse			635	5	215	7
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			739	4.6	216.5	ŭ
	6 Q92LN9		618	4.7	220	4
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			79,	4.7	223.5	2
			78	4.7	K 1	õ
P73472 synechocyst			86		225	9
Q93pm2 haemophilus	O		793	4.9	229.5	8
Q8ufl6 agrobacter	6 Q8UFL6		77,	4.9	32	7

## ALIGNMENTS

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RESULT 1
Q91001
ID 0910
AC 0910
DT 01-y
DT 01-(
DF 08-c
OC PSc
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RP SEE
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RC STRAIN=ARCC 15692 / PAO1;

RX MEDILINE=20437337; PubMed=10984043;

RX Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

RA Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,

RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

RA Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an

RT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an

RT "ABO4682; AA605931.1;

DR EMBL; ABO4682; AA605931.1;

DR EMBL; ABO4682; AA605931.1;

RW Hypothetical protein; Complete proteome.

SQ SEQUENCE 579 AA; 63739 MW; 23467005C836FBBF CRC64;
                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 178
                   266
                                                                                                                                                                                                     210
                                                                                                            41
                                                                                             ANIEAYYGSLGERD----EAALQRFRRNAEAQAEKAAQALGYFQ-----AQIDSE 86
                   IHD---
                                                                                                                                                                                           ANIKAALEDITQESAMDLNGSIPRLRQTALV----AARAVGYYDIDLSIIRNSIGEVDVI 265
                                                                                                                                                                                                                                                                                         h 13.0%;
Similarity 24.5%;
78; Conservative 11
-----LGEPVYIDYRAVEVRGEGADDKAFTTVADEVPLLIGDVFHHGKYET 314
                                                                                                                                                                                                                                                                                                   117;
                                                                                                                                                                                                                                                                               Score 615.5; DB 16; Length 579;
Pred. No. 4.3e-28;
7; Mismatches 220; Indels 213;
                                                                                                                                                                                                                                                                                    Gaps
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O9CK26;
O1-JUN-2001 (TrEMBLrel. 17, Created)
O1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein PM1809.
PM1809.
                                                                         MEDLINE-21145866; PubMed-11248100; May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam "Complete genomic sequence of Pasteurella multocida proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001). EMBL, AB006218; AAK03893.1; -
Pfam; PF01103; Bac_surface_Ag; 1.
PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                          NCBI_TaxID=747;
                                                                                                                                                                                                                                                                   Pasteurella
                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                         Pasteurella multocida
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                                      InterPro: IPR000184; Bac_surfAg_D15
InterPro: IPR001092; HLH_basic.
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                                                                                                                                                                                                                                                                                    subdivision; Pasteurellaceae;
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                                                                                                                        1 T.S., K
                                                                                                                                         Kapur V.;
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Q8ZB95
ID Q8ZB
AC Q8ZB
DT 01-M
DT 01-J
DT 91-J
DT Puta
GN YPO3
OS Yers
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Query Match
Best Local s
Matches 166
                                                                                             Q8ZB95
Q8ZB95;
Q8ZB95;
Q1-MAR-2002 (TIEMBLIEL 20, C)
Q1-MAR-2002 (TIEMBLIEL 20, L)
Q1-JUN-2002 (TIEMBLIEL 21, L)
                                                                                      Putative YPO3524.
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NCBI_TaxID=632
                       Yersinia
                                          Bacteria;
                                                                 Yersinia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QNTQLNNNVRIYVGMIDKEEADGSERHKQLVREAIDKALRAYGYYQSEVEFQIESQKPPK 100
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                                                                                                                                                                                                                                                                                                                                      YIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENASAEHGYFDGRWLDRSVDVILPDNTADVSLIYDTGTQYRFDEVVFFTIDPKTNQLTTD:: | | | | | | | | | | |
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                                                                                                                                                                                                                                                                                                                                                                                                                             YPDWWLATFADTGLAANQFTTKELRYGAGMGVRWASPVGAIKFDIATPVRDKDNSKNIQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       \tt MKDLRLAVFGDIGNAYDKGFTNDTKIGAGVGVRWASPVGQVRVDVATGVKEEGNPIKLHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNLVNPMRGYRQRYSLEVGSSGLVSDANMAIARAGISGVYSFGDNAYGSNRAHQMTGGIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIIQNGGWNRTYSLRYRLDKLKTQAPPETWQDLPVDFVNGKPSQEALLA--GVAVHKTVA 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RLSEDKKGVK-LYATKPLSHPLNDQLRATLGYQQEVFGHSTNGFDLS---TRTLEHEISR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YVSAPKQTLEATYKMPLLKNPLNYYYEYSAGLENE-NKNDTESFASSLSAIRYWNHE---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----AGWQHSLGLRVRYD-----
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                                          pestis.
Proteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -KKNSMEVGIGWASDVGPRLQLGWTKPWINNRGHSFRTNL
                                              gamma subdivision; Enterobacteriaceae;
                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----SFIQANVKDKTLLVFPTASVRRTRL
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Best Local Sin
Matches 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G., Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M., Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G., Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V., Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CO-92 / BIOVAR ORIENTALIS; MEDLINE=21470413; PubMed=11586360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00213; LIPOCALIN; UNKNOWN_1
Hypothetical protein; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AJ414157; CAC92753.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000566; Lipocln_cytFABP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           *Genome sequence of Yersinia pestis, the causative agent of plague
 520
                                                                   460
                                                                                                                                    407
                                                                                                                                                                                                      363
                                                                                                                                                                                                                                       684
                                                                                                                                                                                                                                                                         309
                                                                                                                                                                                                                                                                                                          625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      211 NIKAALEDI-TQESAMDLNGSI-PRLRQTALVAARAVGYYD--IDLSIIRNSIGEVDVII 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38
FVDSGEAVNNFSKSDLKTGAGVGVRWASPVGPIKLDIAAPI-GDNETHGVQFYIG
                               FGDIGNAYDKGFTNDTKIGAGVGVRWASPVGQVRVDVATGVKEEGNPIKLHFFIG 916
                                                                                               FNHVPYRLRFFAGGDQSIRGYAHDSLSPISDKGYLTGGQVLAVGTAEYNYEFMKDLRLAV
                                                                                                                                  GDSQRYSIDVSDTTWGSDVDFGIFQAQNVWIRTLGEK-----NRFVARGNVGWIETNN
                                                                                                                                                                  GYRQRYSLEVGSSGLVSDANMAIARAGISGVYSFGDNAYGSNRAHQMTGGIQAGYIWSDN
                                                                                                                                                                                                      QRAINLRWSLD-----
                                                                                                                                                                                                                                     NRTYSLRYRLDKLKTQAPPETWQDLPVDFVNGKPSQEALL - - AGVAVHKTVADNLVNPMR
                                                                                                                                                                                                                                                                       EQTLDFSYRIPLLRNPLEQYYLIQGGFRR-----
                                                                                                                                                                                                                                                                                                       KKGVKL-YATKPLSHPLNDQLRATLGYQQEVFGHSTNGFDLSTRTLEHEISRSIIQNGGW
                                                                                                                                                                                                                                                                                                                                                                        VYQSKKVPLYVFVASDKPRDGQIGLGWGSDTGTRLVTKFEHNLINRDGYQAGAELRLSED
                                                                                                                                                                                                                                                                                                                                                                                                                                            MPDDRVLAINHDDGVNRSILGRISDAVSAVARAILPDESENEVIDLPERTALANRKTPAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSSSRTEPAQVDESTLEPVIETVELTDGILMDISPIEFSASNLIQDKLNLVAAKARHLYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VKRELLEQLLTVNMGEAYNLQAVRALSNDLIATRYFNMVNTEIVFPEREQIQNDQVSFEQ 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RRGYFDANMIKSQLGVAAQLHEAFWDIDFDSGQRYRFGKVIF------QGSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EHGYFDGRWLDRSVDVILPDNTADVSLIYDTGTQYRFDEVVFFTIDPKTNQLTTDPDKLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AKVVPGEPVLIAGVDIVLQGGAKTDPDYQALVRRDTPKIGSVLNHGDFDNFTSSLTGLAL 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HDL--GEPVYIDYRAVEVRGEGADDKAFTTVADEVPLLIGDVFHHGKYETKKNLIENASA 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NVRARLSTIGTDEVTAD--GRFRSRVDEAIRQGLRALGYYDPTITFELQNRPAPARSVLI 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64405 MW;
                                                                                                                                                                                                                                                                                                                                       ----ELGGGYATDVGPRLTASWRKPWMNSFGHSLTTTTALSAP
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                                                                                                                                                                                                      ----HFTQGRVTDTTMLLYPGVSINRTRQRGGAMPVW
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Pred. No. 6.
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69AD3780BFDC20F1 CRC64;
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                                                                                                                                                                                                                                                                       -TDLNDTNSDTTTLNVARFWDLSSGW
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5.5e-21;
les 255;
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
Nature 413:848-852(2001).
EMBL; AE008906; AAL23229.1; -
EMBL; AE008906; AAL23229.1; -
EMBL; AL627283; CAD06889.1; -
InterPro; IPR000184; Bac_surfay_D15.
InterPro; IPR000184; Bac_surfay_D15.
InterPro; IPR000566; Lipocln_cytrABP.
pfam; PF01103; Bac_surface_A9; 1.
PROSITE; PS00213; LIPOCALIN; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M. Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamilin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D. Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720 MEDLINE=21534948; PubMed=11677609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Salmonella typhimurium, Salmonella typhi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Putative outer membrane protein YTFM OR STM4409 OR STY4768.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2002
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8XEL5;
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8XEL5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES=S.typhi; STRAIN=CT18; MEDLINE=21534947; PubMed=11677608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein; Complete proteome. SEQUENCE 577 AA; 64765 MW; FBA4A190173BF18C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete genome sequence of Salmonella enterica serovar Typhimurium
                              431
                                                                197
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                                                                                                                                                                 311
                                                                                                                                                                                                                                                                                                       210 ANIKAALEDITQESAMDLNGSIPRLRQTALVAAR----
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E-----FEKSRKTKILP----
                              EREQIQNDQVSFEQSSSSRTEPAQVDESTLEPVIETVELTDGILMDISPIEFSASNLIQD
                                                                                              PKTNQLTTDPDKLPVKRELLEQLLTVNMGEAYNLQAVRALSNDLIATRYFNMVNTEIVFP
                                                                                                                                 DYDNFKKSLTSVSLRKGYFDSEFIKSQLGIALGRHQAFWDIDYDSGERYRFGPVTF----
                                                                                                                                                                 KYETKKNLIENASAEHGYFDGRWLDRSVDVILPDNTADVSLIYDTGTQYRFDEVVFFTID
                                                                                                                                                                                                     DLLPPPAKGRQVLIARVTPGQPVLIGGTEVILRGGARTDKDYLALLKTRP-AIGTVLNQG
                                                                                                                                                                                                                                       SIIRNSIGEVDVIIHDL--GEPVYIDYRAVEVRGEGADDKAFTTVADEVPLLIGDVFHHG
                                                                                                                                                                                                                                                                     ANVRLKVEGLSGELEKNVRAQLSTIQSDEVTPDRRFRARVDDAIREGLKALGYYEPTIKF
                                                                                                                                                                                                                                                                                                                                         166;
                                                                                                                                                                                                                                                                                                                                                           Similarity
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(TremBLrel. 20, Last sequence update)
(TremBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                EGSQIRDEYLQNLLPFKEGDEYESKDLAELNRRLSATGWFNSV---VVAP
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                                                                                                                                                                                                                                                                                                                                                         10.1%;
22.7%;
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255
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Q9KP31
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Best Local S
Matches 164
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                                                                                                                                                     Hypothetical protein; Complete proteome.
SEQUENCE 582 AA; 65644 MW; E96946FB85F1C426 CRC64;
                                                                                                                                                                                                            Pfam; PF01103; Bac_surface_Ag; 1.
PROSITE; PS00213; LIPOCALIN; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-EL TOR N16961 / SEROTYPE 01;
MEDLING-20406833; PubMed-10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers
MCDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C
                  211
                                                                                                                                                                                                                                                              InterPro; IPR000184; Bac_surfAg_D15.
InterPro; IPR000566; Lipocln_cytFABF
                                                                                                                                                                                                                                                                                                                     TIGR; VC2548; -
                                                                                                                                                                                                                                                                                                                                            EMBL; AE004323;
                                                                                                                                                                                                                                                                                                                                                                                                   cholerae
                                                                                                                                                                                                                                                                                                                                                                       Nature 406:477-483(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
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NCBI_TaxID=666;
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NIKAALEDITQESAMDLNGSI---PRLRQTALVAARAVGYY--DIDLSIIRNS-----
                                                                 164;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VHKTVADNLVNPMRGYRQRYSLEVGSSGLVSDANMATARAGISGVYSFGDNAYGSNRAHQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --AVSRYWDLSSGWQRAINLRWSFD--------HFTQGNVTNTTMLFYPGVM
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                                                                                      Similarity
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                                                              Conservative
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                                                                                   9.68;
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                                                         104;
                                                    Score 454; DB 16;
Pred. No. 1.5e-18;
4; Mismatches 237;
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                                                                                                      582;
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EMBL; AY010120; SEQUENCE 593 F

Submitted (AUG-2001) to the EMBL/GenBank/DDBJ EMBL; AY010120; AAG38834.1;

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Sonti R.V from

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SEQUENCE FROM N.A.

Xanthomonas NCBI_TaxID=64187;

subdivision; Xanthomonas

group;

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RESULT
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O9EY32;
O1-MAR-2001 (TrEMBLrel. 16, Created)
O1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                     Xanthomonas oryzae pv. oryzae.
Bacteria; Proteobacteria; gamma
                                                                                                                                                Putative outer membrane protein.
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                                                                                                                                                                                                                                                                                                       EEGNPIKLHFFIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNLSLERHWQLDGGWHRTVFIRYLLENYR-----QGLQDD-----NSQFLLPGMTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KTNQLTTDPDKLPVKRELLEQLLTVNMGEAYNLQAVRALSNDLIATRYFNMVNTEIVFPE 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YDNLKSGIRNLALQKGYFNGDFQASRLEVIPELNQARVILHFDSGIRYLF------
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01-OCT-2000 (TrEMBLrel. 15, L
01-JUN-2002 (TrEMBLrel. 21, L
Hypothetical protein Xf1231.
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Best Local Similarity
   MEDLINE=20365717; PubMed=10910347; Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencic Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones
                                                        STRAIN-9A5C
                                                                                                                                                                                                      Q9PDZ7;
                                                                                                                                                                                                                   Q9PDZ7
                                                                   SEQUENCE FROM N.A.
                                                                                                                  Bacteria;
                                                                                                         Xylella
                                                                                                                                Xylella fastidiosa
                                                                                            NCBI_TaxID=2371;
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                                                                                                                                                                                                                                                                            GFGLRWRSPVGPVRVDIAHGLNDPDAQFQLYIDIG
                                                                                                                                                                                                                                                                                                   GVGVRWASPVGQVRVDVATGVKEEGNPIKLHFFIG
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                                                                                                                                                                                                                                                                                                                                                  DSLSPISDK--GYLTGGQVLAVGTAEY-NYEFMKDLRLAVFGDIGNAYDKGFTNDTKIGA
                                                                                                                                                                                                                                                                                                                                                                             VYGQLRWFLGAGDNSRLILRG
                                                                                                                                                                                                                                                                                                                                                                                                                        FSSGDDFEGAVYETSTLIYPQLQANYINVDDRLFPRSGVSGQMFIRGGAEGAGSDTNFGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                 FVNGKPSQEALL-AGVAVHKTVADNLVN-----PMRGYRQRYSLEVGSSGLVSDANMAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSESGAGVRGGVERRYVNARGHKMDTQLDYAQNRKSLTTSYRIPAFRWLDGWYTAS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSDTGTRLVTKFEHNLINRDGYQAGAELRLSEDKKGVKLYATKPLSHPLNDQLRATLGYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----KPEEADDQ------GRVPVDVKLTRAKRTVYT-----AGLSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ILMDISPIEFSASNLIQDKLNLVAAKARHLYDMPDDRVLAINHDDGVNRSILGRISDAVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           153;
                                                                                                                  Proteobacteria;
                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                  gamma
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Pred. No. 1.4e-12;
11; Mismatches 260
                                                                                                                                                                                                                  PRT;
                                                                                                                 subdivision;
                                                                                                                                                                                                                                                                                                                                                                          -EGGTTWTSDLVAMPPSLRFFAGGSNSIRGYAF
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     M.R.S.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein; Complete proteome. SEQUENCE 617 AA; 69579 MW; A875FA462C470D21 CRC64;
                                                                                                              657
               769
                                                                                      358
                                                                                                                                                             599
                                                                                                                                                                                                                                                                                     234
                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 AARAVGYY--DIDLSIIRNSIGEVDVIIHDLGEPVYIDYRAVEVRGEGADDKAFTTVADE
                                                                                                                                                                                                                                                                                                                                                                                     163
                                                                                                                                                                                                                                                                                                                                                                                                                                     103
ISGVYSFGDNAYGSNRAHQMTGGIQAGYIWSDNFNHVPYRLRFFAGGDQSIRGYAHDSLS : | :: | || || || || || || : : |
                                    DGTNTVAYQQSTLVYPQLEASYVDVDDATFPRNGSAATVLLRGGASALGSKSNFTQLHGQ
                                                          DFVNGKPSQEALLAGVAVHKTV--ADNLVNPMRGYRQRYSLEVGSSGLVSDANMAIARAG
                                                                                    DGWY1FFARAYDEQTKY1DLRNVKLSAARSGQ1NRHLTATASLNALRGR----
                                                                                                          ----HSTNGFDLSTRTLE-HEISRSIIQNGGWNRTYSLRYRLDKLKTQAPPETWQDLPV
                                                                                                                                    LRAGVERRYMNARGHKMNARLDYAQNLKSL--
                                                                                                                                                          LVTKFEHNLINRDGYQAGAELRLSEDKKGVKLYATKPLSHPLNDQLRATLGYQQEVFG--
                                                                                                                                                                                                           LPDESENEVIDLPERTALANRKTPADVYQSKKVPLYVFVASDKPRDGQIGLGWGSDTGTR
                                                                                                                                                                                                                                     KLDYFSSIDIQPK--
                                                                                                                                                                                                                                                          PIEFSASNLIQDKLNLVAAKARHLYDMPDDRVLAINHDDGVNRSILGRISDAVSAVARAI
                                                                                                                                                                                                                                                                                                          YFNMVNTEIVFPEREQIQNDQVSFEQSSSSRTEPAQVDESTLEPVIETVELTDGILMDIS
                                                                                                                                                                                                                                                                                                                                      YDMGPVRFH - - -
                                                                                                                                                                                                                                                                                                                                                          YRFDEVVFFTIDPKTNQLTTDPDKLPVKRELLEQLLTVNMGEAYNLQAVRALSNDLIATR
                                                                                                                                                                                                                                                                                                                                                                                  FKPKLGEIFNHPTYEASKVRITRRLAERGYFDADFTHRRVEVTRAAHAADIDLIWESGRR
                                                                                                                                                                                                                                                                                                                                                                                                         VPLLIGDVFHHGKYETKKNLIENASAEHGYFDGRWLDRSVDVILPDNTADVSLIYDTGTQ 358
                                                                                                                                                                                                                                                                                                                                                                                                                                  ALEPFGYYAPTIRIDAPRQNDHITVVIYVDKGEPVRVRQAHVAMTGAAAQDHYLQRDLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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21.6%;
                                                                                                                                                                                  -----GNVPVDVKLERAKSKIYTAGISYGSESGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 347; DB 16;
Pred. No. 3.5e-12;
96; Mismatches 252
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Indels

Gaps

17;

222

162

WRYRAD

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265 478 233

828 472 768

617; 194;

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Q8RHT4
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-ATCC 25586;
MEDLINE-21886394; PubMed-11889109;
Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidi.
Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
Vasieva O., Chu L., Koyan Y., Chaga O., Goltsman E., Bernal A.,
Larsen N., D'Souza M., Walinas T., Pusch G., Haselkorn R.,
Fonstein M., Kyrpides N., Overbeek R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE 678 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fusobacterium nucleatum
Bacteria; Fusobacteria;
NCBI_TaxID=76856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genome sequence and analysis of the oral bacterium Fusobacterium nucleatum strain ATCC 25586.";
J. Bacteriol. 184:2005-2018(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Outer membrane protein. FN1911.
                    660
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NGFDLSTRTLEHEIS----RSIIQNG-GWNRTYSLRYRLDKLKTQ---:
                                                                     EHNLINRDGYQAGAE----LRLSEDKKGVKLYATKPLSHPLNDQLRATLGYQQEVFGHST
                                                                                                   TVDNLMRLG IFKNVKYEARSIPGDPEGIDLILLIDEDRTAELQGGVAYGSETG-----F
                                                                                                                          LANRKTPADV-----YQSKKVP------LYVFVASDKPRDGQIGLGWGSDTGTRLVTKF
                                                                                                                                                        LHISIVEGIYRRIEVKKMYTKQKGNRRTPNDDVLKTKDYVIDREIEIQPGKIFNVKEYDA
                                                                                                                                                                                                                                                                                                SNDLIATRYFNMVNTEIVFPEREQIQNDQ--VSFEQSSSSRTEPAQVDESTLEPVIETVE
                                                                                                                                                                                                                                                                                                                                                                                                      KYETKKNLIE-NASAEHGYFDGRWLDRSVDVILPDNTADVSLIYDTGTQYRFD----EVV
                                          LGTLSLKDSNWRGKNQQFGFTFEKSNKNYTGFALDFYDPWIKDTDRVSWGW----
                                                                                                                                                                                    LAINHDDGVNRSILGR-----ISDAVSAVARAILPDESE---NEVIDLPERTA
                                                                                                                                                                                                              ITGNNTIPTSTIMSELTTKPGSVQNYNNLREDRDKILGLYQAQGYTLVNITDMSTDENGT
                                                                                                                                                                                                                                                                     QRRLLATGKFSEVRPD-----AQVANGKMALSFE------VVEN---PIVKSVI 178
                                                                                                                                                                                                                                                                                                                            VDLLKEKGVAINTLREDTDKSIVLSSVKFTGNKRVTTSELLDITQLKAGEYFSRSRVEDA
                                                                                                                                                                                                                                                                                                                                                      FFTIDPK---TNQLTTDPDKLPV-----KRELLEQLLTVNM---GEAYNLQAVRAL 410
                                                                                                                                                                                                                                                                                                                                                                                    KFSTEALLADFNALKETGYFE-----DVILQ-----PVSYDGGVRIVVDVVEKENV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRTAKPDAFALGAKHVFSAGAEFEYYYKGGPFGGAVFVDSGSAFNR--YPDWHTGVGIGL 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LRWFHGLGASSRLILRG------EAGTTWASDLVAMPPSLRFFAGGVNSIRGYAFREVG
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Fusobacterium
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Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 262.5; D
Pred. No. 4e-07
.1; Mismatches
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Best Local S
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P95359;
01-MAY-1997
01-MAY-1997
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                         Microb. Pathog. 23:0-0(1998).
EMBL; U81959; AAC17600.1; -.
InterPro; IPR000184; Bac_surfAg_D15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Manning D.S., Reschke D.K., Judd R.C.;
"Omp85 proteins of Neisseria gonorrhoeae and Neisseria meningitidis are similar to Haemophilus influenzae D-15-Ag and Pasteurella multocida Oma87.";
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-FA19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria gonorrhoeae.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S84WO
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    450
                               284
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                                                                                                                                                                   270
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                                                                                                                                                                                                                                                                                                                           116 TPLSLEELFAQESTEMGINPND-----YIPEYQGEQPNSEVVVPPTLEPEKPGLIKRLY 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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  TEPAQVDESTLEPVIETVELTDGILMDISP---
                                                   LEQLLTVNMGEAYNLQAVRALSNDLIATRYFNMVNTEIVFPEREQIQNDQVSFEQSSSSR
                                                                                                DGRWLDRSVDVILPDNTADVSLIYDTGTQYRFDEVVFFTIDPKTNQLTTDPDKLPVKREL
                                                                                                                                                                                                                                                                                                 SPLAFADFTIQDIRVEGLQRTEPSTVFNYLPVKVGDTYN------DTHGSAIIKSLY
                                                                                 DFRILDTDIQTNEDKTRQTIKITVHEGGRFRWGKV---SIEGDTNE-----VPKAE
                                                                                                                                     GNQVYSDRKLMR-----QMSLTEGGIWTWLTRSDRFDRQKFAQDMEKVTDFYQNNGYF
                                                                                                                                                                GEPVYIDYRAVEVRGEGADDKAFTTVADEVPLLIGDVFHHGKYETKKNLIENASAEHGYF
                                                                                                                                                                                          ATLNQAVAGLKEEY---LGRGKLNIQITPKVTKLARNRVDIDITIDEGKSAKITDIEFE- 182
                                                                                                                                                                                                                  ANIKAALEDITQESAMDLNGSIPRLRQTALVAARAVGYYDIDLSIIRNSIGEVDVIIHDL
                                                                                                                                                                                                                                              ATGFFDDVRVETADGLLLLTVIVCPTIGSLNITGAKMLQNDAIKKNLESFGLAQSQYFNQ
                                                                                                                                                                                                                                                                        ARLFNDGV------NKVPRLKAKFYQSSQ-SGETSAIGSSHQKTEPY 209
                             LEKLLTMKPGKWYERQQMTAVLG--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGNFGNATLELRTYHKGLFKNNIF----AYKVVGGVAT-----NNTKESQKFWVGGG 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DANMAIARAGISGVYS--FGDNAYGSNRAHQMTGGIQAGYIWSDNFNHVPYRLRFFAGGD 816
                                                                                                                                                                                                                                                                                                                                                                                                                               PF01103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YKEKNKWRE--IEGVDDKYWLWSIYPYISY--DTRNNYLNPTSGFYGKFQVEAGHAGGYK 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TSYGDEDSILFHEIDTIGFRTNIGKGLGKNFTLSLGTKVEYIKEKHEDGKLRQANNGKWY
                                                                                                                                                                                                                                                                                                                                                               189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -APPETWQDLPVDFVNGKPSQEALLAGVAVHKTVADNLVNPMRGYRQRYSLEVGSSGLVS 758
                                                                                                                                                                                                                                                                                                                                                                         Similarity
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7 (TrEMBLrel. 03,
L (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                792 AA;
                                                                                                                                                                                                                                                                                                                                                            Conservative 119;
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                                                                                                                                                                                                                                                                                                                                                                                                              90E32D24AA0513D8 CRC64;
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                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                       No. 7.9e-07
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----IEFSASNLIQDKLNLVAAKARH
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                           -----EIQNRMGSAGYAYS--
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                                                                                                                                                                                                                            Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Elsen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Clecko A., Parksey D.S., Blair E., Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C., "Complete genome sequence of Neisseria meningitidis serogroup B strain "Complete genome sequence of Neisseria meningitidis serogroup B strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O9K1H0, PRELIMINARY; PRT; 797 AA.

O9K1H0;
O1-OCT-2000 (TrEMBLrel. 15, Created)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                    Science 287:1809-1815(2000).

EMBL; AE002275; AAF40639.1; -.

TIGR; NMB0182; -.

InterPro; IPR000184; Bac_surfag_D15.

Pfam; PF01103; Bac_surface_Ag; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-MC58 / SEROGROUP B;
MEDLINE-20175755; PubMed-10710307;
   Complete proteome. SEQUENCE 797 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neisseria meningitidis (serogroup
Bacteria; Proteobacteria; beta sub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NMB0183
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Proteobacteria; beta subdivision;
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Best Local Similarity
                                                                             766
                                                                                                                                        706
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                                                                                                                                                                                                    649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67
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                                                                                                                                                                                                                     LRFFAGGDQSIRGYAHDSLSPISDKGYLTGGQVLAVG---TAEYNYEFM------KD
                                                                                                      PVGQVRVDVATGVKE--EGNPIKLHFFIGTPF 919
                                                                                                                                                                   LRLAVFGDIGNAYD ---
                                                                                                                                                                                                                                                                                                                                            N--GK-PSQEALLAGVAVHKTV-----ADNLVNPMRGYRQRYSLEVGSSGLVSDANMAI
                                                                             PLGPMKFSYAYPLKKKPEDEIQRFQFQLGTTF
                                                                                                                                     VRLSLFADAGSVWDGKTYDDNSSSATGGRVQNIYGAGNTHKSTFTNELRYSAGGAVTWLS
                                                                                                                                                                                                  ENFYGGGLGSVRGYESGTLGP---KVYDEYGEKISYGGNKKANVSAELLFPMPGAKDART
                                                                                                                                                                                                                                                             ALPGSKLQY----YSATHNQTWFFPLSKTFTLMLGGEVGIAGGY---GRTKEIPFF
                                                                                                                                                                                                                                                                                            ARAGISGVYSFGDNAYGSNRAHQMTG------
                                                                                                                                                                                                                                                                                                                           KKYGKTDGTDGSFKGWLYKGTVGWGRNKTDSALWPTRGY--
                                                                                                                                                                                                                                                                                                                                                                                      RKASTSIKQYKTTTA----GAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHYADFI
                                                                                                                                                                                                                                                                                                                                                                                                                   FDLSTRTLEHEISRSIIQNGGWNR----TYSLRYRLDKLKTQAPPETWQDLP---VDFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SAGVSQDNLFGTGKSAALRASRSK--TTLNGSLSFTDPYFTADGVSLGY--DVYGKAFDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KFEHNLINRDGYQAGAELRLSEDKKGVKLYATKPLSHPLNDQLRATLGYQQEVFGHSTNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DKLPVKRELLEQLLTVNMGEAYNLQAVRALSNDLIATRYFNMVNTEIVFPEREQIQNDQV 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----VDL--NMSLTERST-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENEVIDLPERTALANRKTPADVYQSKKVPLYVFVASDKPRDGQIGL--GWGSDTGTRLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NLVAAKARHLYDMPDD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SAGYAYS ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SFEQSSSSRTEPAQVDESTLEPVIETVELTDGILMDISP-----IEFSASNLIQDKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DFYQNNGYFDFRILDTDIQTNEDKTKQTIKITVHEGGRFRWGKV---SIEGDTNE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NASAEHGYFDGRWLDRSVDVILPDNTADVSLIYDTGTQYRFDEVVFFTIDPKTNQLTTDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GNQVYSDRKLMR------QMSLTEGGIWTWLTRSNQFNEQKFAQDMEKVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GEPVYIDYRAVEVRGEGADDKAFTTVADEVPLLIGDV-----FHHGKYETKKNLIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MD---LNGSIPRLRQ-----TALVAARAVGYYDIDLSIIRNSIGEVDVIIHDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDA---IKKNLESFGLAQSQY 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARLFNDGVNKVP---RLKAKFYQSSQSGETSATGSSHQKTEPYANIKAALED--ITQESA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPLALADFTIQDIRVEGLQRTEPSTVFNYLPVKVGDTYN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -VVRRELRQMESAPYDTSKLQRSKERVELLGYFDNVQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----VPKAELEKLLTMKPGKWYERQQMTAVLG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----EISVQPLPNAETKTVDFVLHIEPGRKIYVNEIHITGNNKTRDE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.5%; Score 259; DB 16; 20.5%; Pred. No. 8.6e-07; ative 121; Mismatches 342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ~ -- RVLAINHDDGVNRSILGRISDAVSAVARAILPDES
                                                                             797
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                                                                                                                                                                   -KGFTNDTKIGAGVGVRWAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSLDLSAGWVQDTG - - LVM
                                                                                                                                                                                                                                                                                            -GIQAGYIWSDNFNHVPYR 808
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STRAIN=22491 / SEROGROUP A / SEROTYPE 4A;

RX MEDLINE=2022255; PubMed=10761919;

RA MEDLINE=20222556; PubMed=10761919;

RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,

RA Parkhill J., Achtman M., Brown D., Chillingworth T.,

RA Navies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,

RA Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,

RA Ajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,

RA RAJandream M.A., Rutherford K.M., Simmonds M., Skelton J.,

RA RAJandream M.A., Rutherford K.M., Simmonds M., Skelton J.,

RA RAJANDREAM S., Spratt B.G., Barrell B.G.;

RT "Complete DNA sequence of a serogroup A strain of Neisseria meninglitidis 22491 ";

RT meninglitidis 22491 ";

RT Mature 404:502-506(2000).

DR EMBL; Al162752; CAB83401.1; -.

DR Ffam; PF01103; Bac_surface_Ag; 1.
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Best Local S
Matches 191
                662
                                       441 SAGVSQDNLFGTGKSAALRASRSK--TTLNGSLSFTDPYFTADGVSLGY--DVYGKAFDP 496
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OMP85 OR NMA0085.

Neisseria meningitidis (serogroup A).

Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                       544
                                                                                                                                                                                                                                                                                           314
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                              364
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FDLSTRTLEHEISRSIIQNGGWNR-----TYSLRYRLDKLKTQAPPETWQDLP---VDFV 713
                                                                              KFEHNLINRDGYQAGAELRLSEDKKGVKLYATKPLSHPLNDQLRATLGYQQEVFGHSTNG
                                                                                                                                                             ENEVIDLPERTALANRKTPADVYQSKKVPLYVFVASDKPRDGQIGL--GWGSDTGTRLVT
                                                                                                                                                                                                                                       NLVAAKARHLYDMPDD-----RVLAINHDDGVNRSILGRISDAVSAVARAILPDES 543
                                                                                                                                                                                                                                                                                                                      SFEQSSSSRTEPAQVDESTLEPVIETVELTDGILMDISP-----IEFSASNLIQDKL 492
                                                                                                                                ----VDL--NMSLTERST-----
                                                                                                                                                                                                  VVRRELRQMESAPYDTSKLQRSKERVELLGYFDNVQ------FDAVPLAGTPDK- 411
                                                                                                                                                                                                                                                                                 SAGYAYS-----EISVQPLPNAETKTVDFVLHIEPGRKIYVNEIHITGNNKTRDE-
                                                                                                                                                                                                                                                                                                                                                                 ----VPKAELEKLLTMKPGKWYERQQMTAVLG-----
                                                                                                                                                                                                                                                                                                                                                                                        DKLPVKRELLEQLLTVNMGEAYNLQAVRALSNDLIATRYFNMVNTEIVFPEREQIQNDQV 440
                                                                                                                                                                                                                                                                                                                                                                                                                                            DFYQNNGYFDFRILDTDIQTNEDKTKQTIKITVHEGGRFRWGKV---SIEGDTNE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GEPVYIDYRAVEVRGEGADDKAFTTVADEVPLLIGDV-----FHHGKYETKKNLIE 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FNQATLNQAVAGLKEEYLGRGKLNIQITPKVTKLARNRVDIDITIDEGKSAKITDIEFE- 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MD---LNGSIPRLRQ------TALVAARAVGYYDIDLSIIRNSIGEVDVIIHDL 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGFFDDVRVETADGOLLLTVIERPTIGSLNITGAKMLONDA---IKKNLESFGLAQSQY 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPLALADFTIQDIRVEGLQRTEPSTVFNYLPVKVGDTYN------DTHGSAIIKSLY 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88404 MW; 65DE47E00C9E1D1F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------QMSLTEGGIWTWLTRSNQFNEQKFAQDMEKVT 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 259; DB 16; Length 797; Pred. No. 8.6e-07;
                                                                                                                          ------GSLDLSAGWVQDTG--LVM
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                                                                                                                                                                                                                                                                                                                                                               -----EIQNRMG 313
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24	Qy 368 TIDPKTNQLTTDPDKLPVKRELLEQLLTVNMGEAYNLOAVRALSNDLTATRYFNMVN 42	0
83	227 SEERLAADEEALRRFYYNRGYADFRVISSKAVFDEARNAYEIDFVLDEGVRYKIG	
67	308 HHGKYETKKNLIEN	_
26	67 TINLGKGRVNVVFNIVEGRRTKISNITFKGNHAFGSSRLRDVISTKPSGILSLLLRGDVY	_
07	EVDV-IIHDLGEPVYIDYRAVEVRGEGA-DDKAFTTVADEVPLLIGDVF 3	_
	: : :   :       ::  VNVIREAYKTVGRNDIAVTIQ 1	m
S S	1 2	_
23	Db 64 KVGKSFSSGDVDFAVKRLFALGLFYDVKINQVGDRLVVLVKEYEVVNQVLFQGNKSLKDP 1:	_
97	S 1	_
ω	NIDI 6	_
51	PPLGLDMSVIEETTPLSLEELFAQESTEMGINPNDYIPEYQGEQPNSEV 1	_
š 52;	Query Match 5.4%; Score 254; DB 2; Length 798; Best Local Similarity 21.9%; Pred. No. 1.7e-06; Matches 203; Conservative 136; Mismatches 352; Indels 236; Gaps	
	SEQUI	
	InterPro; IPR000184; Bac_surfAg_ Pfam: PF01103: Bac_surfAce_ac: 1	
	Submitted (DEC-2001) EMBL; AF461795; AAL66	
	<pre>protein of Bartonella henselae.";</pre>	
	SEQUENCE FROM N.A. Zimmermann R., Augustin K., Schaal K., Sander A.;	
	oteobacteria; alpha bae; Bartonella.	
	OMP89. Bartonella henselae (Rochalimaea henselae)	
	01-JUN-2002 (TrEMBLrel. 21, Omp89.	
	01-MAR-2002 (TrEMBLICE) 20, Created)	
	~ ~	
	SULT 12	
	Db 766 PLGPMKFSYAYPLKKKPEDEIQRFQFQLGTTF 797	
	ATGVKEEGNPIKLE	
765	Db 706 VRLSLFADAGSVWDGKTYDDNSSSATGGRVQNIYGAGNTHKSTFTNELRYSAGGAVTWLS 7	
689	RLAVFGDIGNAYDKGFTNDTKIGAGVGVRWAS	
705	VRGYESGTLGPKVYDEYGEKISYGGNKKANVSAELLEPMPGAKDART	
856	ISDKGYLTGGQVLAVGTAEYNYEFMKD	
648	Db 600 ALPGSKLQYYSATHNQTWFFPLSKTFTLMLGGEVGIAGGYGRTKEIPFF (	
808		
599	Db 553 KKYGKTDGTDGSFKGWLYKGTVGWGRNKTDSALWPTRGYLTGVNAEI!	
764	K-PSQEALLAGVAVHKTVADNLVNPMRGYRQRYSLEVGSSGLVSDANMAI	
552	Db 497 RKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHYADFI	

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RESULT 13
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ID 03091
AC 03091
DT 01-JA
DT 01-DE
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GN 01-DE
OC Neiss
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RN (1)
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       Query Match
Best Local Sim
Matches 190;
                                                             Microb. Pathog. 23:0-0(1998).
EMBL; APC21245; AAC17599.; -
InterPro; IPR000184; Bac_surfag_D15.
Pfam; PF01103; Bac_surface_Aq; 1.
SEQUENCE 797 AA; 88539 MW; CF911
                                                                                                                                                                                                                                                                                       O30912 PRELIMINARY; PRT; 797 AA.
O30912: 01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Outer membrane protein Omp85.
                                                                                                                                      Manning D.S., Reschke D.K., Judd R.C.;
"Omp85 proteins of Neisseria gonorrhoeae and Neisseria meningitidis are similar to Haemophilus influenzae D-15-Ag and Pasteurella multocida Oma87.";
                                                                                                                                                                                                    STRAIN-HH
                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                    Neisseria meningitidis.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria
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                  5.4%;
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    Score 253; DB 2;
Pred. No. 1.9e-06;
11; Mismatches 343
                                                            CF911B5F70B999CF
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AC Q8XZI
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                                                                                                                            PLGPMKFRYAYPLKKKPEDEIQRFQFQLGTTF
                                                                                                                                                                                                                                                                                                        ARAGISGVYSFGDNAYGSNRAHQMTG-------GIQAGYIWSDNFNHVPYR
                                                                                                                                                    PVGQVRVDVATGVKE -- EGNPIKLHFFIGTPF 919
                                                                                                                                                                                                      LRLAVEGDIGNAYD-----
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                                                                                                                                                                                                                                                                                                                                                                                                       FDLSTRTLEHEISRSIIQNGGWNR-----TYSLRYRLDKLKTQAPPETWQDLP----VDFV
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Q8XZI3 PRELIMINARY; Q8XZI3; Q1-MAR-2002 (TrEMBLrel. 2) Q1-MAR-2002 (TrEMBLrel. 2) Q1-JUN-2002 (TrEMBLrel. 2) Putative outer membrane s

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-21691879; PubMed-11823852;
Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.
Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange
Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,
Weissenbach J., Boucher C.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AL646064; CAD15114.1; ...
InterPro; IPR002198; ADH_short.
InterPro; IPR000184; Bac_surfAq_D15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RSC1412 OR RS05280.
Ralstonia solanacearum (Pseudomonas solanacearum).
Ralstonia Proteobacteria; beta subdivision; Ralstonia
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                                   784
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KSFTLAFNNEIGYGHGYGNKDFPVFKNYYAGGIGSVRGYETSTLGPRDANGVAIGGASKF
                           RAHQMTGGIQAGYIWSDNFNHVPYRLRFFAGGDQSIRGYAHDSLSPISDKGYLTGGQVLA 843
                                                            T-IGWSKDQRDSALVPTRGRYQQANLEFGIPG----GDLQYYRAYYQHQY
                                                                                         AGVAVHKTVADNLVNPMRGYRQRYSLEVGSSGLVSDANMATARAGISGVYSFGDNAYGSN 783
                                                                                                                                                           *IIQNGG------WNRT----YSLRYRLDKLK-TQAPPETWQDLPVDFVNGKPSQEALL
                                                                                                                            RIVQQGGN1KFGVPFSETDTVFFGIGYERTTIDVTSNTPLVYQNYVAK--NGRISNNFPI
                                                                                                                                                                                           QDNVFGSGTSLGLDVNTSKSNRTISVTQYDPYFTVDGISRSTELYYRTYRPLYYTGDQDY
                                                                                                                                                                                                                                                           QNRINRTGYFTDTNITTEDVPGMSDQVDVNVNVTEKPTGQISLGVGFSSTDKLVLSAGIR
                                                                                                                                                                                                                             QE-VFGHSTN-GFDLST----RTLE-----HEISRS-----
                                                                                                                                                                                                                                                                                          HNLINRDGYQAGAELRLSE-----DKKGVKLYAT-KP-----LSHPLNDQLRATLGYQ
                                                                                                                                                                                                                                                                                                                          RTVALTLVVDPGRRVYVRRVNV---VGNSKTRDEVVRREMRQMESSWFD--GEKL--QLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NKAFSEGDLRDEMQLSTPNWLSWYTKNDLYSKQKLTADLEALRSFYLDRGYLEF----AI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DKLPVKRELLE--QLLTVNMGEAY---NLQAVRALSNDLIATRYFNMVNTEIVFPEREQI 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLIDRAEQELKRQYVSRGYYAADVQ---TTVTPVDANRVSVTFTVDEGPVAKIRQINIVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RWLDRSVDVILPD-----NTADVSLIYDTGTQYRFDEV-VFFTID----PKTNQLTTDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FKDVQIRAEG---NVLVVRVEERPAISQLEFIG-IKEFDKDTLRRSLRGVGVAEARYYDK 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YRAVEVRGEGADDKAFTTVADEVPLL----IGDVFHHGKYETKKNLIENASAEHGYFDG
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Pred. No. 5.7e-06;
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W., Schiex T.,
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Best Local Similarity 21.2%; range 105; Conservative 105;
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Q8XWT6;
Q1-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Crunac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RSC2384 OR RS02766.
Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; beta subdivision; Ralstonia
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01-MAR-2002 (TrEMBLrel.
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Nature 415:497-502(2002).
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         336
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                                                   NDQLRATLGYQQEVFG--HSTNGFDLSTRTLEHEISRSIIQNGGWNRTYSLRYRLDKLKT
         PDGKR----
                                                                                                                PNRITSGVGYSTDTGAQVEGRYQYLNLFDK-AWVLDTQARIEQRRQYLFGSVTLP----
                                                                                                                                                                                                                                      GEDYSADRLQALAAAIQGQPYFANAIVDLGD------
                                                                                                                                                                                                                                                                                         GR--ISDAVSAVARAILPDE-SENEVIDLPERTALANRKTPADVYQSKKVPLYVFVASDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KAKEDSLAALQSKRYY-----195
                                                                                                                                                                         PRDGQIGLGWGSDTGTRLVTKFEH-NLINRDGYQAGAELRLSEDKKGVKLYATKPLSHPL
                                                                                                                                                                                                                                                                                                                                                               LSVAYDSGPAYTLGPLD
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YVNSLYGSLDRTNLSGTDTRSYRSGFKQTRVR-GIYETSFTIDFYYDDLRP
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21.2%; Pred. No. 4.8e-06;
tive 105; Mismatches 268;
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Last annotation update)
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Hypothetical protein Atu2615.
ATU2615 OR AGR_C_4742.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L. Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Raymond C., Rouse G. Saenphimmachak C., Wu Z., Romero P., Gordo Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V., Nester F. W.
                                                                                                                                                                                                                                                                     Hypothetical protein; Complete proteome. SEQUENCE 641 AA; 68281 MW; ECOAllDA3BBDF61E CRC64;
                                                                                                                                                                                                                                                                                                                                    EMBL; AE009208; AAL43596.1; ALT_INIT EMBL; AE008175; AAK88337.1; -.
                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of the plant pathogen Agrobacterium tumefaciens C58."; Science 294:2323-2328(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE-21608551; PubMed-11743194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 294:2317-2323(2001).
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MEDLINE=21608550; PubMed=11743193;

Wood D.W., Setubal J.C., Kaul R., Monks D.E.,
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                                                                                GSSHQKTEPYANIKAALEDITQESAMDLNGSI-PRLRQTALVAARAVGYYDIDLSIIRNS
IGEVDVIIHDLGEPV-YIDYRAVEVRGEGADDKAFTTVADE---VPLLI--
                                                   GSEEPEVEVINPVKYA---VTLDAA-DADKSLKSSLENSSLLLADKDKPASGDLGLLIKA
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Q8UFL6; PRT; 274 AA.
Q8UFL6
O1-JUN-2002 (TrEMBLrel. 21, Created)
O1-JUN-2002 (TrEMBLrel. 21, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation updat
                                                                                                                                                                                                                                                                              Agrobacterium tumefaciens (strain C58 / ATCC Bacteria; Proteobacteria; alpha subdivision;
                                                                                                                                                                                                                                                                                                                                         Group 1 outer membrane protein. OMP1 OR ATU1381 OR AGR_C_2554.
                                                                                                                               SEQUENCE FROM N.A. MEDLINE-21608550; PubMed-11743193;
                                                                                                                                                                                                                     NCBI_TaxID=176299;
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Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Chapman P., Clendenning J., Deatherage G., Gillet W., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri

Jr., Grant C., Sr., J.P

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M. Nester E.W.;
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                             SLRYRLDKLKTQAPPETWODLPVDFVNGKPSQEALLAGVAVHKTVADNLVNPNRGYRQRY 747
                                                                         FKNQSKSEDYYNYDEQGFAL
                                                                                                                                       VEEKNFLGRGQYIRVAAGAG---EDDARTYSLSFTEPY-----FLGYRLAAGFDL
                                                                                                                                                                        FEH-NLINRDGY----QAGAELRLSEDKKGVKLYATKPLSHPLNDQLRATLGYQ------
                                                                                                                                                                                                                                              SENEVIDLPERTALANRKTPADVYQSKKVPLYVFVASDKPRDGQIGLGWGSDTGTRLVTK
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774 AA;
                                                                                                      -QEVFGHSTNGFDLSTRTLEHEISRSIIQN----
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   AEPYQAL --
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Pred. No. 3e-05;
9; Mismatches 3
-IRGEDWTQSILSNTLNYNTLDDRNM-PREGWQAAL
                                                                   -RVTAPITENLSTTFKYTYKQINYEGKGDWQNNA
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Dolan M.,
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q93PM2;

01-DEC-2001 (TrEMBLrel. 19, Created)

01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPRO00184; Bac_surfag_D15. Pfam; PF01103; Bac_surface_Ag; 1. SEQUENCE 793 AA; 88661 MW; E4E9D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Infect. Immun. 69:4438-4446(2001).
EMBL; AF329831; AAK70345.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=21295095; PubMed=11401984;
Thomas K.L., LeDuc I., Olsen B., T
    323
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PKFNEEDHTVQ--INFIVDAGRRIY----VRKIRFEGNDVTADSTLRREMRQQEGAWLST
                        PIEFSASNLIQDKLNLVAAKARHLYDMPDDRVLAINHDDGVNRSILGR------ISD 529
                                                                      DGVNK------VPRLKAKFYQSSQSGETSAIGSSHQKTEPYANIKAALEDIT------
                                                      LFRKTELSIIEEQIKQILGDR----GYGSAK--
                                                                                                                 YNISEM---
                                                                                                                                     YRFDEVVFFTIDPKTNQLTTDPDKLPVKRELLEQLLTVNMGEAYNLQAVRALSNDLIATR 418
                                                                                                                                                               IFESSKFQQQEYNKDIEILRDFYMDHGY--AKFTLKDTDVKFNENKTEVDLTYKINEGSQ
                                                                                                                                                                                       VFHHGKYETKK-----NLIENASAEHGYFDGRWLDRSVDVILPDNTADVSLIY--DTGTQ 358
                                                                                                                                                                                                                       QTITTPNNNGSINVELNITEGEIAYVK----KINFEGNNAFSYDELIKELEIKPNAPWWN
                                                                                                                                                                                                                                               SIIR--NSIGEVDVIIH-DLGEPVYIDYRAVEVRGEGADDKAFTTVADEVPLLIG----D
                                                                                                                                                                                                                                                                            PLINNLTIKGNNAIPKNALEQNLKANLIVAGEVYDKAKLEAFKQALVDHYHTMGRYQADI
                                                                                                                                                                                                                                                                                                       ---QESAMDLNGSIPR-----LRQTALVAA---
                                                                                                                                                                                                                                                                                                                                DGVQTETGNAIIASLPVKVGQTATDGDVTNIVKQLFSQNRFENVSAAREGQTLVIKVAER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THEF--AGLGGDSEYYKIYAKARYYYTLSDEYDVIGS-----LTG--QAGHVMPTGDNLL 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VFD-QFKFGGRQ-VRGFKNDGIGPRIGSDS---IGGTTYFAASAEVTAPMPGVPEDF--G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLEVGSSGLVSDANMAIARAGISGVYSFGD--NAYGSNRAHQMTGGIQAGYIWSDNFNHV 805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PYRLRFFAGGDQSIRGYAHDSLSPI--SDKGYLTGGQVLAVGTAEYN-----YEFMKD 856
                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                           Conservative 134;
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                                                                                                             -----RIIGDTQKLDNE---LNQLLT
                                                                                                                                                                                                                                                                                                                                                                                                         4.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 88661 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gamma subdivision;
                                                                                                                                                                                                                                                                                                                                                                                         Score 229.5; DB 2
Pred. No. 4.7e-05;
84; Mismatches 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                E4E9DB62A8F9903F CRC64;
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Matches
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P73472;

P01-FEB-1997 (TrEMBLrel. 02, Created)

P10-FEB-1997 (TrEMBLrel. 02, Last sequence update)

P10-JUN-2002 (TrEMBLrel. 21, Last annotation update)

Chloroplast import-associated channel IAP75.

E1P75 OR SLR1227.

Synechocystis sp. (strain PCC 6803).

Bacteria; Cyanobacteria; Chroococcales; Synechocystis.

NEB_TaxID-1148;
                                                                                                                              pfam; PF01103; Bac_surfaq_D15.
Pfam; PF01103; Bac_surface_Ag; 1.
TIGRPAMs; TIGR00992; 3a0901s03IAP75; 1.
Complete profeome.
SEQUENCE 861 Aa.
                                                                                                                                                                                                                "Sequence analysis of the genome of the unicellular cyanobacterium synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.", DNA Res. 3:109-136(1996).
EMBL; D90906; BAA17512.1; ...
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=97061201; PubMed=8905231;

MEDLINE=97061201; PubMed=8905231;

Maneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,

Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,

Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,

Miyajima N., Naruo K., Okumura

Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura

Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.
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SPYYRLLLLTSGLVLGASPAQATQAFSPLNMLADGDNTELLVSPSSEL-NFPGPTSESEA
                             SPISRIGEQSPPLGLDMSVIEETTPLS-LEELFAQESTEMGINPNDYIPEYQGEQPNSEV 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NLPDFGDYKRVRASAGIALOWOSPIGPLSFSYAKPIKKYAGDEIEQFQFTVGSTF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAYDKGFTNDTKIGAGVGVRWASPVGQVRVDVATGVKE-EGNPI-KLHFFIGTPF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QR----YSLEVG-----SSGLVSDANMAIARAGISG------VYSFGDNAYG--
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                                                                                     Similarity
                                                                     Conservative
                                                                                     4.8%;
19.7%;
                                                                     130;
                                                                 Score 225; DB 16;
Pred. No. 0.0001;
0; Mismatches 399;
                                                                                                                                   1C5DFFD394DA5B44 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synechocystis
                                                                                                 Length 861;
                                                                   Indels
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Q8YHHO PRELIMINARY;
Q8YHHO;
Q1-MAR-2002 (TrEMBLrel.)
Q1-MAR-2002 (TrEMBLrel.)
Q1-JUN-2002 (TrEMBLrel.)
Quier membrane protein.

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update) update)

Created) Last sequence up

PRELIMINARY;

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Bacteria; Proteobacteria; Brucellaceae; Brucella. Brucella melitensis.

alpha

subdivision; Rhizobiaceae

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QGAVPGFPAIVRGLPG-SGVGYGLGVRIQSPVGPIRIDL--GFTGEGES-RINFGIGEKF
               -----AYDKGFTNDTKIGAGVGVRWASPVGQVRVDVATGVKEEGNPIKLHFFIGTPF
                                                                             FAGGDQSIRGYAHDSLSPISDKGYLTGGQVLAVGTAEYNYEFMKDLRLAVFGDIGN----
                                                               ILGGSNSVRGY-----
                                                                                                                                                    MAIARAGISGVYSF----
                                                                                                                                                                                                                                                                                                                                   INRDGYQAGAELRLSEDKKGVKLYATKPL--SHPLNDQLRATLGYQQEVFGHSTNGFDLS
                                                                                                                      IMMTR--LRGSYSYYIPVNWLDLTGFGLVESTQPQTVAFNVQAGTVLGD----LPPYEAF
                                                                                                                                                                                 PLNGFNSQPLSFSDYGVDELFTLSFGASQDNRNNALQPTSGSLVRFGAE--QTIPVGTGN
                                                                                                                                                                                                              PVDFVNGKP-----SQEALLAGVAVHKTVADNLVNPMRGYRQRYSLEVGSSGLVSDAN
                                                                                                                                                                                                                                            {\tt IRTFNGFDSPRVVRTGLGLTFFRPIADDVFAPPDWRLSAGFGYQNVRIENAAGALSPFSA}
                                                                                                                                                                                                                                                                           TRTLEHEISRSIIQNG----
                                                                                                                                                                                                                                                                                                         LGGNNQTIGVEAQVGQRELLFDVSFTDPWIGGDPFRTSYTANL-FRRRTISLVFDGADSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNYSTLQEAAPSVINALNGE---NGEISVIPP-EIEQIDGDRLGQTMEISA----
                                                                                                                                                                                                                                                                                                                                                                                                 ---PLYVFVASD--KPRDGQIGLGWG--SDTGTRLVTKFEHNL
                                                          -QEGELGNGRSFFQATAEYRFPIIAAVGGALFVDYGSNLGS
                                                                                                                                                   -GDNAYGSNRAHQMTGGIQAGYIWSDNFNHVPYRLRF
                                                                                                                                                                                                                                                                          -----GWNRTYSLRYRLDKLKTQAPPETWQDL
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SEQUENCE
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MEDLINE-20020109; PubMed-11756688;
DelVecChio V.G. Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,
Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
Selkov E., Kyrpides N., Overbeek R.;
"The genome sequence of the facultative intracellular pathogen
Brucella melitensis.";
Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
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Pfam; PF01103; Bac_surface_Ag; 1.
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                                                                                                             SVSYSLTYSSIDDIKN--
                                          ---YYQTLSQEADIVGLLG-----VGAGYIHEFGDD------GVRI----
                                                                        MRGYRORYSLEVGSSGLVSDANMAIARAGISGVYSFGDNAYGSNRAHQMTGGIQAGYIWS
                                                                                                                                   --TYSLRY-RLDKLKTQAPPETWQDLPVDFVNGKPSQE-ALLAGVA--VHKTVADNLVNP
                                                                                                                                                                 YDVEQTGGTIRFGLPITDNFSAGIAYSLVQEKYDLFRGDAENYYAPALLEAAENSPWLRS
                                                                                                                                                                                               ----QLRATLGYQQEVFGHSTNG-----FDLSTRTLEHEISRSII---
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                                                                                                         -PHDGLYGKFIQEFAGLGGDAKYVKTTFKGN----
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Q98MC3; 01-OCT-2001 (TremBLrel. 18, C
01-OCT-2001 (TremBLrel. 18, L
01-OCT-2001 (TremBLrel. 18, L
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DNA Res. 7:331-338(2000).
EMBL; AP002995; BAB48190.1;
InterPro; IPR000184; Bac_surfAg_D15.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
                                482
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MEDLINE=21082930; PubMed=11214968;
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                        FSASNLIQDKLNLVAAKARHLYDMPDDRVLAINHDDGVNRSILGRISDAVSAVARAILPD 541
 IRGNDRTRDYV----IRREFD-----
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-VSEGDAFNQVLIQR---
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Best Local S
Matches 131
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                                                                                                                                                             SEQUENCE 615 AA;
                                                                                                                                                                                                    "Complete DNA sequence of a meningitidis Z2491.";
Nature 404:502-506(2000).
                                                                                                                                                                                                                                                                                                                              STRAIN=Z2491 / SEROGROUP A / SEROTYPE 4A;
MEDLINE=20222556; Pubmed=10761919;
                                                                                                                                                                                                                                                                                                                                                                                                        Neisseria meningitidis (s. Bacteria; Proteobacteria;
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01-DEC-2001 (TrEMBLrel.
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                                            48
             SI--LGRISDAVSA--
                                        PDTESVKLKPKFPVRIDTQDSEIKDMVEEHLPLITQQQEEVLDKEQTGFLAEEAPDNVKT
                                                                   PVIETVELTDGILMDISPIEFSASNLIQDKLNLVAAKARHLYDMPDDRVLAINHDDGVNR 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QVRVDVATGVKEEGNP--IKLHFFIGTPF 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YNYEF-----KIGAGVGVRWASPVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EGYGNDGDLRIFDH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---WSDN----FNHVPYRLRFFAGGDQSIRGYAHDSLSPISD--KGYLTGGQVLAVGTAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLEVGSSGLVSDANMAIARAGISGVYSF----GDNAYGSNRAHQM-----TGGIQAGYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GPTDPPNPPGGTCN---ISQAILDGIAESPWIKSSVSLGLVYNTI-DDMKNPHEGIY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPETWQDLPVDFVNGKPSQEALLAGVA------VHKTVADNLVNPMRGYRQRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---GFDIYKSTREYNNNYDSDTVGATVRFGLPITNSITTQLAYNISQE-KYKVD---NSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SVEGSITERNFLGRGQFIKLSAGGGKNSRDYSVSFTEP--YFLGRRIAA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KFEHNLINRDGYQAGAELRLS----EDKKGVKLYATKPLSHPLNDQLRATLGYQQEVFGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESENEVIDLPERTALANRKTPADVYQSKKVPLYVFVASDKPRDGQIGLGWGSDTGTRLVT
                                                                                                                                                                                      AL162752; CAB83602.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AQFPLPVIPESFGLRGAVFADAATLYGNKIADQTLVDQDSTGMKLRASVGVGLMWASPFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LNYFDKVEI-----STVPGS--QPDQVVLVVDVVEKSTGEFSVGAGY-STGGDSAGP
                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence up
(TrEMBLrel. 19, Last annotation
                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                           A
X
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                                                                                                                                                          67775 MW;
                                                                                                                4.7%;
                                                                                                                                                                                                                                                                                                                                                                                                        (serogroup A).
ia; beta subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FQSTDRMIRGFAYGGIGPVASGTSGDHLGGTTYFNASAE
                                                                                                                                                                                                                               serogroup
                                                                                              Pred. No. 0.00
2; Mismatches
                                                                                                                Score 220;
Pred. No. 0.
                                                                                                                                                          B9A64607638E1CCB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 - ISRSIIQNGGWNRTYSLRYRLDKLKTQA
                                                                                                                                                                                                                               A strain of Neisseria
             VARAILPDESENEVIDLPERTALAN
                                                                                                                .00011;
                                                                                                                            DB 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               update)
                                                                                                                            Length
                                                                                                 Indels
                                                                                                 148;
                                                                                                                                                                                                                                                                                                                                                                                                      Neisseria
                                                                                               Gaps
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     Matches
                              Query Match
Best Local
                                                                                                                                                           DNA Res. 7:331-338(2000).

EMBL; AP002998; BAB48984.1;
InterPro; IP000184; Bac_surfag_D15.
InterPro; IP0003975; Shal_channel.

Pfam; PF01103; Bac_surface_Ag; 1.

PRINTS; PR01497; SHALCHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                               Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamo Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T Watanabe A., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A. Mochizuki Y., Kiyokawa C., Kohara M., Shimpo S., Sugimoto Makayama S., Nakazaki N., Shimpo S., Sugimoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhizobium loti (Mesorhizobium loti).
Bacteria: Proteobacteria: alpha subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical MLL1662.
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                                                                                                            Hypothetical protein; SEQUENCE 617 AA; 65
                                                                                                                                                                                                                                                                                                                       "Complete genome structure Mesorhizobium loti ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-MAFF303099;
MEDLINE=21082930; PubMed=11214968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; alpha su
Phyllobacteriaceae; Mesorhizobium
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01-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                              akeuchi C., Yamada M., Tabata S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TALIRTSARAG-----YFFTPENKKLGTFIIRGQAGYTVARDNAN-VPSGLMFR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANM--AIARAGISGVYSFGDNAYGSNRAHQMTGGI----QAGY-IWSDNFNHVPYRLRFF 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QEALLAGVAV---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WQQPVGSDFDQDSWENSKTSVLGAVTRKAYPLAKLGNTRAAVNPDTATADLNVVVDSGRP 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGGASSVRGYELDSIGLAGPNGSVLPERALLVGSLEYQLPFTRTLSGAVFHDMGDAAANF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MDKYETTLAAGISQPRNYRGNYWTSNVSYNRSTTQNLEKRAFSGGIWYVRDRAGIDARLG 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FDLSTRTLEHEISRSIIQNGGW----NRTYSLRYRLDKLKTQAPPETWQDLPVDFVNGKPS 718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADFDRLQGDRVPVKVSVTEVKRHKLETGIRLDSEYGLGGKIAYDYYNLFNKGYIGSVVWD
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                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 18, Created)
(TrEMBLrel. 18, Last sequence update)
(TrEMBLrel. 21, Last annotation updat)
1 protein mll1662.
     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         z
                         4.78;
                                                                                                      o; Complete proteome.
65759 MW; 83FB8C176201A444 CRC64;
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     95;
                                                                                                                                                                                                                                                                                                                                                        of
                           Score 220; DB 16;
Pred. No. 0.00011;
                                                                                                                                                                                                                                                                                                                                                     the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
     Mismatches
                                                                                                                                                                                                                                                                                                                                                nitrogen-fixing
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                                                    DB 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      , Kato T., Juliana T
  246;
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                                                  Length
  Indels
                                                                                                                                                                                                                                                                                                                                                symbiotic bacterium
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                                                       617;
  186;
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QY

313 ETKKNLI---ENASAEHGYFDGRWLDRSVDVILPDNTADVSLIYDTGTQYRFDEVVFFTI 369

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Q92LN9;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update
01-UN-2002 (TrEMBLrel. 21, Last annotation update
Hypothetical protein R02996.
R02996 OR SMC03097.
R02996 OR SMC03097.
R01996 OR SMC03097.
R019976 OR SMC03097.
R01996 OR SMC03097.
R019976 OR SMC03097.
R01996 OR S
STRAIN-1021;
STRAIN-1021;
MEDLINE-21396507; PubMed-11481430;
Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut Boistard P., Becker A., Boutry M., Cadleu E., Dreano S., Gloux Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Penard C., Thebault P., Vandenbol M., Weidner S., Galibert F.; "Analysis of the chromosome sequence of the legume symbiont Sinorhizobium meliloti strain 1021.";

Sinorhizobium scal. U.S.A. 98:9877-9882(2001).
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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Matches 168
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InterPro; IPR001064; Crystallin.
InterPro; IPR001064; Crystallin.
InterPro; IPR001412; trNA-synt_I.
Pfam; PF01103; Bac_surface_Ag; 1.
PROSITE; PS00178; AA_TRNA_LIGASE_I; UNKNOWN_1.
PROSITE; PS001278; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
Hypothetical protein; Complete proteome.
SEQUENCE 618 AA; 65656 MW; E51276BB29B1FB78 CRC64;
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                                                                                                                                                                                                    FVLAGKLGAGVLVGGDELSDIPATRRFFLGGGGSVRGYSYQEISPRDADDELTGGRSYVS
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Pred. No. 0.00011;
8; Mismatches 279
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Q9PIZ8
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RC STRAIN=NCTC 11168;

RX MEDLINE=20150912; pubMcd=10688204;

RA MEDLINE=20150912; pubMcd=10688204;

RA Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,

RA Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,

RA Dagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,

RA Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,

RA Whitehead S., Barrell B.G.;

RA Whitehead S., Barrell B.G.;

RT The genome sequence of the food-borne pathogen Campylobacter jejuni

RT reveals hypervariable sequences.";

RL Nature 403:65-668(2000).

DR EMBL; AL139074; CAB72613.1; -.

DR InterPro; IPR000184; Bac_surfag_D15.

PGM Tomnlete Troteoma
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Best Local S
Matches 172
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01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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                                                  472 GILMDISPIEFSASNLIQDKLNLVAAKARHLYDMPDDRVLAINHDDGVNRSILGRISDAV 531
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hes 172;
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GILLNAS---LSDTNIFGSGI----KSSVSVDKSDD----
                                                                                                                                             TEIVFPEREQIQNDQVSFEQSSSSRTEPAQVDESTLEPVIETVEL------TD 471
                                                                                                                                                                                                                                                                VFFTIDPKTNQLTTDPDKLPVKRELLEQLLTVNMGEAYNLQAVRALSNDLIATRYFNMVN 424
                                                                                                                                                                                                                                                                                                                                                                          DVFHHGKYETKKNLIENASAEHGYFDGRWLDRSVDVILPDNTADVSLIYDTGTQYRFDEV 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                       QVSSPYLKTYTDTYQANLTYFIKE-GKPYKI--KSISIENPLFDDKQNAQTVKDLRSSAG
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                                                                                                                                                                                                                          YIRNVIISGNSRTVD----RVIRRELY-----ITEGNLYNRTDLSESKNALKRTSYFDDVN 395
                                                                                                                                                                                                                                                                                                                                       KTINIEDIRKDVKTIETQSADLGY---AFVEVYPDIQKNDQTQEATVVFKV---IPHDKV 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AKKESYSDIEPAVVNKEKEFMGWMWGRNDGKLKVFELSNDSSRIADEYM----KKGYLDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QKTEPYANIKAALEDITQE------SAMDLNGSIPRLRQTALVAARAVGYYDI 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEGNIKEAIERIKAYYEAKSYFDTIVEYKKKTLENTDGLELEFIVNRGENIIIDNVHLSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KONYFENIAVE---NNNGILEIIVTEKPTIAKVTITGIASNDRKQVESILGIKR--GTLL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LEELFAQESTEMGINPNDYIPEYQGEQPN-SEVVVPPTLEPEKPGL-----IKRLYARLF 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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     TLSGRIS---
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	555 ALANRKTPADVYOSKKVDIVVEVASDKBBDGOTGIGGGGGGGGGGGGG	οv
	MAGELVRLNGVDVVTKGRTNPEWVGRL	Db
	505 MPDDRVLAINHDDGVNRSILGRISDAVSAVARAILPDESENEVIDLPERT 554	Qy
	456 DESTLEPVIETVELTDGILMDISPIEFSASNLIQDKLNLVAAKARHLY 504	Оу
17	Match 4.6%; So Local Similarity 21.8%; Pr Local Similarity 21.8%; Pr les 110; Conservative 87;	
	Hypothetical protein; Complete proteome.  SEQUENCE 628 AA; 68203 MW; 92DAD1722CF82295 CRC64;	SQ
	Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001). EMBL; AE005835; AAK23582.1;	DR RL
	Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva I Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M., "Complete denome sequence of Caulobacter crescatus".	RA RA
	Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Sherty J., Bay	RA RA
	Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddo	RA RA
	SEQUENCE FROM N.A. STRAIN=ATCC 19089 / CB15; MEDLINE=21173698: Dubmed=11250	7 7 X
	NCBI_Ta:	RNOX
	Bacteria; Proteobac Caulobacter.	88
	CC1603. Caulobacter crescentus.	S G G
	01-MAR-2002 (TrEMBLrel. 20, Last annotation upda Hypothetical protein CC1603.	D Di
	01-JUN-2001 (TrEMBLrel. 17, Created) 01-JUN-2001 (TrEMBLrel. 17, Last sequence	DI
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	SU A7	Q R Q 9
	692 DEIKRMSTGIGIEWITPIGPLQLVFAKPLNDKKGDDTNSFEFNLGTRF 739	Дb
	874 TNDTKIGAGVGVRWASPVGQVRVDVATGVK	Qy
	632	фq
	816	Qy
	578 GGDQEFISSSSKFNFYQGLQDYIGYDLIYRYKASFYKVWDEGYLPINQRIYLGG 631	ф
	770 SGVYSEGDNAYGSNRAHQMTGGIQAGYIWSDNENH	Qγ
	523 SDIYHLSPTLLRTGYELGKSIKSS-ITPAITFNDTDDYYLPRSGIIASTSLEYAGL 577	dα
	710 VDFVNGKPSQEALLAGVAVHKTVADNLVNPMRGYRQRYSLEVGSSGLVSDANW	Qγ
	488 YEWDNYSEKNYGFDITIGRQFARYYNVSLTYNLEQ 522	Db
	650 YQQEVFGHSTNGFDLSTRTLEHEISRSIIQNGGWNRTYSLRYRLD	Qγ
	480 GGT 487	Db
	590 GWGSDTGTRLVTKFEHNLINRDGYQAGAELRLSEDKKGVKLYATKPLSHPLNDQLRATLG 649	Qy
	467PRVLDSQYSL 479	Db
	/ 532 SAVARAILPDESENEVIDLPERTALANRKTPADVYQSKKVPLYVFVASDKPRDGQIGL 589	QY

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STRAIN-CS / SEROGROUP B;

MEDLINE-20175755; PubMed-10710307;

MEDLINE-20175755; PubMed-10710307;

Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.

Elsen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,

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Scalld J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L.,

Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;

Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 287:1809-1815(2000).
EMBL; AE002561; AAF42442.1;
TIGR; NMB2134; -
                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein; Complete SEQUENCE 635 AA; 69801 MW;
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Q9JXB7;
               559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical
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                                                                       128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=491;
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                                                                                                                                                                                                                            PVIETVELTDGILMDISPIEFSASNLIQDKLNLVAAKARHLYDMPDDRVLAINHDDGVNR
            RKTPA - -
                                                    MLRSKGYFSSKVSLTEKDGAYTVHITPGPRTKIANVGVAILGDILSDGNLAEYYRNALEN
                                                                                                                                                                       PDTESVKLKPKFPVLIDTODSEIKDMVEEHLPLITOOOEEVLDKEOTGFLAEEAPDNVKT 127
                                                                                                                            SI--LGRISDAVSA----
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
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            DVYQSKK
                                                                                                                                                                                                                                                                                                                            4.5%; Score 215; DB 16; 22.1%; Pred. No. 0.00023;
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- VPLYVFVASDKP
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RA SIMPSON A.U.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Colauto N.B., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa N.R.S.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa N.R.
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Marques M.V., Marcca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Moon D.H., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA de Rosa V.B., Roberto P.G., Rodriques V., de Rosa A.J.M.,
RA de Rosa V.B. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
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01-OCT-2000 (TrEMBLrel. 15,
01-MAR-2002 (TrEMBLrel. 20,
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"The genome sequence of the plant pathogen Xylella Nature 406:151-159(2000).
EMBL; AE003941; AARB3856.1; -.
InterPro; IPRO00184; Bac_surfaq_D15.
Pfam; PF01103; Bac_surface_Ag; 1.
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MEDLIND-21470413; PubMed-11586360;

Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,

Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,

Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,

Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,

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Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;

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Nature 413:523-527(2001)
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Q1-MAR-2002 (TrEMBLrel. 20,
Q1-JUN-2002 (TrEMBLrel. 21,
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InterPro; IPR000184; Bac_surfag_D15.
Pfam; PF01103; Bac_surface_Ag; I.
Hypothetical protein; Complete proteome.
SEQUENCE 795 AA; 87838 MW; 8C4581328D38F821 CRC64;
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VTYKVKERNTGSLNFGIGYGTESG----VSFQVGVQQDNWLGTGNTVGINGTKNDYQTYA
                                  FVASDKPRDG---QIGLGWGSDTGTRLVTKFEHNLINRDGYQAGAELRLSEDKKGVKLYA
                                                                             NR -- LGYF --
                                                                                                                                                                                                                                 GSKYTRMEDDIKKMLGRYGYAYPRVVTQPE----IND---
                                                                                                                                                                                                                                                                          LQAVRALSNDL--IATRYFNMVNTEIVFPEREQIQNDQVSFEQSSSSRTEPAQVDESTLE
                                                                                                                                                                                                                                                                                                              KKGIYVTINITEGPQFKLNSVIV-----SGNLAGHQSEAEKLTKIEPGELFN
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                                                                                                                                                                                                                                                                                                                                                                                                                                ----VADEVPL--LIGDVFHHGKYETKKNLIENASAEHGYFDGRWLDRSVDVILPDNTAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KGLEDFYYSVGKYSASVKAVVTPLPRNRVDLKLVFTEGVSAKIQQINIVGNHSFTTDELI 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NMPVRVGDTVSDDDIGKTIRALFATGNFEDVRVLRDGNTLIVQVK-----ERPTI 94
                                                                                                                 NRSTLGRISDAVSAVARATLPDESENEVIDLPERTALANRKTPADVYQSKKVP----
                                                                                                                                                      ---LHINVDAGNRFYVRHIRFEGNDTSKD--SVLRREMRQMEGAWLGNDQVEA--GKERL
                                                                                                                                                                                           PVIETVELTDGILMDISPIEFSASNLIQDKLNLVAAKARHLYD--MPDDRVLAINHDDGV
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19.1%;
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Last annotation update)
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Pred. No. 0.00055;
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                                                                             ETVDV - - -
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Matches 146
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OI-MAR-2002 (TrEMBLrel. 201-MAR-2002 (TREMBLRel.
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STRAIN-16M / ATCC 23456 / BIOTYPE 1;

MEDLINE-20020109; PubMed-11756688;

DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G. Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Golts Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J. Haselkorn R., Kyrpides N., Overbeek R.;

"The genome sequence of the facultative intracellular pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. EMBL; AE009623; AAL53076.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brucella melitensis.";
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Brucellaceae; Brucella.
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NDQVSFEQSSSSRTEPAQVDEST-LEPVIETVELTDGILMDISPIEFSASNLIQDKLNLV
                                                                                                                                               GREANDIPPDTEIPNNAKVAITVDPGPQFLFSRTAISNIAPPPGNRR----DKVQTPEEAG
                                               FAPGQEAKSGTILKAERLAVEAWRQEGYAKARVTGEDVVADHADNRVSADIALDPGRKAY
                                                                                                                                                                                             -RSVDVILPD----NTADVSLIYDTGTQYRFDEVVFFTIDPKTNQLTTDPDKLPVKRE--
                                                                                                                                                                                                                                               GKEADLKSVIEGASGLVSDADKPASGSAGLLAKARGDYRRILSALYGEGRYGGTISIKVD
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                                                                                                                                                                                                                                                                                                                                                                           Score 209; DB 16;
Pred. No. 0.00051;
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RESULT 31
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 Query Match
Best Local Similarity
                                                                                                                                                                               SEQUENCE ***... STRAIN-2685/ ATCC 700392;

STRAIN-2695/ ATCC 700392;

MEDLINE-97394467; PubMeds-9252185;

Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G., Fleischmann R.D., Ketchum K.A., Klenk H.-F., Gill S., Dougherty B.A., Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S., Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A., Ketchney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K., McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M., Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E., Cotton M.D., Weidman J.M., Kaip P.D., Smith H.O., Fraser C.M.,
                                                                                                      pylori.";
Nature 388:539-547(1997).
EMBL; AE000579; AAD07720.1;
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025369;
01-JAN-1998;
01-JAN-1998;
01-DEC-2001;
                                          InterPro; IPR000184; Bac_surfAg_D15.
Pfam; PF01103; Bac_surface_Ag; 1.
Hypothetical protein; Complete prote
SEQUENCE 916 AA; 102671 MW; 186D
                                                                                                                                                                                                                                                                                                                                                                                                               Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter
                                                                                                                                                                    "The complete genome sequence
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                                                                                                                                                                                                                                                                                                                                                                                                       Helicobacter
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(TTEMBLrel. 05, Last sequence up
(TTEMBLrel. 19, Last annotation
surface antigen D15.
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19.3%;
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Score 206.5;
Pred. No. 0.
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                                          proteome.
186D8E301CD9408A CRC64;
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                 DB
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                                                                                                                                                                    pathogen
              16;
              Length
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Matches

202;

143;

Mismatches

318;

Indels

383;

Gaps

51;

31 24

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WLGGDGIFTASTELSYGVLKAAKMRLAWFFDFGFLTFKTPTRGSFFYNAPVTTANFKDYG 844
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                                                                                                                                                                                                                                                                                                                                        SYDNTDDYYFPRNGVIFS----SYATMSGLPSSGTLNSWNGLGGNVRNTKVYGKFAAYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KPSQEALLAGVAVHKTVA------DNLVNP-----MRGYRQR-----YSLEV
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                                                                                                                                                                                                                                                                                IATGGGRSYPGMFKGAGRMFAGNLSLTNP-----RIF----RIF----DSWYSSTINLY
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Matches 171
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Q9ZE03;
01-MAY-1999 (TrEMBLrel. 10, C
01-MAY-1999 (TrEMBLrel. 10, L
01-DEC-2001 (TrEMBLrel. 19, L
Outer membrane protein OMP1 (
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STRAIN-MADRID E;

MEDLINE-99039499; PubMed=9823893;

Andersson S.G.E., Zomorodipour A., Andersson J.O.,

Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund .

Eriksson A.-S., Winkler H.H., Kurland C.G.;

"The genome sequence of Rickettsia prowazekii and the origin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome. SEQUENCE 768 AA;
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EMBL; AJ235270; CAA14627.1;

InterPro; IPR000184; Bac_surfAg_D15.

Pfam; PF01103; Bac_surface_Ag; 1.
                                      652
                                                                                           446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=782;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65
QEVFGHSTN-----GFDLSTRTLEHE----ISRSIIQNGGWNRTYSLRYRLDKLKTQAPP 702
                                                                             RNLVG-TGKLLNAGVQVSKNSTSYYGCITDPHFLDRDLSLSVNAFRNYTGRGASVLNTTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                     FPEREQIQNDQVSFEQSSSSRTEPAQVDESTLEPVIETVELTDGILMDISPIEFSASNLI
                                                                                                                                                                                                                                         DLPERTALANRKTPA-DVYQSKKVPLYVFVASDKPRDGQIGLGWGSDTGTRLVTKF---E
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                                                                                                                                  HNLINRDGYQAGAELRLSEDKKGVKLYATKP--LSHPLNDQLRATLGY------Q
                                                                                                                                                                                          DYFEKVSISLAQTKAKDKYD------VNVEVDEKSTSSIGFDLGYNTAGGLFGRFSFLE
                                                                                                                                                                                                                                                                                                 INKINII--NNLKTEDHVIRRAFKIEEGDVMNRSYIEK------GERNLRNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KELLREFYQSVGFADFRVI--SASVALNDTKEYFTITYSIEEGEKYRFGNV---TID---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -KVIFDIAEGPKTVIKSIYFSGNEHYSDSELKSIVLTKESRWFRFLESNDTYDPDRVEYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87196 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.3%; Score 205.5; DB 16; 20.1%; Pred. No. 0.0012; tive 111; Mismatches 297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation updat
(OMP1).
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AYDKGFTNDT-KIGAGVGVRWASPVG 892

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                                                                                                                                                                                                                                                            Matches 172;
                                                                                                                                                                                                                                                                           Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q92J67;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 21, Last annotation update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                               "Mechanisms of evolution in Rickettsia Science 299:2093-2098(2001).
EMBL: ABC008587; AAL02740.1;
                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-21442074: PubMed-11557893;
Ogata H., Audic S., Renesto-Audlff
Samson D., Roux V., Cossart P., We
Raoult D.;
               372
                                                                                                                                                                                                                                                                                                                 Complete proteome. SEQUENCE 768 AA;
                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000184; Bac_surfAg_D15.
Pfam; PF01103; Bac_surface_Ag; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-MALISH 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; alpha subdivision; Rickettsiaceae; Rickettsieae; Rickettsia.
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         KTNQLTTDPDKLPVKRELLEQLLTVNMGEAYNLQAVRALSNDLIATRYFN---
                                   DKELLRDFYQSVGFADFRVISASAEL---NNTKEYFTLTYSIEEGEKYSFGNI---TIDN
                                                                                         --KVIFDIAEGPKTGINYIYFSGNENYSDSELKSIVLTKESRWFRFLESNDTYDPDRMEY
                                                                                                                                                                        SHOKTEPYANIKAALEDITQESAMDLNGSIPRLRQTALVAARAVGYYDIDLSIIRNSIGE
                                                                                                                                                                                                  VIKRLYATSLFRNINMHITNDGNLIVNVTETPFISSVVFSGNSKIKTNMLAKEIYTMSGE
                                                            KKNLIENASAEHGYFDGRWLDRSVDVILPDNTAD-VSLIY--DTGTQYRFDEVVFFTIDP
                                                                                                                                                 SLSQAKIELDVKKILE-IYKRSGRFATTVTPKIE-----
                                                                                                                     VDVIIHDL--GEPVYIDYRAVEVRGEGADDKAFTTVADEVP-----LLIGDVFHHGKYET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VPEEF--NFTGAVFIDLGSVWGVGLNKKQYKTPNGFYNDQSLRASVGFGFIWVTRFAPIR
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                                                                                                                                                                                                                                                            Conservative 122;
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                                                                                                                                                                                                                                                                        4.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                     Renesto-Audiffren P., Fournier P.-E., Barbe V., Cossart P., Weissenbach J., Claverie J.-M.,
                                                                                                                                                                                                                                                                                                                 86881 MW;
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                                                                                                                                                                                                                                                                     Score 202.5; DB 16; Length 768; Pred. No. 0.0017;
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           ---MVNTE
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                                          Query Match
Best Local S
Matches 176
                                                                                                                                                                                                                                                                   Q9X3V8 PRELIMINARY; PRI; (2007)
Q9X3VB;
Q9X3VB;
Q1-NOV-1999 (TrEMBLrel. 12, Created)
Q1-NOV-1999 (TrEMBLrel. 12, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 81.1 kDa protein.
Zymomonas mobilis.
Zymomonas mobilis.
                                                                                             Hypothetical protein. SEQUENCE 738 AA; &
                                                                                                                       InterPro; IPR000184; Bac_surfAg_D15
Pfam; PF01103; Bac_surface_Ag; 1.
                                                                                                                                               "Sequence analysis of 42C11 fosmid clone of Zymomonas mobilis Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases. EMBL; AF088896; AAD21534.1;
                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN=ZM4;
                                                                                                                                                                                                                                               NCBI_TaxID=542;
                                                                                                                                                                                                                                                                Zymomonas
                                                                                                                                                                                           Lee H.J., Kang H.S.;
                 127
                                                                                                                                                                                                                                                                                                                                                                                                                                            747
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FPIKKKKYDDTQHFHL 762
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ilarity 20.6%;
Conservative 12:
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                                                                                             81140 MW;
                                Score 198; DB 2;
Pred. No. 0.003;
Pred. No. 344;
                                                                                             F169545D09168114
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SEQUENCE
                                      Anabaena sp. (strain PCC Bacteria; Cyanobacteria;
                                                                   Hypothetical ALR2269.
                          NCBI_TaxID=103690;
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al protein Alr2269.
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                                    7120).
Nostocales;
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                                 Nostocaceae; Nostoc
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"Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";
DNA Res. 8:205-213(2001).
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Pfam; PF01103; Bac_surface_Ag; Z.
Hypothetical protein; Complete proteome.
B33 AA; 89633 MW; 7F52B1E52FEA1BE9 CRC64;
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                                                                                                                 -GINDDGDS-RINFGIGERF
                                                                                                                                                                                                                                                  AFNIQGGTVLGD----LPPYEAFTLGGSNSVRGY-----EEGALGSGRSFVQASVE
                                                                                                                                                                                                               YNYEFMKDLRLAVFGDIGNAYDKGFTNDTK-----IGAGVGVRWASPVGQVRVDVA
                                                                                                                                                                                                                                                                                                                   QPTSGSFLRFG--VDQSVPVGSGNIFLTR--FRGSYSQYLPVKFTGF-----SKGPETI
                                                                                                                                                                                                                                                                                                                                                                                     --RVSTRDADGNLRKDGAVFDDNGNRTSEIVPLSF-SGTGEDDLLLVQLGAQRDLRNNPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --PGRTTTRSQLQEDINAIFGTGFFSNVQASPEDTPLGVRVSFIVQPNPVL---SKVEIQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PNATPETTEP-----RVLVSEVL------VRPQSGQLTPELETQVYNVIRTQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ESENEVIDLP-----ERTALANRKTPADVYQSKKVPL-----YVFVASDKPRDGQI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASNLIQDKLNLVAAKARHLYDMPDDRVLAINH-DDGVNRSILGRISDAVSAVARAI-LPD 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative 104; Mismatches 255; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.2%; Score 197.5; DB 19.7%; Pred. No. 0.004;
                                                                                                                                                                                                                                                                                                                                                                                                                       -----ETWQDLPVDFVNGKPSQEALLAGVAVHKTVADNLV
                                                                                                                 833
                                                                                                                                                 919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
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Q92Q48 Q92Q48; Q1-DEC-2001

(TrEMBLrel.

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PRELIMINARY;

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J., Boltard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S., Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F., Analysis of the chromosome sequence of the legume symbiont Sinchizoblum meliloti strain 1021.*;

Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OMP OR R01502 OR SMC02094.

Rhizobium meliloti (Sinorhizobium meliloti).

Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
           601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21396507; PubMed=11481430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rhizobiaceae; Sinorhizobium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Putative outer membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 01-MAR-2002 (TrEMBLrel.
                                                                                                                                                    494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              223 SAMDLNGSIPRLRQTALVAARAVGYY-DIDLSIIRNSIGEVDVIIHD----LGEPVYIDYR 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70
GLGGTSDFYKLTGKA--KWYYTLHDEA-----DIIGSLSGSAGHLFETSGSLEVFDQ-
                                                                                                        DKLKTQAPPETWQDLPVD-FVNGKPSQEALLAGVAVHKTVADNLVNPMRGYRQRYSLEVG
                                                                                                                                             GYRLAAGFDLFKNENDFDDDNYSYNDQGFSL----RVTAPITE----NLSTTLRYNY
                                                                                                                                                                             SHPLN---DOLRATLGYQQEVFGHSTNGFDLSTRTLEHEISRSIIQNGGWNRTYSLRYRL
                                                                                                                                                                                                                  GIGAGYSAGDGGGFLVEASIEEKNFLGRGQY-----IRLAAGKGEDSQTYNVSFTEPYFL
                                                                                                                                                                                                                                                   QIGLGWGSDTGTRLVTKF---EHNLINRDGYQAGAELRLS----EDKKGVKLYATKP--L
                                     SSGLVSDANMAIARAGISGVYSFGDNAYGSNRAHQMTGGI--QAGYIWSDN----
                                                                      TELEYFGDRDELSS-PYDRVIDGSPWTRSSISQSITYNTL-DDAQLPHEGILASVTQEFA
                                                                                                                                                                                                                                                                                                                          ---DESENEVIOLPERTALANRKTPADVYQSK------KVPLYVFVASDKPRDG
                                                                                                                                                                                                                                                                                                                                                              RVASEGY -- PFARVTPRGNRDLANHTI--AVDYLVDQGERAYVERIEIRGNTRTRDYVIR
                                                                                                                                                                                                                                                                                                                                                                                                                                  VTITIEEGPRYDFGPVNI-ESTVEG-IDAEELR-GLVQSREGTVYKAKD-IQSTMSEISK 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DQVSFEQSSSSRTEPAQVDESTLEPVIETVELTDGILMDISPIEFSASNLIQDKLNLVAA 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YNPDKLRADEELLRQFY-YNRGYA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QVVPIAEGRVNLAFVINEGERTKITQINFVGNEVYSDGRLQSVIATKESGIFSFLTRKDV
                                                                                                                                                                                                                                                                                         REFDVGEGDAFN-QEMVARAKRRLEALGYFSSVNISTQPGSAADRVVIVVDVQDQSTGSF
                                                                                                                                                                                                                                                                                                                                                                                                 K-ARHLYDMPDDRVLAINHDDGVNRSILGRISDAVSAVARAILP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TDPDKLPVKRELLEQLLTVNMGEAYNLQAVRALSNDLIATRYFNMVNTEIVFPEREQIQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DVI-LPDNTADVSLIYDTGTQYRFDEVVFF-----TIDPK------TNQLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KIK-----DDKLQGVVRTQ-PL---GPYSEATVETDIQAIRDAYAAIGRSD----VTVTT 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AVEVRGEGADDKAFTTVADEVPLLIGDVFHHGKYETKKNLIENASAEHGYFDGRWLDRSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNADIDASYKRL-----YATGYFSDYSITV---SGGSLVVSVSENQLVNQVVFNGNR 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pro; IPR000184; Bac_surfAg_D15
PF01103; Bac_surface_Ag; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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776 AA;
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21.2%;
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20, Last annotation updat
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Pred. No. 0
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                                   -FNHV
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01-MAY-1999
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
EMBL; AE001492; AAD06181.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-99120557; PubMed-9923682;
Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G., Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000184; Bac_surfAg_D15.
Pfam; PF01103; Bac_surface_Ag; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9ZLH9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Helicobacter pylori J99 (Campylobacter pylori J99)
Bacteria; Proteobacteria; epsilon subdivision; Hel
    469
                               344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-85963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Helicobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genomic sequence comparison of two unrelated
                                                                                                                                                                                                                                                                                                                                                  154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 705
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                                                                                                                                                                                                                                                                                                                                                                                37
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37
LTDGILMDISPIEFSASNLIQDKLNLVAAKARHLYDMPDDR----VLAINHDDGVNRSILG
                               ILKTEIADKGYAFA---VVKPDLDK
                                                                                     VKEGIQYRISDIL-----IEIDNPVVPLK--TLEKALKVKRKDVFNIEHLRADAQ
                                                                                                   T--GTQYRFDEVVFFTIDPKTNQLTTDPDKLPVKRELLEQLLTVNMGEAYNLQAVRALSN 412
                                                                                                                                                                                                                                                                                                                                                                                                      TPLSLEELFAQEST------EMGINPNDYIP-EYQ-------GEQPNSEVVV 153
                                                     DL---IATRYFNMVNTEIVFPEREQIQNDQVSFEQSSSSRTEPAQVDEST-LEPVIETVE
                                                                                                                                            RDFMGWMWGLNDGKLRLDQLEYDSLRIQDVYMRRGYLDAHISSPFLKTDFSTHDAKLHYK
                                                                                                                                                                                                                              EPVYIDYRAVEVRGEGADDKAFTTVAD---EVPLLIGDVFHHGKYETKKNLIENASAEH-
                                                                                                                                                                                                                                                            MGIKKGDTFDEQKLE-----HAKTALKTALEGQGYY---
                                                                                                                                                                                                                                                                                                                   TAVLALFNQGYFKDVYA-TFENGI-----LEFHFDEKARIAGVEIKGYGTEKEKDGLKSQ
                                                                                                                                                                                                                                                                                                                                              PPTLEPEKPGLIKRLYARLENDGVNKVPRLKAKFYQSSQSG--ETSAIGSSHQKTEPYAN 211
                                                                                                                                                                                                                                                                                 TPKEAQKNEAQNETSQSNQTPKEMKVKSISYVGLSYMSDMLANEIAKIRVGDMVDSKKID 96
                                                                                                                                                                                                                                                                                                                                                                                                                                       192;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VFGDIGNAYDKGFTNDTKIGAGVGVR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PYRLREFAGGDQSIRGYAHDSLSPISDKGYLTGGQVLAVGTAEYNYEFM-----KDLRLA 860
                                                                                                                                                                                                    ----VEVRTEKVSEGALLIVFDVNRGDSIYIKQSIYEGSDKLKRRVIESLSANKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -FQLNSNDIRGFERNGLGPRMNNGDALGGTTYFTASAEATFPLPGLPRDSGFRGA 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               906 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative 131;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.1%;
19.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101438 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 194.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  .5; DB 16;
                                                                                                                                                                        -WLDRSVD--VILPD-NTADVSLIYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q., Taylor D.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ₽
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                                                                                                                                                                                                                                                                                                                                                                                                                                    311; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              isolates of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WASPVGQVRVDVATGVKEE 905
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                            DEKNGLVKVIYRIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                    333;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                        468
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SS

SEQUENCE

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AA,

87437 MW;

DC1D004AAFB2CD9E CRC64;

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ID Q51930
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               "Characterization of the Pasteurella multocida Gene 161:39-43(1995).

EMBL: U60439: AAC44600.1; -.

EMBL: X74357; CAA52399.1; -.

InterPro; IPR0010184; Bac_surfAg_D15.

InterPro; IPR0010184; Caystallin.

Pfam; PF01103; Bac_surface_Ag; 1.

PROSITE: P$00225; CRYSTALLIN_BETAGAMMA; UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q51930 PRELIMINARY; PRT; 789 AA. Q51930; Q51921; Q51930; Q51921; Q51930; Q5196 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
                                                                                                                                                                                                                            MEDLINE-95369730; PubMed=7642134; Delamarche C., Manoha F., Behar G., Wroblewski H.;
                                                                                                                                                                                                                                                                                                     STRAIN-9222
                                                                                                                                                                                                                                                                                                                                                                              Ruffolo G.C., Adler B.;
Infect. Immun. 64:0-0(0).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Pasteurella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pasteurella multocida
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RESULT 39
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AC Q8YMP
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DT 01-JU
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Best Local :
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Q8YMP0;
01-MAR-2002
01-MAR-2002
01-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69
                                                                                                                                                                                   VGQVRVDVATGVKE-EGNPI-KLHFFIGTPF
                                                                                                                                                                    IGPLVFSYAKPLKKYQGDEIEQFQFSIGGTF
                                                                                                                                                                                                                                                                                    QYYSAGGIGSLRGFAYGAIGPNAIYRTRQCPDSYCLVSSDVIGGNAMVTASTELIVPTPF
                                                                                                                                                                                                                                                                                                              LRFFAGGDQSIRGYAHDSLSP-------ISDKGYLTGGQVLAVGTAE
                                                                                                                                                                                                                                                                                                                                                                       GLV----SDANMAIARAGISGVYSFGDNAYGSNRAHQMTGGIQAGYIWSDNFN--HVPYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GRTSYGGNLTLGFPVNE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QQEVF-GHSTNGFDLSTRTLEHEISRSIIQNGGWNRTYSL--RYRLDKLKTQAPP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QDNFLGMGSSISLGGTRNDYGTTVNLGYNEPYFTKDGVSLGGNVSFEEYDSSKSNTSAGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KLRLDRTGYFESVETKTEA-IPGSDQVDVIYKVKERNTGSINFGIGYGTESGLSYQASIK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LYDMPDDRVLAINHDDGVNRSIL-----GRISDAVSAVARAILPDES---ENEVIDLP 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RVSGGMWGGMSAELAPILETIQL-NGLFRRTSVLEVEQRN--KSKLGERGYATAQVNVHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LNRAKLEEFRKGIVEHYNSV-----GRY-NAKVDAIVNTLPNNSAEIKIQINEDDVALFK 175
                                                                                                                                                                                                                              VADKNQNSVRTSLFVDAASVWNTRWKAEDKAKFAKLNVPDYSDPSRVRASAGVALQWQSP
                                                                                                                                                                                                                                                          YNYEFMKDLRLAVFGDIGNAYDKGFTNDTK-----
                                                                                                                                                                                                                                                                                                                                              GRVTIPGSDNKYYKLNAEAQGFYPL-----DREHGWVLSSRISASFADGFSGKRLPFY
                                                                                                                                                                                                                                                                                                                                                                                                      YRQSMKYNDSWTFKSHDF----
                                                                                                                                                                                                                                                                                                                                                                                                                                -----ETWODLPVDFVNGKPSQEALLAGVAVHKTVADNLVNPMRGYRQRYSLEVGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EHNLI------NRDGYQAGAELRLSE---DKKGVKLYATKPLSHPLNDQLRATLGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VRALSNDLIATRYFNMVNTEIVFPEREQIQNDQVSFEQSSSSRTEPAQVDE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EVVF-----FTIDPKTNQ--LTTDP------DKLPVKRELLEQLLTVNMGEAYNLQA 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FHHGKYET-KKNLIENASAEHGYFDGRWLDRSVDVI---LPDNTADVSLIYDTGTQYRFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YDDVKASREGNTL-----VVTVMPKPVISN--VVIVGNKSIPDEAIKONLDANGFKVGDV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----ERTAL---ANRKTPADVYQSKKVPLYVFVASDKPRDGQIGLGWGSDTGTRLVTKF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ETTFEGNEAFSSGKLADQMELQTDSWWKLFGNKFDQTQFNKD-LETLRSYYLDRGY----
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                                        2 (TrEMBLrel. 20,
2 (TrEMBLrel. 20,
2 (TrEMBLrel. 21,
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                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -STLEPVIETVELTDGILMDISPIEFSASNLIQDKLN-----LVAAKARH
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Last annotation updat
                                                                      Created)
                                                                                                PRT;
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                                        update)
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                                                                                                                                                                                                                                                         --IGAGVGVRWASP
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Hypothetical ALR4893.

protein Alr4893. (strain PCC 7120).

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MEDLINE-21595285; PubMed-11759840;

Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,

Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,

Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,

Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,

Yasuda M., Tabata S.;

Yasuda M., Tabata S.;

Complete genomic sequence of the filamentous nitrogen-fixing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cyanobacterium Anabaena sp. strain PCC 7120.";
DNA Res. 8:205-213(2001).
EMBL; AP003597; BABF76592.1; -.
InterPro: IPR000977; DNA_LIGASE_A1; UNKNOWN_1.
Hypothetical protein: Complete proteome.
SEQUENCE 676 AA; 72411 MW; C5779633037D1223 CRC64;
                          701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Cyanobacteria;
NCBI_TaxID::103690;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 MPVALAAYLPLMTSQALAQQNNPANIINHVPAHDTAINQAKAGNPPVLLTPEQIQARLNA 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73
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PPETWQDLPVDFVNGKPSQEALLAGVAVHKTVADNLVNPMRGYRQRYSLEVGSSGLVSDA
                                                                                                                         GL---
                                                                                                                                             GLGWGSDTGTRLVTKF--EHNLINRD--GYQAGAELRLSEDKKGVKLYATKPLSHPLNDQ
                                                                                                                                                                                N-----YQDQNIGGKNDTLLAN-----
                                                IKLANGDKVRE-GKVGTGISLQ-RPID------GWNASLGFNYSRTSIRDRQGNI
                                                                              LRATLGYQQEVFGHSTNGFDLSTRTLEHEISRSIIQNGGWNRTYSLRYRLDKLKTQ---A
                                                                                                                                                                                                            SDAVSAVARAILPDESENEVIDLPERTALANRKTPADVYQSKKVPLYVFVASDKPRDGQI 587
                                                                                                                                                                                                                                                                        TDGILMDISPIEFSASNLIQDKLNLVAAKARHLYDMPDDRVLAINHDDGVNRSI--LGRI 527
                                                                                                                                                                                                                                                                                                                                       LSNDLIATRYFNMVNTEIVFPEREQIQNDQVSFEQSSSSRTEPAQVDESTLEPVIETVEL 469
                                                                                                                                                                                                                                                                                                                DVQQLYRTGLFQSVN-----
                                                                                                                                                                                                                                                                                                                                                                                                     IYDTGTQYRFDEVVFFTIDPKTNQL--TTDPDKLPVKRELLEQLLTVNMGEAYNLQAVRA 409
                                                                                                                                                                                                                                                                                                                                                                       VSD--IKFRFVNDDGKTIDSNGNPVGGRTKPD-----FLRQQLKLQPGQVFQENIVKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRFQSQI---GKPISPEGLKQAVAQVNQWYADNGYNLARVLSIEPNRQGILNINVAE-GL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AARAVGYYDIDLSIIRNSIGEVDVIIHDLGEPVYIDYRAVEVRGEGADDKAFT-TVADEV 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VIAQ-----NSPVVLPSTPRPVVPPAPKP--ATTVNELVVTATDVQIVGATPEL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INPNDYIPEYQGEQPNSEVVVPPTLEPEKPGLIKRLYARLFND------GVNKVPRL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGLNAKPQSQALDVVNFDDQSPISRIGEQSPPLGLDMSVIEETTPLSLEELFAQESTEMG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLLIGDVFHHGKYETKKNL-----IENASAEHGYFDGRWL--DRSVDVILPDNTADVSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASANVN------SRTTPSGLNVVYQ--VQPVIV--RSLQLTGA----KALTYSVAQ--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 K---AKFYQSSQSGETSAIGSSHQKTEPYANIKAALEDITQESAMDLNGSIPRLRQTALV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----QNENL-VIPVVEETPV-QLGNVTPP-----ET-----EVTPQFSTKSR
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                                                                                                                    -SRTDLQFDTKFISPYRDTNSDRLGYTVNA--
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                                                                                                                                                                                                                                            -VAFAGD-----ATKLDMIYELKENGARAINLGGSYNGDVGLMGTL
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20.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 193.5; DB 16;
Pred. No. 0.0048;
9; Mismatches 323;
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                                                                                                                 -----FRREISETFDDE
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Best Local (
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Q9A711;
01-JUN-2001 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
01-MAR-2002 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                           Complete
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                               Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E., Elsen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B. DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K., Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White C salzberg S.L., Venter J.C., Shapiro L., Fraser C.M., "Complete genome sequence of Caulobacter crescentus."; Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000184; Bac_surfAg_D15.
Pfam; PF01103; Bac_surface_Ag; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=ATCC 19089 / CB15;
      542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-21173698;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Caulobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caulobacter crescentus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Outer membrane protein
                                                                                                                                                                                    366
                                                                                                                                                                                                                 211
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                                                                                                                                                                                                                                                                                   250 IDLSIIRNSIGEVDVI-IHDLGEPVYI--DYRAVEVRGEGADDKAFTTVADEVPLLIGDV 306
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      ESEN---
                                                        FSASNLIQDKLNLVAAKARHLYDMPDDRVLAINHDDGVNRSILGRISDAVSAVARAILPD
                                                                                                                 EIVFPEREQIONDOVSFEOSSSS----RTEPAOVDESTLEPVIETVELTDGILMDISPIE 481
                                                                                                                                                                         FFTIDPKTNQLTTDPDKLPVKRELLEQLLTVNMGEAYNLQAVRALSNDLIATRYFNMVNT 425
                              ---PRVYVDRIDIV-GNTRTL-DYVLRRELEVAEGDAYNR---
                                                                                                                                                 --TVETELKKLDGN------LLAQILPVRTGQLYE----
                                                                                                                                                                                                        YDPDRIEYDREQLRKHYRNRGYFDFRVIS-SVAELAPDKNGFAVTYTLEEGPKYKFGKI-
                                                                                                                                                                                                                                  FHHGKYETKKNLIENASAEHGYFDGRWLDRSVDVILPD-NTADVSLIYDTGTQYRFDEVV 365
                                                                                        ----DERIEQATDALTFAAGAAGFAFVDVRPRYVPNRETKTVDVVFQVREG
                                                                                                                                                                                                                                                                VDLVFEINEGAKSGVLGINFLGNAEYSDNDLRDVIVTKESRWYKILTS-----NDN
                                                                                                                                                                                                                                                                                                                                 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GYAHDSLSPISDKGYLTGGQVLAVGTAEYNYEFMKDLRLAVFGDIGNAYDKGFT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GVRGKPGSGFGYGAGIRVDSPLGLIRADY--GINDQGES-RVHLGIGQRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----NDTKIGAGVGVRWASPVGQVRVDVATGVKEEGNPIKLHFFIGTPF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TPTDAQGNPLS-VSGTGVDDLTTVSFSATKDQRDNPINPTQGSVVRVSTE--QSVPIGQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NISMNRLKADYSQYVPVNIFNSQTPQVFALNVQAGTVLG---NLPPYE-TFNLGGSNSVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NMAIARAGISGVYSFGDNAYGSNRAHQMTGGIQAGYIWSDNFNHVPYRLRFFAGGDQSIR 820
                                                                                                                                                                                                                                                                                                                                             Similarity
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769 AA;
                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=11259647;
-EVID-----LPERTALANRKTPADVYQSKKVPLYVFVASDKPRDGQ
                                                                                                                                                                                                                                                                                                                                                                                      85938 MW;
                                                                                                                                                                                                                                                                                                                                          4.0%;
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17,
20,
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Last annotation update)
                                                                                                                                                                                                                                                                                                                             Pred. No. 0.00
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                    Score 190.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                    7B12A1FEB6226F2B CRC64;
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                             ---VLVD
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                             381
                                                          541
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Searc	рь	Qy	DЬ	Qy	Db	Qy	В	ν	Ъ	Qy	В	Qy	DЪ	Qy	Db
Search completed: April 28, 2003, 16:23:06	719 KDNLGLRASAGISIDWKSPMGPIRFDISRILSKE 752	878KIGAGVGVRWASPVGQVRVDVATGVKEE 905	662 NSMGAKLYAISTFELTVPTFLPEQYGIKAALFSDVGTAGLLDDVDRQRSPGVFDPNI 718	835 YLTGGQVLAVGTAEYNY-EFMKDLRLAVFGDIGNAYDKGFTNDT	605 YWGFTKDLVFSATGSFGYIEGWGGDNVRINDRFYRGG-TSFRGFEIAGIGPRDISSSF 661	786HQMTGGIQAGYIWSDNFNHVPYRLRFFAGGDQSIRGYAHDSLSPISDKG 834	565 IDKRNDPINPTRGWFADLNQDLAGVGGDVKYLKTEADAGW 604	737 VNPMRGYRQRYSLEVGSSGLVSDANMAIARAGISGVYSFGDNAYGSNRA 785	505 GGDVRFGFPLTNDSSMSLRYTVRQDEVSVADSLCASGSVSQILCLQRGAYITSLIGYGLR 564	705 WQDLPVDFVNGKPSQEALLAGVAVHK-TVADNL 736	458 SVGSLRQQIDFGFSEPRF	647 TLGYQQEVFGHSTNGFDLSTRTLEHEISRSIIQNGGWNRTYSLRYRLDKLKTQAPPET 704	423 LSFSAGYSSIDKLVLDVGITERNFRGRGQNLRARA 457	587 IGLGWGSDTGTRLVTKFEHNLINRDGYQAGAELRLSEDKKGVKLYATKPLSHPLNDQLRA 646	:

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